

Table 42: Comparative Sequences relating to SAG 0764

SEQ ID NO. 4201: 2603 V/R STRAIN

ATGGTAAATAGTATTCGCACGCCACGGTGAATCTGAGTGAATAAAGCTAACCTTTTC
 ACTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGG
 AAATTAATTAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTTAAACGT
 GCCATCAAAACAACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA
 AAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATAAGCAGAA
 GCAGCTGAACAATTTGGTGATGAGCAAGTTTATTTGGCGTCGTTTATATGATGATTG
 CTTCCAGATATGGCTAAAGATGATGAACATTTCAGCACATACTGATCGTCGCTATGCTTCA
 CTAGATGATTCTGTTATTCAGATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTT
 CCTTTCTGGGAAGATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGT
 GCACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAGATGATGAA
 ATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTTCGAATTGATGAAAAATTA
 AACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4202: 090 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTG
 GAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 ATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAAC
 AACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAA
 AATCATGGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAAT
 AAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCG
 TCGTTTATATGATGATTGCTTCCAGATATGGCTAAAGATGATGAACATT
 CAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCA
 GATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 AGATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG
 CACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 CGAATTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4203: A909 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
 ATCATGGGCGCTTAAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCGT
 CGTTTATATGATGATTGCTTCCAGATATGGCTAAAGATGATGAACATT
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
 ATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 GATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4204: H36B STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAG
 TGGAATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAA
 AAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAG
 GTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAA
 ACAAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAA
 AAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAA
 AATAAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGG
 CGTCTTATATGATGATTGCTTCCAGATATGGCTAAAGATGATGAACA
 TTCAGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATT
 CAGATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGG
 GAAGATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGG
 TGACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 TTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAA
 A

SEQ ID NO. 4205: 18RS21 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT
 TTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCAGTTGAAAA
 ATCATGGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAAATA
 AAGCAGAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCAATTTGGCGT
 CGTTTATATGATGATTGCTTCCAGATATGGCTAAAGATGATGAACATT
 AGCACATACTGATCGTCGCTATGCTTCACTAGATGATTCTGTTATTCCAG
 ATGCAGAAAAACCTTAAAGTTACTTTAGAGCGTGCTCTTCTTTCTGGGA
 GATAAAATTTGCTCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTG
 ACACGGTAACTCAATCCGTGCTCTTGTAAAAACATATCAACAATTTGTCAG
 ATGATGAAATCATGGACGTTGAAATTCCTAACTTCCCACCACTTGTTTT
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4206: M732 STRAIN

GTAAAAATTAGTATTCGCACGCCACGGTGAATCTGAGTGG
 AATAAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTCAGAAAA
 AAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAGCAGGT

Table 42: Comparative Sequences relating to SAG 0764

TTGAGTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATCAAAACA
 ACTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACAGTTGAAAA
 ATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAAAAATA
 AAGCAGAGCAGCTGAACCAATTGGTGATGAGCAAGTTTCATATTTGGCGT
 CGTTTCATATGATGATTGCTCCAGATATGGCTAAAGATGATGAACATTC
 AGCACAATCTGATCGTTCGCTATGCTTCACTAGATGATTCGTTATTCCAG
 ATGCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCTTCCITTCGGGAA
 GATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGTTGGTGC
 ACACGGTAACTCAATCCGTGCTCTTGTAAACATATCAACCAATTGTGAG
 ATGATGAAATCATGGACGTTGAATTCCTAACCTCCACCACTTGTTTC
 GAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4207: COH1 STRAIN

GTAAATTTAGTATTTCGACGCCACGG
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTGCTGATGAGCAAGT
 TCATATTTGGCGTCGTTTCATATGATGTTATGCTCCAGATATGGCTAAAG
 ATGATGAACATTTCAGCACAATGATCGTCGCTATGCTTCACTAGATGAT
 TCTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT
 TCCITTCGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTGTTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAACATATC
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCC
 ACCACTTGTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4208: CJB110 STRAIN

GTAAATTTAGTATTTCGACGCCACGG
 TGAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAG
 ATCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 CAAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 TGCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGG
 TACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTG
 ACAGGAAAAAATAAGCAGAGCAGCTGAACAATTGCTGATGAGCAAGT
 TCATATTTGGCGTCGTTTCATATGATGTTATGCTCCAGATATGGCTAAAG
 ATGATGAACATTTCAGCACAATGATCGTCGCTATGCTTCACTAGATGAT
 TCTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT
 TCCITTCGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
 TGTGTTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAACATATC
 AAACAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCC
 ACCACTTGTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 ACTTAGGTAAA

SEQ ID NO. 4209: 1169NT STRAIN

AGTATTTCGACGCCACGGTGAATCTGAGTGGAAATAAGCTAACCTTTTCA
 CTGGATGGGCTGACGTAGATCTTTTCAGAAAAAGGTACACAACAAGCTATT
 GATGCTGGGAAATTAATTCAAGCAGCAGGTATTGAGTTTCGACCTTGCTTT
 TACATCAGTTCTTAAACGTCGCATCAAAACAATAACCTTGCCCTTGAAG
 CAGCTGATCAACTTTGGGTACAGTTGAAAAATCATGGCGCTTGAACGAA
 CGTCAATTCGGTGGATTGACAGGAAAAATAAGCAGAGCAGCTGAACA
 ATTTGGTGATGAGCAAGTTTCATATTTGGCGTCGTTTCATATGATGATTGC
 CTCAGATATGGCTAAAGATGATGAACATTTCAGCACAATGATCGTCGCT
 TATGCTTCACTAGATGATCTGTTATTCCAGATGTCAGAAAACTTAAAGT
 TACTTTAGAGCGTGCTCTTCCITTCGGGAAGATAAAATTGCTCCTGCTC
 TTAAAGATGGTAAAAATGTGTTGTTGGTGACACGGTAACTCAATCCGT
 GCTCTTGTAAACATATCAACAATTGTCAGATGATGAAATCATGGACGTT
 TGAATTCCTAACCTCCACCACTTGTTTTCGAATTTGATGAAAAATTA
 ACCTTGTTTCAGAAATATTACTTAGGTAAA

SEQ ID NO. 4210: M781 STRAIN

GTAAATTTAGTATTTCGACGCCACGGT
 GAATCTGAGTGGAAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGA
 TCTTTTCAGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATT
 AAGCAGCAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACG
 GCCATCAAAACAATAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGT
 ACCAGTTGAAAAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGA
 CAGGAAAAAATAAGCAGAGCAGCTGAACAATTGCTGATGAGCAAGTT
 CATATTTGGCGTCGTTTCATATGATGATTGCTCCAGATATGGCTAAAGA
 TGATGAACATTTCAGCACAATGATCGTCGCTATGCTTCACTAGATGATT
 GTGTTATTCCAGATGTCAGAAAACTTAAAGTTACTTTAGAGCGTGCTCT
 CCTTTTCGGGAAGATAAAATTGCTCCTGCTCTTAAAGATGGTAAAAATG
 GTTGTGTTGGTGACACGGTAACTCAATCCGTGCTCTTGTAAACATATCA
 AACAAATTGTCAGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCA
 CCACCTTGTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATT
 CTTAGGTAAA

SEQ ID NO. 4211: JM930013 STRAIN

GTAAATTTAGTATTTCGACGCCACGGTGAATCT
 GAGTGAATAAGCTAACCTTTTCACTGGATGGGCTGACGTAGATCTTTTC
 AGAAAAAGGTACACAACAAGCTATTGATGCTGGGAAATTAATTCAAGCAG

Table 42: Comparative Sequences relating to SAG 0764

CAGGTATTGAGTTTCGACCTTGCTTTTACATCAGTTCTTAAACGTGCCATC
 AAAACAACCTAACCTTGCCCTTGAAGCAGCTGATCAACTTTGGGTACCACT
 TGAATAATCATGGCGCTTGAACGAACGTCATTACGGTGGATTGACAGGAA
 AAAATAAAGCAGAAGCAGCTGAACAATTTGGTGATGAGCAAGTTTCATATT
 TGGCGTGGTTTCATATGATGATTTGCTCCAGATATGGCTAAAGATGATGA
 ACATTGAGCAGCATACTGATCGTGGCTATGCTTCACTAGATGATTCTGTTA
 TTCCAGATGAGAAAACCTAAAGATTACTTTAGAGCGTGCTCTTCCITTC
 TGGGAAGATAAAATTTGCTCCTGCTCTTAAAGATGGTAAAAATGTGTTGT
 TGGTGACACCGGTAACCTCAATCCGTGCTCTTGTAAACATATCAACAAT
 TGTGATGATGAAATCATGGACGTTGAAATTCCTAACCTCCCAACCTT
 GTTTTCGAATTTGATGAAAAATTAACCTTGTTTCAGAAATATTACTTAGG
 TAAA

PRETTY of: /biotmp/msa63264.2{*} March 10, 2003 09:30 ..

msa63264.2{110_090}	1	---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	50
msa63264.2{110_1169NT}		-----	-AGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC		
msa63264.2{110_18RS21}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_2603}		atg	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_CJB110}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_COH1}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_H36B}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_JM9130013}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_M732}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_M781}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
msa63264.2{110_A909}		---	gtaaaat	tAGTATTGCG	ACGCCACGGT	GAATCTGAGT	GGAATAAAGC	
Consensus		*****	-----	*****	*****	*****	*****	
msa63264.2{110_090}	51	TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC	100	
msa63264.2{110_1169NT}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_18RS21}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_2603}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_CJB110}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_COH1}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_H36B}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_JM9130013}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_M732}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_M781}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
msa63264.2{110_A909}		TAACCTTTTC	ACTGGATGGG	CTGACGTAGA	TCITTCAGAA	AAAGGTACAC		
Consensus		*****	*****	*****	*****	*****		
msa63264.2{110_090}	101	AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC	150	
msa63264.2{110_1169NT}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_18RS21}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_2603}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_CJB110}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_COH1}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_H36B}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_JM9130013}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_M732}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_M781}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
msa63264.2{110_A909}		AACAAGCTAT	TGATGCTGGG	AAATTAATTC	AAGCAGCAGG	TATTGAGTTC		
Consensus		*****	*****	*****	*****	*****		
msa63264.2{110_090}	151	GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT	200	
msa63264.2{110_1169NT}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_18RS21}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_2603}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_CJB110}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_COH1}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_H36B}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_JM9130013}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_M732}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_M781}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
msa63264.2{110_A909}		GACCTTGCTT	TTACATCAGT	TCTTAAACGT	GCCATCAAAA	CAACTAACCT		
Consensus		*****	*****	*****	*****	*****		
msa63264.2{110_090}	201	TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC	250	
msa63264.2{110_1169NT}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_18RS21}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_2603}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_CJB110}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_COH1}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_H36B}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_JM9130013}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_M732}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		
msa63264.2{110_M781}		TGCCCTTGAA	GCAGCTGATC	AACCTTGGGT	ACCAGTTGAA	AAATCATGGC		

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_A909}	TGCCCTTGAA	GCAGCTGATC	AACITTTGGGT	ACCAGTTGAA	AAATCATGGC
Consensus	*****	*****	*****	*****	*****
251					
msa63264.2{110_090}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_1169NT}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_18RS21}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_2603}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_CJB110}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_COH1}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_H36B}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_JM9130013}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M732}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_M781}	GCTTgAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
msa63264.2{110_A909}	GCTTaAACGA	ACGTCATTAC	GGTGGATTGA	CAGGAAAAAA	TAAAGCAGAA
Consensus	*****	*****	*****	*****	*****
301					
msa63264.2{110_090}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_1169NT}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_18RS21}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_2603}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_CJB110}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_COH1}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_H36B}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_JM9130013}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M732}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_M781}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
msa63264.2{110_A909}	GCAGCTGAAC	AATTTGGTGA	TGAGCAAGTT	CATATTTGGC	GTCGTTTCATA
Consensus	*****	*****	*****	*****	*****
351					
msa63264.2{110_090}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_1169NT}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_18RS21}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_2603}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_CJB110}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_COH1}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_H36B}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_JM9130013}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M732}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_M781}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
msa63264.2{110_A909}	TGATGTATTG	CCTCCAGATA	TGGCTAAAGA	TGATGAACAT	TCAGCACATA
Consensus	*****	*****	*****	*****	*****
401					
msa63264.2{110_090}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_1169NT}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_18RS21}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_2603}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_CJB110}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_COH1}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_H36B}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_JM9130013}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M732}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_M781}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
msa63264.2{110_A909}	CTGATCGTCG	CTATGCTTCA	CTAGATGATT	CTGTTATTCC	AGATGCAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa63264.2{110_090}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_1169NT}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_18RS21}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_2603}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_CJB110}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_COH1}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_H36B}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_JM9130013}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M732}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_M781}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
msa63264.2{110_A909}	AACCTAAAAG	TTACTTTAGA	CGGTGCTCTT	CCTTTCTGGG	AAGATAAAAT
Consensus	*****	*****	*****	*****	*****
501					
msa63264.2{110_090}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_1169NT}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_18RS21}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_2603}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_CJB110}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_COH1}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_H36B}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_JM9130013}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_M732}	TGCTCCTGCT	CTTAAAGATG	GTA AAAATGT	GTTTGTGGT	GCACACGGTA

Table 42: Comparative Sequences relating to SAG 0764

msa63264.2{110_M781}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
msa63264.2{110_A909}	TGCTCCTGCT	CTTAAAGATG	GTAAAAATGT	GTTTGTGGT	GCACACGGTA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	551				600
msa63264.2{110_1169NT}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_18RS21}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_2603}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_CJB110}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_COH1}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_H36B}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_JM9130013}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_M732}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_M781}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
msa63264.2{110_A909}	ACTCAATCCG	TGCTCTTGTA	AAACATATCA	AACAATGTGC	AGATGATGAA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	601				650
msa63264.2{110_1169NT}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_18RS21}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_2603}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_CJB110}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_COH1}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_H36B}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_JM9130013}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_M732}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_M781}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
msa63264.2{110_A909}	ATCATGGACG	TTGAAATTCC	TAACTTCCCA	CCACTTGTTC	TCGAATTGGA
Consensus	*****	*****	*****	*****	*****
msa63264.2{110_090}	651				690
msa63264.2{110_1169NT}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_18RS21}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_2603}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_CJB110}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_COH1}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_H36B}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_JM9130013}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M732}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_M781}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
msa63264.2{110_A909}	TGAAAAATTA	AACCTTGTTC	CAGAATATTA	CTTAGGTAAA	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 4212: 2603 V/R STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4213: 090 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4214: A909 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4215: H36B STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4216: 18RS21 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4217: M732 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKTTNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLV
 PDMAKDDEHSAHTDRRYASLDDSVI PDAENLKVTLEALPFWEDKIAPALDKGKNVFGA
 HGNSIRALVKHIKQLSDEIMDVEIPNFPPLVFEFDEKLNLVSEYLLGK

SEQ ID NO. 4218: COH1 STRAIN

Table 42: Comparative Sequences relating to SAG 0764

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
 PDMAKDEHSAHTDRRYASLDDSVIPDAENLKVTTLERALPFWEDKIAPALKDGNVVFVGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4219: CJB110 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
 PDMAKDEHSAHTDRRYASLDDSVIPDAENLKVTTLERALPFWEDKIAPALKDGNVVFVGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4220: 1169NT STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
 AKDDEHSAHTDRRYASLDDSVIPDAENLKVTTLERALPFWEDKIAPALKDGNVVFVGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4221: M781 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
 PDMAKDEHSAHTDRRYASLDDSVIPDAENLKVTTLERALPFWEDKIAPALKDGNVVFVGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

SEQ ID NO. 4222: JM9130013 STRAIN

VKLVFARHGESEWNKANLFTGWADVDLSEKGTQQAIDAGKLIQAAGIEFDLAFTSVLKRA
 IKITNLALEAADQLWVPVEKSWRLNERHYGGLTGKNKAEAAEQFGDEQVHIWRRSYDVLPPDM
 PDMAKDEHSAHTDRRYASLDDSVIPDAENLKVTTLERALPFWEDKIAPALKDGNVVFVGA
 HGNSIRALVKHIKQLSDDEIMDVEIPNFPPLVFEFDEKLNLVSEYYLGK

PRETTY of: /biotmp/msa70722.2{*} March 10, 2003 09:33 ..

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      msa70722.2{110_090}      1
msa70722.2{110_18RS21}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_2603}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_A909}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_CJB110}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_COH1}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_H36B}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_JM9130013} vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M732}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_M781}      vklVFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
msa70722.2{110_1169NT}    ---VFARHGE SEWNKANLFT GWADVDLSEK GTQQAIDAGK LIQAAGIEFD
      Consensus            - - - * * * * *
                                     50

      msa70722.2{110_090}      51
msa70722.2{110_18RS21}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_2603}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_A909}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_CJB110}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_COH1}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_H36B}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_JM9130013} LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M732}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_M781}      LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
msa70722.2{110_1169NT}    LAFTSVLKRA IKITNLALEA ADQLWVPVEK SWRLNERHYG GLTGKNKAE
      Consensus            * * * * *
                                     100

      msa70722.2{110_090}      101
msa70722.2{110_18RS21}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_2603}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_A909}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_CJB110}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_COH1}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_H36B}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_JM9130013} AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M732}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_M781}      AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
msa70722.2{110_1169NT}    AEQFGDEQVH IWRRSYDVLPPDMAKDDEHS AHTDRRYASL DDSVIPDAEN
      Consensus            * * * * *
                                     150

      msa70722.2{110_090}      151
msa70722.2{110_18RS21}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_2603}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_A909}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_CJB110}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_COH1}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_H36B}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_JM9130013} LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI
msa70722.2{110_M732}      LKVTTLERALP FWEDKIAPAL KDGNVVFVGA HGNSIRALVK HIKQLSDDEI

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Table 42: Comparative Sequences relating to SAG 0764

msa70722.2{110_M781}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
msa70722.2{110_1169NT}	LKVTLERALP	FWEDKIAPAL	KDGKNVFGA	HGNSIRALVK	HIKQLSDDEI
Consensus	*****	*****	*****	*****	*****
	201		229		
msa70722.2{110_090}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_18RS21}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_2603}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_A909}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_CJB110}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_COH1}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_H36B}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_JM9130013}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M732}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_M781}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
msa70722.2{110_1169NT}	MDVEIPNFPP	LVFEFDEKLN	LVSEYYLGK		
Consensus	*****	*****	*****		

Table 43: Comparative Sequences relating to SAG0079

SEQ ID NO. 4301: 2603 V/R STRAIN

ATGAATCTTTTAATTATGGGTTTGCTGCTGGTAAAGGTACTCAAGCAGCTAAGATC
 GTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCT
 AATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCT
 GATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAA
 GGTTTTTTACTTGGATGGATATCCAGTACTATTGAACAAGCACAGCCCTTAGATGCTACG
 CTTGAAGAAGCTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGT
 CTTATAGAGCGTTTGGTGTGCTGATATTAATCGTAAAACTGGTGAACTTTCCACAAA
 GTGTTCAACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAG
 CCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAA
 CACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTT
 TTTGCAGATGTTGAAAAAGCGTTGCTAGAACTCAA

SEQ ID NO. 4302: 090 STRAIN (reverse complement)

AATCTTTTAATTATGGGTTTGCTGCTGGTAAAGGTACTCA
 AGCAGCTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCG
 CGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGG
 TGAATTTGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGA
 TATCGCAGAAAAAGGTTTACTTGGATGGATATCCAGTACTATTGAACAAGCACAGC
 CTTAGATGCTACGCTTGAAGAAGCTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGT
 GGATCCATCATGTCTTATAGAGCGTTTGGTGTGCTGATTAATCGTAAAACTGGTGA
 AACTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACG
 TGAAGATGATAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGA
 ACCATCTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGA
 AATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4303: 1169NT STRAIN (REVERSE COMPLEMENT)

TGGTAAAGGGACTCAAGCAGCTAAGATTGTTGAAGAATTTGGTGTGCGCACATCTCAAC
 AGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAG
 TTATATTGATAAAGGTGAATTGGTTCCTGATCAAGTAACAAACGGGATTGTAAAGAGCG
 CTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGGATGGGTATCCAGTACTAT
 TGAACAAGCACAGCGCTTAGATGCTACGCTTGAAGAAGCTAGGACTACGCTTAGATGGTGT
 TATTAAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGTGCTGATTAATCAA
 TCGTAAACTGCTGGTGAAGCTTTCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGA
 AGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTCA
 TATTGCTCAAGGAGAACCTATTCTTGAACACTATAGTAAGCTTGGCCTTGTACAGATAT
 TGAAGGTAATCAAGAAATAA

SEQ ID NO. 4304: 18RS21 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCACGGGTTTCGCTGGTGGTAAAGGTACTCAAGCAGCTAAGATCG
 TTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTA
 ATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTG
 ATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAG
 GTTTTTTACTTGGATGGATATCCAGTACTATTGAACAAGCACAGCCTTAGATGCTACGC
 TTGAAGAAGCTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATCATGTG
 TTATAGAGCGTTTGGTGTGCTGATTAATCGTAAAACTGGTGAAGCTTTCCACAAAG
 TGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGC
 CTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAAC
 ACTATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTT
 TTGAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4305: A909 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCTGCTGGTAAAGGTACTCAAGCAG
 CTAAGATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCG
 CAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAAT
 TGGTTCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCG
 CAGAAAAAGGTTTTTACTTGGATGGATATCCAGTACTATTGAACAAGCACAGCCTTAG
 ATGCTACGCTTGAAGAAGCTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATC
 CATCATGTCTTATAGAGCGTTTGGTGTGCTGATTAATCGTAAAACTGGTGAAGCTTT
 TCCACAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAG
 ATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTA
 TTCTTGAACACTATCGAAAGCTTGGTCTTGTACAGATATTGAAGGTAA

SEQ ID NO. 4306: CJB110 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAACCACGGGTTTGCTTGGTGGTAAAGGTACTCAAGCAGCTAA
 GATCGTTGAAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAAT
 GGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGT
 TCCTGATGAAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGA
 AAAAGGTTTTTACTTGGATGGATATCCAGTACTATTGAACAAGCACAGCCTTAGATGC
 TACGCTTGAAGAAGCTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCATC
 ATGCTTATAGAGCGTTTGGTGTGCTGATTAATCGTAAAACTGGTGAAGCTTTCCA
 CAAAGTGTTCACCCACAGTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGA
 TAAGCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCT
 TGAACACTATAG

SEQ ID NO. 4307: COH1 STRAIN (REVERSE COMPLEMENT)

ATCTTTTAATTATGGGTTTGCTGCTGGTAAAGGTACTCAAGCAGCTAAGATGTTG
 AAGAATTTGGTGTGCTCAGATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATC
 AAACCAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATG
 AAGTAACAAACGGGATTGTAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTT
 TTTTACTTGGATGGATATCCAGTACTATTGAGCAAGCACAGCCTTAGATGCTACGCTTG
 AAGAAGTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCACATGCTTTA
 TAGAGCGTTTGGTGGCCGATTATCAATCGTAAAACTGGTGAAGCTTTCCACAAAGTGT

Table 43: Comparative Sequences relating to SAG0079

TCAACCCACCACTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTG
AAACTGTCAAACGTCGCTTGGACGTTAAATTGCTCAAGGAGAACCTATCTTGAACACT
ATCGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTG
CAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4308: H36B STRAIN (REVERSE COMPLEMENT)

CAGGGGATATGTTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAA
GTTATATTGATAAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATGTAAAAAGAGC
GCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTA
TTGAACAAGCACACGCCCTTAGATGCTACGCTTGAAGAAGTACGACTACGCTTAGATGGTG
TTATTAATATTAAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCA
ATCGTAAAACTCGCAGAAAAAGCTTTCCACAAAGTGTTCAACCCACCACTAGATTATAAAGAAG
AAGATTACTATCAACGTGAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTA
ATATTGCTCAAGGAGAATCTATTCTTGAACACTATCGTAAGCTTGGTCTTGTACAGATA
TTGAAGGTAATCAAGAAATAACAGAAGTTTTTGCAGATGTTGAAAAAGCGTTG

SEQ ID NO. 4309: JM9130013 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTATGGGTTTGCCTGGTCTGGTAAAGGT
ACTCAGCAGCTAAGATCGTTGAAGAATTTGGTGTCTCATCTCAACAGGGGATATG
TTCCGCGCCGCAATGGCTAATCAAACCGAAATGGGACGTTTAGCTAAAAAGTTATATTGAT
AAAGGTGAATTGGTTCCTGATGAAGTAACAAACGGGATGTAAAAAGAGCGCTTAGCTGAG
GATGATATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAACAAGCA
CAGCGCTTAGATGCTACGCTTGAAGAAGTACGACTACGCTTAGATGGTGTATTAAATATT
AAAGTGGATCCATCATGTCTTATAGAGCGTTTGGTGGTTCGATTATCAATCGTAAAACT
GGTGAACCTTTCCACAAAGTGTTCAACCCACCACTAGATTATAAAGAAGAAGATTACTAT
CAACGTGAAGATGATAAGCCTGAAACTGTAAACGTGCTTGGACGTTAATATTGCTCAA
GGAGAACCTATTCTTGAACACTATAAAAAAGCTTGGTCTTGTACAGATATTGAAGGTAAT
CA

SEQ ID NO. 4310: M732 STRAIN (REVERSE COMPLEMENT)

CTTTAATTATGGGTTTGCCTGGTCTGGTAAAGGTACTCAAGCAGCTAAGATGTTGAA
GAATTTGGTGTGTGCTCATCTCAACAGGGGATATGTTCCGCGCCGCAATGGCTAATCAA
ACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGTGAATTGGTTCCTGATGAA
GTAACAAACGGGATGTAAAAAGAGCGCTTAGCTGAGGATGATATCGCAGAAAAAGGTTTT
TTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCGCTTAGATGCTACGCTTGAA
GAACTAGGACTACGCTTAGATGGTGTATTAAATATTAAAGTGGATCCAACATGCCCTTATA
GAGCGTTTGAAGTGGCGCTTATTCAATCGTAAACTGGTGAACCTTTCCACAAAGTGTTT
AACCCACCACTAGATTATAAAGAAGAAGATTACTATCAACGTGAAGATGATAAGCCTGAA
ACTGTCAAACGTGCTTGGACGTTAATATTGCTCAAGGAGAACCTATTCTTGAACACTAT
CGTAAGCTTGGTCTTGTACAGATATTGAAGGTAATCAAGAAATAACAGAAGTTTTGCA
GATGTTGAAAAAGCGTTG

SEQ ID NO. 4311: M781 STRAIN (REVERSE COMPLEMENT)

AATCTTTTAATTACGGGTTTGCCTGGTCTGGTAAAGGTACTCAA
GCAGCTAAGATTGTTGAAGAATTTGGTGTGCTCATCTCAACAGGGGATATGTTCCGCG
GCCGCAATGGCTAATCAAACCCAAATGGGACGTTTAGCTAAAAGTTATATTGATAAAGGT
GAATTTGGTTCCTGATGAAGTAACAAACGGGATGTAAAAAGAGCGCTTAGCTGAGGATGAT
ATCGCAGAAAAAGGTTTTTACTTGATGGATATCCACGTACTATTGAGCAAGCACACGCGC
TTAGATGCTACGCTTGAAGAAGTACGACTACGCTTAGATGGTGTATTAAATATTAAAGTG
GATCCAACATGCCCTTATAGAGCGTTTGGTGGCGGCTATTATCAATCGTAAAACTGGTGAA
ACTTTCCACAAAGTGTTCAACCCACCACTAGATTATAAAGAAGAAGATTACTATCAACGT
GAAGATGATAAGCCTGAAACTGTCAAACGTGCTTGGACGTTAATATTGCTCAA

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25038.2{*} April 17, 2002 08:53 ..
PRETTY of: /biotmp/msa25229.2{*} January 31, 2003 03:05 ..

	1		50
msa252229.2{114_COH1}	----atcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M732}	-----cttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_M781}	---Aatcttt taattacggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_A909}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_JM9130013}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_CJB110}	---Aatcttt taaccacggg tttgcttggg gctggtaaag gtactcaagc		
msa252229.2{114_090}	---Aatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_2603}	atgAatcttt taattatggg tttgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	---Aatcttt taaccacggg ttcgcctggg gctggtaaag gtactcaagc		
msa252229.2{114_1169NT}	-----		
Consensus	*****		
	51		100
msa252229.2{114_COH1}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M732}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_M781}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_A909}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_JM9130013}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_CJB110}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_090}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_2603}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_H36B}	-----		
msa252229.2{114_18RS21}	agctaagatt gttgaagaat ttggtgttgc tcacatctca aCAGGGGATA		
msa252229.2{114_1169NT}	agctaagatt gttgaagaat ttggtgttgc gcacatctca aCAGGGGATA		

Table 43: Comparative Sequences relating to SAG0079

Consensus	-----	-----	-----	-----	-----	*****
	101					150
msa252229.2{114_COH1}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M732}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_M781}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_A909}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_JM9130013}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_CJB110}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_090}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_2603}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_H36B}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_18RS21}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
msa252229.2{114_1169NT}	TGTTCCGCGC	CGCAATGGCT	AATCAAACCC	AAATGGGACG	TTTAGCTAAA	
Consensus	*****	*****	*****	*****	*****	*****
	151					200
msa252229.2{114_COH1}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M732}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_M781}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_A909}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_JM9130013}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_CJB110}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_090}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_2603}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_H36B}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_18RS21}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
msa252229.2{114_1169NT}	AGTTATATTG	ATAAAGGTGA	ATTGGTTCCT	GATgAAGTAA	CAAACGGGAT	
Consensus	*****	*****	*****	*****	*****	*****
	201					250
msa252229.2{114_COH1}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_M732}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_M781}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_A909}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_JM9130013}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_CJB110}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_090}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_2603}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_H36B}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_18RS21}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
msa252229.2{114_1169NT}	TGTAAAAGAG	CGCTTAGCTG	AGGATGATAT	CGCAGAAAAA	GGTTTITTTAC	
Consensus	*****	*****	*****	*****	*****	*****
	251					300
msa252229.2{114_COH1}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M732}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_M781}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_A909}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_JM9130013}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_CJB110}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_090}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_2603}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_H36B}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_18RS21}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
msa252229.2{114_1169NT}	TTGATGGaTA	TCCACGTACT	ATTGAGCAAG	CACACGCCTT	AGATGCTACG	
Consensus	*****	*****	*****	*****	*****	*****
	301					350
msa252229.2{114_COH1}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M732}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_M781}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_A909}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_JM9130013}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_CJB110}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_090}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_2603}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_H36B}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_18RS21}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
msa252229.2{114_1169NT}	CTTGAAGAAC	TAGGACTACG	CTTAGATGGT	GTTATTAATA	TAAAGTGGA	
Consensus	*****	*****	*****	*****	*****	*****
	351					400
msa252229.2{114_COH1}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M732}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_M781}	TCCAaCATGc	CTTATAGAGC	GTTTGAGTGg	cCGTATTATC	AATCGTAAAA	
msa252229.2{114_A909}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_JM9130013}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_CJB110}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_090}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_2603}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_H36B}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	
msa252229.2{114_18RS21}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTGg	tCGTATTATC	AATCGTAAAA	

Table 43: Comparative Sequences relating to SAG0079

msa252229.2{114_1169NT}	TCCAtCATGt	CTTATAGAGC	GTTTGAGTg	tCGTATTATC	AATCGTAAAA
Consensus	****-****	*****	*****	-*****	*****
	401				450
msa252229.2{114_COH1}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M732}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_M781}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_A909}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_JM9130013}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_CJB110}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_090}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_2603}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_H36B}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_18RS21}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
msa252229.2{114_1169NT}	CTGGTGAAAC	TTTCCACAAA	GTGTTCAACC	CACCAGTAGA	TTATAAAGAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa252229.2{114_COH1}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M732}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_M781}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_A909}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_JM9130013}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_CJB110}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_090}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_2603}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_H36B}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_18RS21}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
msa252229.2{114_1169NT}	GAAGATTACT	ATCAACGTGA	AGATGATAAG	CCTGAAACTG	TcAAACGTCG
Consensus	*****	*****	*****	*****	*-*****
	501				550
msa252229.2{114_COH1}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M732}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_M781}	CTTGGACGTT	aATATTGCTC	AA-----	-----	-----
msa252229.2{114_A909}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgaa
msa252229.2{114_JM9130013}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactataaaa
msa252229.2{114_CJB110}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatag--
msa252229.2{114_090}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_2603}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_H36B}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_18RS21}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatcgta
msa252229.2{114_1169NT}	CTTGGACGTT	aATATTGCTC	Aaggagaacc	tattcttgaa	cactatagta
Consensus	*****	*****	*****	-----	-----
	551				600
msa252229.2{114_COH1}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M732}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	agcttggtct	tggtacagat	attgaaggta	a-----	-----
msa252229.2{114_JM9130013}	agcttggtct	tggtacagat	attgaaggta	atca-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_2603}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_H36B}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_18RS21}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aacagaagtt
msa252229.2{114_1169NT}	agcttggtct	tggtacagat	attgaaggta	atcaagaaat	aa-----
Consensus	-----	-----	-----	-----	-----
	601				636
msa252229.2{114_COH1}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M732}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_M781}	-----	-----	-----	-----	-----
msa252229.2{114_A909}	-----	-----	-----	-----	-----
msa252229.2{114_JM9130013}	-----	-----	-----	-----	-----
msa252229.2{114_CJB110}	-----	-----	-----	-----	-----
msa252229.2{114_090}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_2603}	tttgcatag	ttgaaaaagc	gttgctagaa	ctcaaa	-----
msa252229.2{114_H36B}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_18RS21}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
msa252229.2{114_1169NT}	tttgcatag	ttgaaaaagc	gttg-----	-----	-----
Consensus	-----	-----	-----	*****	*****

SEQ ID NO. 4312: 2603 V/R STRAIN

MNLLIMGLPGAGKGTQAAKIVVEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP
 EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDLELGLRLDGVINIKVDPSC
 LIERLSKRIINRKTGETFHKVFNPVVDYKEDDYQREDDKPETVKRRLDVNIAQGEPILE
 HYRKLGLVTDIEGNQETVEFADVEKALLELK

SEQ ID NO. 4313: 090 STRAIN

NLLIMGLPGAGKGTQAAKIVVEFGVAHISTGDMFRAAMANQTEMGRILAKSYIDKGELVP
 EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDLELGLRLDGVINIKVDPSC
 IERLSGRIINRKTGETFHKVFNPVVDYKEDDYQREDDKPETVKRRLDVNIAQGEPILEH

Table 43: Comparative Sequences relating to SAG0079

YRKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4314: 1169NT STRAIN

GKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDQVTNGIVKER
LAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI IN
RKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEHYSKLGVLTDI
EGNQEI

SEQ ID NO. 4315: 18RS21 STRAIN

NLLITGSPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH
YRKLGLVTDIEGNQEITEVFADVEKALLE

SEQ ID NO. 4316: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4317: A909 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGESILEH
YRKLGLVTDIEG

SEQ ID NO. 4318: CJB110 STRAIN

NLLITGGLGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH
Y

SEQ ID NO. 4319: COH1 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDE
VTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPCL
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH
RKLGLVTDIEGNQEITEVFADVEKALL

SEQ ID NO. 4320: H36B STRAIN

GDMFRAAMANQTEMGRKLSYIDKGELVPDEVTNGIVKERLAEDDIAEKGFLLDGYPRIT
IEQAHALDATLEELGLRLDGVINIKVDPSCLIERLSGRI INRKTGETFHKVFNPVDYKEE
DYQREDDKPETVKRRLDVHIAQGESILEHYRKLGLVTDIEGNQEITEVFADVEKAL

SEQ ID NO. 4321: JM9130013 STRAIN

NLLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPSCLI
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH
YKLGVLTDIEGN

SEQ ID NO. 4322: M732 STRAIN

LLIMGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPDE
VTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPCL
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQGEPILEH
RKLGLVTDIEGNQEITEVFADVEKALLELK

SEQ ID NO. 4323: M781 STRAIN

NLLITGLPGAGKGTQAAKIVEEFGVAHISTGDMFRAAMANQTEMGRKLSYIDKGELVPD
EVTNGIVKERLAEDDIAEKGFLLDGYPRITIEQAHALDATLEELGLRLDGVINIKVDPCL
ERLSGRI INRKTGETFHKVFNPVDYKEEDYYQREDDKPETVKRRLDVHIAQ

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa32357.2{*} April 17, 2002 09:17 ..

	1				50
msa252352.2{114_18RS21}	~nllttgspg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_M781}	~nllitglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_CJB110}	~nllttgllg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_090}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_JM9130013}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	tGDMFRAAMA
msa252352.2{114_A909}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_1169NT}	-----	~gkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_2603}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_COH1}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTqMGRlak
msa252352.2{114_M732}	~nllimglpg	agkgtqaaki	veefgvahis	tGDMFRAAMA	NQTeMGRlak
msa252352.2{114_H36B}	-----	-----	-----	~GDMFRAAMA	NQTeMGRlak
Consensus	*	-----	-----	*****	*****
	51				100
msa252352.2{114_18RS21}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_M781}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT
msa252352.2{114_CJB110}	SYIDKGELVP	DeVINGIVKE	RLAEDDIAEK	GFLLDGYPRT	IEQAHALDAT

Table 43: Comparative Sequences relating to SAG0079

msa252352.2{114_090}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_JM9130013}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_A909}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_1169NT}	SYIDKGELVP	DqVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_2603}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_COH1}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_M732}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
msa252352.2{114_H36B}	SYIDKGELVP	DeVTNGIVKE	RLAEDDIAEK	GFLLDGYPR	IEQAHALDAT
Consensus	*****	*-*****	*****	*****	*****
101					
msa252352.2{114_18RS21}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M781}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_CJB110}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_090}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_JM9130013}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_A909}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_1169NT}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_2603}	LEELGLRLDG	VINIKVDPsC	LIERLSxRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_COH1}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_M732}	LEELGLRLDG	VINIKVDPtC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
msa252352.2{114_H36B}	LEELGLRLDG	VINIKVDPsC	LIERLSgRII	NRKTGETFHK	VFNPFPVDYKE
Consensus	*****	*****	*****	*****	*****
151					
msa252352.2{114_18RS21}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M781}	EDYYQREDDK	PETVKRRLDV	nIAQ-----	-----	-----
msa252352.2{114_CJB110}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hy-----	-----
msa252352.2{114_090}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_JM9130013}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hykklglvtd	iegn-----
msa252352.2{114_A909}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	ieg-----
msa252352.2{114_1169NT}	EDYYQREDDK	PETVKRRLDV	hIAQgepile	hysklglvtd	iegnqei---
msa252352.2{114_2603}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_COH1}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_M732}	EDYYQREDDK	PETVKRRLDV	nIAQgepile	hyrklglvtd	iegnqeitev
msa252352.2{114_H36B}	EDYYQREDDK	PETVKRRLDV	nIAQgesile	hyrklglvtd	iegnqeitev
Consensus	*****	*****	-----	-----	-----
201					
msa252352.2{114_18RS21}	fadvekalle	--			
msa252352.2{114_M781}	-----	--			
msa252352.2{114_CJB110}	-----	--			
msa252352.2{114_090}	fadvekalle	LK			
msa252352.2{114_JM9130013}	-----	--			
msa252352.2{114_A909}	-----	--			
msa252352.2{114_1169NT}	-----	--			
msa252352.2{114_2603}	fadvekalle	LK			
msa252352.2{114_COH1}	fadvekal--	--			
msa252352.2{114_M732}	fadvekalle	LK			
msa252352.2{114_H36B}	fadvekal--	--			
Consensus	-----	**			
212					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SEQ ID NO. 4401
STRAIN 2603
 GTGGATAAACCATCACTCAAAAAAGGCTATTTTAAAGTTAACA
 CTTATAACAACCTAGTATTTTATTAATGCATAGCAATCAAGTGAATGCAGAGGAGCAAGAA
 TTAATAAACCAAGAGCAATCACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCG
 GTAACCTACTAATCTGTTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATATTAGAAAGAG
 TTATCTAAAAACCTTGATACGCTTAATTTGGGGGCTGATCTTGAAGAAAGATATCCCTCT
 AAACCAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAAATGCTTCACTGCAATA
 GCACAGAAAGTTCCTCAGCATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGCT
 GTTCTTGATACATCTAAAAATAACAAAAATTACAAGCCATAACCAAGAGGAAAGGGAAAT
 GTAGTAGCTATTATGATACCTGGCTTTGATATTAACCATGATATTTTTCGTTTAGATAGC
 CCAAAAGATGATAAGACACAGCTTTAAACTAAGACAGAAATTTGAGGAATTAAGAACAAAA
 CATAATATCACTTATGGGAAATGGGTAAACGATAAGATTGTTTTTGACATAACTACGCC
 AACAAATACAGAAACGGTGGCTGATATTGCAGCAGCTATGAAGATGTTTATGGTTAGAA
 GCAAGAAATATTTCCGATGGTACACAGCTTGTCTGGTATTTTGTAGGTAATAGTAACAGT
 CCAGCAATCAATGGTCTTCTTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATTAATG
 CGTATTCAGATAGAAATGATTGCGACAAATTTGGTGAAGCATATGCTAAAGCAATCACA
 GACGCTGTTAATCTAGGAGCAAAAACGATTAAATAGATTATGGAAGAAACAGCTGATTCT
 TTAATGCTCTCAATGATAAAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTT
 GCAGTTGTTGCTGCTGCCGAAATGAAGCGCATTTGGTATGGATTATAGCAAAACATT
 TCAACTAATCCTGACTACGCTACGGTTAATAGTCCAGCTATTTCTGAAGATACCTTTGAGT
 GTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTGAACAACTATTGAAGGT
 AAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAACCTTTTGACAAAGGTGAAGCCCTACGAT
 TGGTTTATGCCAATTTATGGTGCAAAAAAGACTTTGAAGGTAAAGGACTTTAAAGGTAAAG
 ATTGCATTAATGAGCGTGGTGGTGGACTTGAATTTATGACTAAATCACTCATGTCTACA
 AATGCAGGTGTTGTTGGTATCGTTATTTTAAAGATCAAGAAAAACGTGGAAATTTTCTA
 ATTCTTACCGTGAATCACCTGTGGGATTTATAGTAAAGTAGATGGCGAGCGTATAAAA
 AATACTTCAAGTCAGTTAAACATTTAACCAGAGTTTGAAGTAGTTGATAGCCAAAGTGGT
 AATCGTATGCTGGAACAAATCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCTGAT
 GTAACAGCTTCTGGCTTTGAAATTTATCTTCAACCTATAATAATCAATACCAAAACATG
 TCTGGTACAAGTATGGCTTACCACATGTTGCAGGATTATGACAAATGCTTCAAGTCAT
 TTGGCTGAGAAATATAAGGGATGAATTTAGATTCTAAAAAATGCTAGAAATTTCTAAA
 AACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAGGATAAGGCGTTTATTCA
 CCACGTCAGCAAGGTGAGGTGATGTTGATGCTGAAAAAGCTATCAAGCTCAATATTAT
 ATTACTGGAACAGATGGCAAGCTAAATTAATCTCAACGAATGGGAGATAAATTTGAT
 ATCAGATTACAATTATAAACTTGTAGAAGGTGTCAAAGAAATGTATTTATCAAGCTAAT
 GTAGCAACAGAAACAGTAAATAAAGGTAAATTTGCCCTTAAACCAAGCCCTTGCTAGAT
 ACTAATTGGCAGAAAGTAATCTTCTGTGATAAAGAAACCAAGTTTCGATTTACTATTGAT
 GCTAGTCAATTTTAGTCAGAAATTAAGAAACAGATGGCAATGGTTATTTCTTAGAAGGT
 TTTGTACGTTTAAAGAGGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTA
 GGATTTAATGGTGATTTTGGCAACTTACAAGCACTTGAACACCCGATTATAAGAGCGCT
 TCTAAAGGTAGTTTCTACTATAACCAATGATACAACTCATAAAGACCAATTTGGAGTAC
 AATGAATCAGCTCCTTTTGAAGCAACAACTATACCTGCTTGTAAACCAATCAGCGTCT
 TGGGGCTATGTTGATTATGTCAAAAATGGTGGGAGTTAGAAATTAGCACCGGAGAGTCCA
 AAAAGAAATATTTTAGGAACCTTTTGAGAAATAGGTTGAGGATAAAACAAATTCATCTTTG
 GAAAGAGATGCAAGCAATAATCCATATTTTGGCAATTTCTCCAAATAAAGATGGAATAGG
 GACGAAATCACTCCCGAGGCACTTTCTTAAGAAATGTTAAGGATATTCTGCTCAAGTT
 CTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGTTTACCATTCTATCGTAAATAAT
 TTCCATTAATTAATCCAAAGCAAGTGTGCTGATGTTATCGTATGATGCTCTTCAGTGGAGT
 GGTTTAGATAAGGATGGCAAGTTGTAGCAGATGGTTTATATCTTATCGCTTACGTTAC
 ACACAGTAGCAGGAAGGAGCAATAGTCAGGAGTCAGACTTTAAGTACAAAGTAAGTACT
 AAGTCACCAATCTTCTTCAAGAGCTCAGTTTGTATGAACTAATCGAACTTAAGCTTA
 GCCATGCTAAGGAGTAGTTATGTTTCTACATATCGTTTACAAATTAGTTTATCTCAT
 GTTGTAAAAGATGAAGAAATATGGGATGAGACTTCTTACCATTATTTCCATATAGATCAA
 GAAGTTAAGTGACACTTCTTAAACCGTTAAGATAGGAGAGAGTGAAGTTGCGGTAGAC
 CCTAAGGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCAACCGTAAATTTG
 TCTGATCTCTTGAATAGGCAAGTATCAGAGAAAGAAACGCTATAGTAATTTCTAAC
 AGTTTCAAAATATTTTGATACTTGAAAAAGAACCTATGTTTATTTCTAAAAAGAAAAA
 GTAGTAAACAGAAATCTAGAAGAAATTAATATTAGTTAAGCCGCAAACTACAGTTACTACT
 CAATCATTTGTCTAAAGAAATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC
 AATAATAGTAGCAGAGTAGCTAAGATCATATCACTAAACATAACGGGGATTTCTGTTAAC
 CATACCTTACCTAGTACATCAGATAGAGCAACGAATGGTCTATTTGTTGGTACTTTGGCA
 TTGTTATCTAGTTTACTTCTTTATTTGAAACCCAAAGACTAAAAATAATAGTAA

SEQ ID NO. 4402
STRAIN 090
 GAGGAGCAAGAAATTAATAAACCAAGAGCAATCACCTGTAATTGCT
 AATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTGTTGAAAA
 AACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAGAAATGGGTG
 ATACATCTGTAATAAATGACAAAAACAGAAGATGAATATTAGAAAGATT
 TCTAAAAACCTTGATACGCTTAATTTGGGGGCTGATCTTGAAGAAATA
 TCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGTAACAA
 ATGCTTCAACTGCAATAGCACAGAAAGTTCCTCAGCGTATGAAGAGGTG
 AAGCCAGAAAGCAAGTCATCGCTTGCTGTTTGTATACATCTAAATAAAC
 AAAATTGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGCTATTA
 TTGATACTGGCTTTGATATTAACCATGATATTTTCGTTTAGATAGCCCA
 AAAGATGATAAGCACAGCTTTAAACTAAGCAGAAATTCGAGGAATTA
 AGCAAAACATAATACCTTATGGGAAATGGGTAAACGATAAGATTGTTT
 TTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGATATTGCAGAC
 GCTATGAAAGATGGTTATGGGTGAGAGCAAGAAATATTTTCGATGGTAC
 ACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAATCAATG
 GTCTTCTTTTAGAAGGTGACGCGCCAAATGCTCAAGTCTTATTATGCGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATCCAGATAAAATTGATTCCGACAAAATTGGAGAAGCATATGCTAAAGC
AATCAGACAGCGCTGTAAATCTAGGAGCAAAAaCGATTAAATATGAGCCCTG
GAAAAACAGCAGATTCTTTAAattGCaCTCAATGATAAAGTTAAATTAGCA
CTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGTGGCTGCCGAAA
TGAAGGTGCACTTTGGTATGGATTATAGCAAACCATATCAACTAATcCTG
ACTACGGTACGGTTAAATAGTCCAGCTATTTCTGAAGATACTTGTAGTGT
GCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACAACTAT
TGaaGGTAAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTTtGACA
AAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCAaaaaaAGAC
TTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATtGAGCGTGGtGG
TGGACTTGATTTTTATGACTAAaatCACTcATGCTACAAATGCAGGTGTTG
tTGGTATCGTtATTTtTAACgAtCAAGAaaaACGtGGAAATTTTtTAATT
CCTTACCCTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGCGAGCG
TATAAAAAAATCTTCAAGTCAGTTAACATTTAACAGAGTTTtGAAGTAG
TTGATAGCCAAAGTGGCAATCGTATGCTGGAAACAAATCAAGTTGGGGCGTG
ACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTTTGAAAT
TTATTCTTCAACCTATAATAATCAATCAAAACAAATGTCTGGTACAAGTA
TGGCTTCAACCATGTGTGAGGATTAAAGACAATGCTTCAAGTCATTG
GCTGAGAAATATAAAGGGATGAATTTAgATTCTTAAAAAATGTCTAGAATT
GTCTAAaACATCCTCATGAGCTCAGCAaCAGCATTATATAGTgAAGAgG
ATAAGGGCTtTtATTcACCAAGTCAGCAAGGtGCAGGtGTAGTTGATGCT
GAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAAACGATGGCAAGC
TAAAAATTAACTCTCAAAACGAGTGGGAGATAAAATTTGATATCACAGTTACA
TTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGTA
GCAACAGAAcAAGTAATAAAGGTAATTTGCCCTTAAACCAACAGCctt
GCTAGATACTAATTGGCAGAAAGTAATTCTTcGTGATAAGAAACACAAG
TTcGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTTAAAGAACAG
ATGGCAAAATGGTTATTCTTAgAAGGTTTGTACGTTTAAAGAACGCCAA
GGATAGTAATCAGGAGTTAaTGAGTATTCCTTtGTAGGATtTAATGGTG
ATTTTGGCAACTTACAAGCACTTGAACACCGATTATAAGACGCTTTCT
AAAGGTAGTTTCTACTATAAACCAAAATGATACAACCTATAAAGCCAATT
GGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTGCCTTGT
TAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATGGTGGG
GAGTTAGAATTAGCACCGGAGAGTcCAAAAAGAATTATTTTAgGAACTTT
TGAGAATAAGGTTGAGGATAAAAACAATTCATCTTTTGGAAAGAGATGCA
GcAATAATCCATATTTTGCCATTCTCCAATTAAGATGGAATAGGGAT
GAATCACTCCCAGGCACTTCTTAAGAAATGTTAAGGATATTCTGCG
TCAAGTTCTAGATCAAAATGGAATGTTATTGGCAAGTAAGGTTTAC
CATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAAGTGATGGTCAT
TATCGTATGGATGCCCTTTCAGTGGAGTGGTTAGATAAGGATGGCAAGT
TGTAGCAGATGGTTTATATCTATCGCCTACGTTACACACAGTAGCAG
AAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAAG
TCACCAATCTTCTTACTAGCTCAGTTTGATGAACTAATCGAACATT
AAGCTTAGCCATGCCTAAGGAAAGTAGTTAAGTTCTTACATATCGTTTAC
AATTAGTTTATCTCATGTTGTAAGAGATGAAGAATATGGGGATGAGACT
TCTTACCATTATTTCCATATAGATCAAGAAGGTAAGTGACACTTCCTAA
AACGGTTAAGATAGGAGAGAGTGAGGTTGCACTAGACCTTAAGGCTTGA
CACTTGTGTGGAAGATAAAGCTGGTAATTTTGAACGGTAAATTTGTCT
GACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAAT
TTCTAACAGTTTCAAATATTTTGATACTTGAaaaaAGAACTATGTTTA
TTTCTAAAGAAAGAAAGTAGTAAACAGAATCTAGAAGAAATAACATTA
GTTAAGCGCAAACTACAGTTACTACTCAATCATTTGCTAAAGAAATAAC
TAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAAATAATAGTAGCA
GAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTAACCAT
ACC

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STRAIN A909

GAGGAGCAAGAATTAAAAAACCAAGAGCAAT
CACCTGTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACT
AATACTGTTGAAAAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGC
GAAAGAAATGGGTGATACATCTGTAAAAATGACAAAACAGAAGATGAAT
TATTAGAAGAGTTATCTAAAAACCTTGATACGCTCAATTTGGGGGCTGAT
CTTGAAGAAGAAATATCCCTCTAAACAGAGACAAACCAATAAAGAAAG
CAATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTCCCTCAG
CATATGAAGAGGTGAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGAT
ACATCTAAATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGGAAA
TGTTAGTAGCTATTATTGATACCTGGCTTGTATTTAACCATGATATTTTC
GTTTAGATAGCCCAAAAGATgaTAAGCACAGCTTTAAaACTAAGGCAGAA
TTTGAGGAATTAAAGCAAAACATAATATCACTTATGGGAATGGGTTAA
CGATAAGATTGtTTTTCACATAACTACGCCaCAATACAGAAACGGTGG
CTGATATTGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAT
ATTTGCGATGGTACACAGTGTGCTGGTATTTTGTAGGTAATAGTAAAGC
TCAGCAATCAATGGTCTTCTTTAGAAGGTGACGCGCAAAATGCTCAAG
TCTTATTATGCGTATPCCAGATAAAATTGATTGCGACAAATTTGGTGAA
GCATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAACGAT
TAATATGAGCCTTGGAAAAACAGCAGATTCTTTAATTGCTCTCAATGATA
AAGTTAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTGTG
TGGCTGCGGAAATGAAGGTGCAATTGGTATGGATTATAGCAAAACCAT
ATCAACTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAG
ATACTTTGAGTGTGCTAGCTATGAATCACTTAAaACTATCAGTGAGGTC
GTTGAACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTC
TAAACCTTTTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GTGCAAAAAAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATT
 AATTGAGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTA
 CAAATGCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGT
 GGAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGGTATATAGTAA
 AGTAGATGGCGAGCGTATAAAAAATACCTCAAGTCAGTTAACATTTAAC
 AGAGTTTGAAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAAACA
 TCAAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGC
 TTCTGGCTTTGAAATTTATTTCTCAACCTATAATAATCAATACCAACAA
 TGCTGGTACAGATATGGCTTACCACATGTGTCAGGATTATGACAAATG
 CTTCAAGTCATTTGGCTGAGAAATATAAAGGATGAATTAGATTCTAA
 AAAATTGCTAGAAATTGTCTAAAAACATCTCATGAGCTCAGCAACAGCAT
 TATATAGTGAAGAGGATAAGGCGTTTATTTACCACGTGAGCAAGGTGCA
 GGTGTAGTTGATGCTGAAAAAGCTATCCAAAGCTCAATATTATGTTACG
 AAACGATGGCAAGCTAAAAATTAATCTCAACAGAGTGGGAGATAAATTTG
 ATATCACAGTTACAATTCATAAATTTAGAGAGGTGTCAAAGAAATTGTAT
 TATCAAGCTAATGTAGCAACAGAACTAAATAAAGGTAATTTGCCTT
 TAAACCAAGCCTTGCTAGATCTAATTTGGCAGAAAGTAATTTCTGCTG
 ATAAAGAAACACAAGTTCCGATTACTATGATTCTAGTCAATTTAGTCAG
 AAATTAAGAAACAGATGGCAATGTTATTTCTAGAAAGTTTGTACG
 TTTTAAAGAAAGCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTG
 TAGGATTTAATGGTATTTTGGCACTTACAAGCACTTGAACACCGGATT
 TATAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAAC
 TCATAAGACCAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACA
 ACTATACCTGCTTGTAAACACATCAGCGTCTTGGGGCTATGTTGATTAT
 GTCAAAAATGGTGGGAGTTAGAAATAGCACCGGAGAGTCCAAAAAGAA
 TATTTTAGGAACCTTTGAGAAATAGGTGAGGATAAAACAAATTCATCTT
 TGGAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAA
 GATGAAATAGGAGTAAATCACTCCCAAGGCAACTTTCTTAAGAAATGT
 TAAGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGC
 AAAGTAAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAG
 CAAAGTGATGGTCATTTATCGTATGGATGCCCTTCAGTGGAGTGGTTAGA
 TAAGGATGGCAAGTTGTAGCAGATGGTTTATATCTTATCGTTACGTT
 ACACACAGTAGCAGAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTT
 CAAGTAAGTACTAAGTCACCAAACTCTTCTTACGAGCTCAGTTTATGA
 AACTAATCGAACATTAAGCTTAGCCATGCTTAAGGAAAGTAGTTATGTT
 CTACATATCGCTACAAATAGTTTATCTCATGTTGTAAAAGATGAAGAA
 TATGAGATGAGAGCTTCTTACCATTAATTTCCATATAGATCGAGAAGGTAA
 AGTGACACTTCTTAAACAGTTAAGATAGGAGAGAGTGGGTTGAGTAG
 ACCCTAAGACCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCGA
 ACGGTAAATTTGCTGACCTCTTGAATAAGGCAAGTAGTATCAGAGAAAGA
 AAACGCTATAGTAATTTCTAACAATTTCAAATATTTTGATAACTTGAAAA
 AAGAACCTATGTTTATTTCTAAAGAAAGGAAAGTAGTAAACAGAACTA
 GAAGAAATAGCATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCAT
 GTCTAAAGAAATAACTCAATCAGGAAATGAGAAAGTCTCACTTCTACAA
 ACAATAATAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGG
 GATTCTGTTAACCATACC

SEQ ID NO. 4404

STRAIN H3B

GAGGAGCAAGAAATTA AAAAACCAGAGCAATCACCTGTAATTGC
 TAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTTGAAA
 AAACATCTGTAAACATCTGCTTCTGCTAGTAATACAGCGAAAGAAATGGGT
 GATACATCTGTAAAAATGACAAACAGAAAGATGAATTTATGAAAGAGTT
 ATCTAAAAACCTTGATACGCTCAATTTGGGGGCTGATCTTGAAGAAGAA
 ATCCCTCTAAACAGAGACAAACCAATAAAGAAAGCAATGTAGTAACA
 AATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAGAGGT
 GAAGCCAGAAAGCAAGTCATCACTTGCTGTTCTTGATACATCTAAATAA
 CAAAATGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGCTATT
 ATTGATAGTGGCTTTGATATTAAACCATGATATTTTCGTTTAGATAGCCC
 AAAAGATGATAAGCACAGCTTTAAACCTAAGGCAGAAATTTGAGGAATTAA
 AAGCAAAACATAATATCACTTATGGGAAATGGGTTAACGATAAGATTGTT
 TTTGCACATAACTACGCCCAATAACAGAAACGGTGGCTGATATTGCAGC
 AGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATTTTCGATGGTA
 CACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAATCAAT
 GGTCTTCTTTAGAAAGTGACAGCGCAAAATGCTCAAGTCTTATTAATCG
 TATTCAGATAAAATTTGATTGGGCAAAATTTGGTGAAGCATATGCTAAAG
 CAATCACAGACGCTGTTAATCTAGGAGCAAAACGATTAATATGAGCCTT
 GSAAAACAGCAGATTCTTTAATTGCTCTCAATGATAAAGTTAAATTAGC
 ACTTAAATTAGCTTCTGAGAAGGGCGTTGCAGTTGTTGGCTGCGCGAA
 ATGAAGGTGCAATTTGGTATGGATTATAGCAACCAATATCACTAATCCT
 GACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGTACTTTGAGTGT
 TGCTAGCTATGAATCACTTAAACCTATCAGTGAGGTGCGTTGAACCACTA
 TTGAAGGTAAAGTTAGTTAAGTTGCCGATTGTGACTCTAAACCTTTGAC
 AAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAAAAAGA
 CTTTGAAGGTAAAGACTTTAAAGGTAAGATTGCATTAATTGAGCGTGGT
 GTGGACTTGATTTTATGACTAAAACTCACTCATGCTACAAATGCAGGTGTT
 GTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGGAATTTCTAAT
 TCCTTACCGTGAATTAACCTGTGGGGGTTATAGTAAGTAGATGGCGAGC
 GTATTAATAAATACTTCAAGTCAGTTAACTTAAACAGAGTTTGTAGGTA
 GTTGATAGCCAAAGGTGGCAATCGATGCTGGAACCAATCAAGTTGGGGCGT
 GACAGCTGAAGGAGCAATCAAGCCTGATGTAAACGCTTCTGGCTTTGAAA
 TTTATTTCTTCAACCTATAATAATCAATACCAACCAATGTCTGGTACAGT
 ATGGCTTCAACCATGTTGCAGGATTAATGACCAATGCTTCAAGTCATTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCTAGAAT
 TGCTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGAAGAG
 GATAAGGCGTTTTATTCCACACGTCAGCAAGGTGCAGGTGTAGTTGATGC
 TGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGATGGCAAG
 CTAATAATTAATCTCAACAGAGTGGGAGATAAATTGATATCACAGTTACA
 ATTCTATAAATCTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCTAATGT
 AGCAACAGAACAGTAATAAAGGTAATTTGCCCTTAAACCcaAAGCCT
 TGCTAGATACTAATTGGCAGAAAGTAATTTCTCGTGATAAAGAAACAA
 GTTCGATTACTATTGATTCTAGTCAATTTAGTCAGAAATTAAGAACA
 GATGGCAAATGGTTATTTCTAGAAGGTTTGTACGTTTAAAGAGCCA
 AGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAATGGT
 GATTTTGCAGACTACAAGCACTGAAACACCGATTTATAAGACGCTTTC
 TAAAGTAGTTTCTACTATAAACCAAATGATACAACTATAAGACCAAT
 TGGAGTACAATGAATCAGCTCCTTTTGAAGCAACCACTATCTGCTCTG
 TTAACCAATCAGCGCTCTGGGGCTATGTTGATTATGTCAAAAAATGGTGG
 GGAATTAgAATTAgCACCGGAGAGTCCAAAAGAATTATTTTAGGAACCT
 TTGAGAAATAGGTTGAGGATAAAACAATTCTCTTTTGAAGAGATGCA
 CGGAATAATCCATATTTGCCATTTCTCAAATAAAGATGGAAATAGGGA
 TGAAATCACTCCCAGGCACTTTCTTAAGAAATGTTAAGGATATTTCTG
 CTCAAGTTCTAGATCAAAATGGAATGTTAATTGGCAAGTAAGGTTTAA
 CCATCTTATCGTAAAAATTTCCATAAATAATCCAAAGCAAGTGATGGTCA
 TTATCGTATGGATGCCCTTCAGTGGAGTGGTTAGATAAGGATGGCAAG
 TTGTAGCAGATGGTTTTTATACCTTATCGTTTACGTTACACACCACTAGCA
 GAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGTACTAA
 GTCACCAATCTTCCCTTACGAGCTCAGTTTGATGAACTAATCGAACAT
 TAAGCTTAGCCATGCCCTAAGGAAAGTAGTTATGTTCTTACATATCGTCTA
 CAATTAGTTTATCTCATGTTGTAAAAGATGAAGAATATGGAGATGAGAC
 TTCTTACCATTAATTTCCATATAGATCAAGAAGGTAAAGTGACACTTCTTA
 AAACAGTTAAGATAGGAGAGAGTGGGTTGCAGTAGACCTTAAGACCTTG
 ACCTTGTGTGGAAGATAAAGCTGGTAATTTTCGCAACGGTAAAAATTTGTC
 TGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATAGTAA
 TTTCTAACAATTTCAAATATTTTGATAACTTGAAAAAGAACCTATGTTT
 ATTTCTAAAGAAGGAAAGTAGTAAACAAGAATCTAGAAGAATAGCAAT
 AGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTAAAGAAATAA
 CTCAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAGTAGC
 AGAGTAGCTAAGATCATATCACCTAAACATAACGGGATTCTGTTAACCA
 TACC

SEQ ID NO. 4405

STRAIN 18RS21

GAGGAGCAAGAAATAAAAACCAAGAGCAATCACC

TGTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATA
 CTGTTGAAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAAATACAGCGAAA
 GAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTAT
 AGAAGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGGCTGATCTTG
 AAGAAGATATCCCTCTAAACCAGAGACAACCAACAATAAAGAAAGCAAT
 GTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATA
 TGAAGAGGTGAAGCCAGAAAGCAAGTCATCGCTTGTGTTCTTGATACAT
 CTAAATTAACAAAATTACAAGCCATAACCCAAAGAGGAAGGAAATGTA
 GTAGCTATTATTGATACTGGCTTTGATATTAAACATGATATTTTCGTTT
 AGATAGCCCAAAAGATGATAAGCAAGCTTTAAACCTAAGACAGAATTG
 AGGAATTAAGCAAAAACATAATATCACTTATGGGAAATGGGTTAACGAT
 AAGATTGTTTTGACATAAATACGCCAACCAATACAGAAACGGTGGCTGA
 TATTGCAGCAGCTATGAAGATGGTTATGGTTCAGAAGCAAGAAATATT
 CGCATGGTACACAGCTTGTCTGTTATTTTGTAGGTAAATAGTAAACGTTCA
 GCAATCAATGGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTT
 ATTAATGGGTATTCAGATAAAATTGATTCCGACAAATTTGGTGAAGCAT
 ATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAAT
 ATGAGTATTGGA AAAACAGCTGATTCTTAAATTGCTCTCAATGATAAAGT
 TAAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGGT
 CTGCCGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCA
 ACTAATCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATAC
 TTTGAGTGTGCTAGCTATGAATCACTTAAACATCATAGTGAGTCTGTTG
 AAACAACCTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAA
 CCTTTTGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATATGGTGC
 AAAAAAGACTTTGAAGGTAAGGACTTTAAGGTAAGATTGCATTAATTG
 AGCGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAT
 GCAGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAA
 TTTTCTAATTCCTTACCGTGAATTACCTGTGGGATTTATTAGTAAAGTAG
 ATGGCGAGCGTATAAAAAATCACTTCAAGTCAGTTAAACATTAAACAGAGT
 TTTGAAGTAgTTGATAGCTAAGGTGGAATCGTATGCTGGAACCAATCAAG
 TTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTG
 GCTTTGAATTTATCTTCAACCTATAATAATCAATACCAaCAATGTCT
 GGTACAAGTATGGCTTCAACACATGTTGCAGGATTAATGACAATGCTTCA
 AAGTCATTGGCTGAGAAATATAAAGGATGAATTTAGATTCTAAAAAAT
 TGCTAGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATAT
 AGTGAAGAGGATAAGGCGTTTATTACCACGTCAGCAAGGTGAGGTGT
 AGTTGATGCTGAAAAAGCTATCCAAGCTCAATATATATATTACTGGAACG
 ATGGCAaAGCTAAAAATTAATCTCAACGAATGGGAGATAAATTTGATATC
 ACAGTTACAATTCAaAACTGTAGAAGGTGTCAAAGAATTGTATTATCA
 AGCTAATGTAGCAACAGAAACAAGTAAATAAAGGTAATTTGCCCTTaAAC
 CACAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTcGTGATAAA
 GAAACCAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTTGTACGTTTTA
 AAGAAGCCAAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGA
 TTTAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACACCGATTATAA
 GACGATTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATA
 AAGACCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATAT
 ACTGCCCTTGTTAACACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAA
 AAATGGTGGGAGTTAGAAATAGCaCCGGAGAGTCCAAAAGAAATTTATTT
 TAGGAACCTTTTGAGAAATAAGGTTGAGGATAAAACAATTCATCTTTTGGA
 AGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAAATAAGATGG
 AAATAGGGACGAAATCACTCCCCAGGCAACCTTTCTTAAGAAATGTTAAGG
 ATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTTGGCAAAGT
 AAGGTTTTTACCATCTTATCGTAAAAATTTCCATAATATCCAAAGCAAAG
 TGATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGG
 ATGGCAAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACA
 CCAGTAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTACAAGT
 AAGTACTAAGTCACCAATCTTCTTCACGAGCTCAGTTTGTAGAACTA
 ATCGAACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTTACA
 TATCGTTTACAATTAGTTTATCTCATGTTGTAAAGATGAAGAATATGG
 GGATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGA
 CACTTCTTAAACCGGTTAAGATAGGAGAGAGTGGGTTGCGGTAGACCCCT
 AAGGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTCCGCAACGGT
 AAAATTGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAACG
 CTATAGTAATTTCTAACAGTTTCAAATATTTTGATACTTGAAGAAAGAA
 CCTATGTTTATTTCTAAAAAGAAAGTAGTAAACAAGAACTTAGAAGA
 AATAATATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTA
 AAGAAATACTAAATCAGGAAATGAGAAAGTCTCACITCTACAAACAAT
 AATAGTAGCAGAGTAGCTAAGATCATATCACTTAAACATAACGGGGATTCT
 TGTTAACCATACC

SEQ ID NO. 4406

STRAIN M732

GAGGAGCAAGAATTAAAAAACCAAGAGCAATCACCT
 GTAATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATAT
 TGTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGTGAAAG
 AAATGGGTGATACATCTGTAAAAAATGACAAACAGAAAGATGAATTATTA
 GAAGAGTTATCTAAAAACCTTGATACGCTCAATTTGGGGCTGATCTTGA
 AGAAGAAATATCCCTCTAAACCAAGAGACCAACAATAAAGAAAGCAATG
 TAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTCCCTCAGCATAT
 GAAGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATC
 TAAATAACAAAAATTACAAGCCACAACCCAAAGAGGAAAGGAAATGTAG
 TAGCTATTTATGTAAGTGGCTTTGATATTAACCATGATATTTTTCGTTTA
 GATAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAAATTTGA
 GGAATTTAAAGCAAAACATAATATCACTTATGGGAAATGGGTTAAGGATA
 AGATTGTTTGTGACATAACTACGCCAACATAACAGAAACGGTGGCTGAT
 ATTGCAGCAGCTATGAAAGATGGTTATGGGTGCAAGCAAGAAATATTTT
 GCATGGTACACAGTTGCTGGTATTTTGTAGGTAATAGTAAACGCTCCAG
 CAATCAATAGTCTTCTTTAGAAGGTGACGCGCAAAATGCTCAAGTCTTA
 TTAATGCGTATTCAGATAAAATGATTGCGGACAAATTTGGAGAAGCATA
 TGCTTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAATA
 TGAGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTT
 AAATTAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTCG
 TGCCGAAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACCATTTCAA
 CTAATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACT
 TTGAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGA
 AACAACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTTGTGACTTCTAAC
 CTTTGACAAAGGTAAGGCCCTACGATGTGGTTTATGCCAATTATGGTGCA
 AAAAAGATTTTGAAGGTAAAGCACTTTAAAGGTAAGATGCAATTAATTGAG
 CGTGGTGGTGGACTTGATTTTATGACTAAAATCACTCATGCTACAAATGC
 AGGTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAAT
 TTCTAATTCCTTACCGTGAATTAACCTGTGGGGGTTATTAGTAAAGTAGAT
 GCGAGCGGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCAAGTTT
 TGAAGTAGTTGATAGCCAAGGTGGCAATCGTATGCTGGAACAATCAAGTT
 GGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGC
 TTTGAAATTTATTTCTCAACCTATAATTAATCAATACTAAACAATGCTGG
 TACAAGTATGGCTTCAACCATGTTGAGGATTAATGACAAATGCTTCAAA
 GTCAATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTG
 CTAGAAATGCTTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAG
 TGAAGAGGATAAGGCGTTTATTCACCAGCTCAGCAAGGTGCAAGGTGATG
 TTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAACAGAT
 GGCAAGTTAAAAATTAACTCTCAACGAGAGGGAGATAAATTTGATATCAC
 AGTTACAATTCATaAACTTGTAAGAGGTGTCAAAGAAATTTGATTATCAAG
 CTAATGTAGCAACAGAAaCAAGTAAATAAAGGTAATTTGCCCTTAAACCA
 CAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTCGTATAAAGA
 AACACAAGTTTCGATTTACTATTGATGCTAGTCAATTTAGTCAGAAATTAA
 AAGACAGATGGCAAATGGTTATTTCTTAGAAGGTTTTGTACGTTTTTAA
 GAAGCCAAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGAT
 TAATGGTGATTTTGCGAACCTTACAAGCACTTGAAACaCCGATTTATAAGA
 CGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAA
 GACCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAATATAC
 TGCTTTGTTAACCAATCAGCGCTTGGGGCTATGTTGATTATGTCAAAA
 ATGGTGGGAGTTAGAAATTAGCACCGGAGAGTCCAAAAGAAATTTATTTA
 GGAACCTTTTGAAGATAAGGTTGAGGATAAAACAATTCATCTTTTGAAG
 AGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGATGGAA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

ATAGGGACGCAAAATCACTCCCCAGGCAACTTTCTTAAGAAATGTTAAGGAT
 ATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAAAGTAA
 GGTTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAGCAAAGT
 ATGGTCATTATCGTATGGATGCTCTTCAGTGGAGTGGTTTAGATAAGGAT
 GGCAAGTTGTAGCAGATGGTTTTTATACCTTATCGCTTACGTTACACACC
 AGTAGCAGAAGGAGCaAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAA
 GTACTAAGTCACCAAACTTTCCTTCACGAGCTCAGTTTGTAGAACTAAT
 CGAACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATA
 TCGTTTACAATTAGTTTTATCTCATGTTGTAAAAGATGAAGAATATGGGG
 ATGAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACA
 CTTCTTAAAACGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCTTAA
 GGCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAA
 AATTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAACCGCT
 ATAGTAAATTTCTAACAGTTTCAAATATTTTGATACTTGAAGAAAGAACCC
 TAGTTTTATTCTTAAAGAAAGGAAAGTAGTAAACAAGAATCTAGAAGAAA
 TAACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAA
 GAAATAACTAAATCAGGAAATGAGAAAGTCCTCACTTCTACAAACAATAA
 TAGTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTG
 TTAACCATACC

SEQ ID NO. 4407

STRAIN COH1

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTaACTACTAATATTG
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
 ATGGGcGATACATCTGTAATAAAATGACAAAAACAGAAGATGAATTATTAGA
 AGAGTTATCTAAAAACCTTGATACGCTCTAATTTGGGGGCTGATCTTGAAG
 AAGAAATATCCCTCTAAACCAGAGaCAACCAACAATAAAGAAAGCAATGTA
 GTAACAAATGCTTCACTGCAATAGCACAGAAAGTTCCTCAGCATATGA
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTA
 AAATAACAAAATTACAAGCCCAACCCAAAGAGGAAAGGGAATAGTAGTA
 GCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCGTTTAGA
 TAGCCCAAAAGATGATAAGCACAGCTTTAAAACTAAGGCAGAAATTGAGG
 AATTAAGCAAAACATAATATCACTTATGGGAATGGGTTAACGATAAG
 ATTGTTTTTGCACATAACTACGCCaCAATACAGAAACGGTGGCTGATAT
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAATATTTTGC
 ATGGTTACACAGCTTGCTGGTATTTTGTAGGTAATAGTAAACGTCACGCA
 ATCAATAGTCTTCTTTAGAAAGGTGCAGCGCCAAATGCTCAAGTCTTATT
 AATGCGTATTCCAGATAAAATGATTCGGACAAATTTGGAGAAGCATATG
 CTAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAACGATTAAATATG
 AGCCTGGGAAAAACGGCTGATTCTTTAATTGCTCTCAATGATAAAGTTAA
 ATTAGCACITTAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTGTGGCTG
 CCGGAAATGAAGGTGCATTGTTGATTTAGGATTATAGCAAAACCTTATCACT
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
 GAGTGTGTGCTAGCTATGAATCACTTAAAACTACAGTGAAGGTGCTTGA
 CAATATTGAAGGTAAGTTAGTTAAGTTGCGGATTGTGACTTCTAAACCT
 TcTGACAAAGGTAAGGCCTACGATGTGGTTTATGCCAATTATGGTGCAAA
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATTGAGCG
 TGGTGGTGGACTTGATTATTATGACTAAAATCACTCATGCTACAAATGCA
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTTGGAATTTT
 CTAATTCCTTACCGTGAATTACCTGCGGGGTTATTAGTAAAGTAGATGG
 CGAGCGTATAAAAAATCTTCAAGTCAGTTAAACATTTAAACAGAGTTTGT
 AAGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAAACAACTCAAGTTGG
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
 TGAaATTATTCTTCAACCTATAATAATCAATACTAAACAATGTCTGGTA
 CRAAGTATGGCTTCAACCATGTTGCAGGATTAATGACAATGCTTCAAAGT
 CATTTGGCTGAGAAATATAAGGGATGAATTTAGATTCTaAAAAATTGCT
 AGaTTGCTCTaAaAACATCCTCATGAGCTCAGCAACAGCATTATATAGT
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT
 GATGCTGAAAAAGCTATCCAAGCTCAATATATGTTACTGGAAACGATGG
 CAAAGTTAAAATTAATCTCAAAACGAGAGGGAGATAAATTTGATATCACAG
 TTACAATTCATaAACTTGTAAGAGGTGTCAAGAAATTGATTATCAAGCT
 AATGTAGCAaCAGAACAAGTAAATAAAGGTAATTTGCCCTTAAACCCACA
 AGCCTTGCTAGATACTAATGGCAGAAAGTAAATCTTcGTGATAAGAAA
 CACAAGTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTA
 GAACAGATGGCAAAATGGTTATTTCTTAGAAGGTTTGTACGTTTAAAGA
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCTTTTGTAGGATTAA
 ATGGTGAATTTGCGAAGCTTACAAGCACTTGAACACCGATTATAAGACG
 CTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACTCATAAAGA
 CCAATTTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACCTATACTG
 CCTTTGTTAAACACAATCAGCGCTTTGGGGCTATGTTGATTATGTCAAAAAT
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAATTATTTTAGG
 aACTTTTGAGAAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAGAG
 ATGCAGCGAATAATCCATATTTTGCCATTTCTCCTAAATAAAGATGGAAT
 AGGAGCGAAATCACTCCCCAGGCaCTTTCTTAAGAAATGTTAAGGATAT
 TTCTGCTCAAGTCTTAGATCAAAATGGAAATGTTATTGGCAAAGTAAGG
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAGCAAAAGTGAT
 GGTCAATTATCGTATGGATGCTCTTCAGTGGAGTGGTTAGATAAGGATGG
 CAAAGTTGTAgCAGATGGTTTATATACTTATCGCTTACGTTACACACCAG
 TAGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTTaAGTTCAAGTAAGT
 AcTAAGTCACCAAACTCTTCTTCACGAGCTCAGTTTGATGaAACTAATCG
 AACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATC
 GTTACAATTAGTTTTATCTCATGCTTTGTAAGAGTAGAAGATATGGGAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
 TCCTAAACGGTTAAGTAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG
 CCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAA
 TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTAT
 AGTAATTTCTAACAGTTTCAAAATATTTTGATAACTTGAAAGAAAGAACCTA
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAGAATCTAGAAGAAATA
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT
 AACCATACC

SEQ ID NO. 4408

STRAIN M781

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGT
 AATTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACCTACTAATATTG
 TTGAAAAAACATCTGTAACAGCTGCTTCTGCTAGTAATACAGTGAAAGAA
 ATGGGTGATACATCTGTAAAAATGACAAACAGAGATGAATTAATTAGA
 AGAGTTATCTAAAAACCTTGATACGTTCTAATTTGGGGCTGATCTTGAAG
 AAGAATATCCCTCTAAACCAGAGACAACCAACATAAAGAAAGCAATGTA
 GTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGA
 AGAGGTGAAGTCAGAAAGCAAGTCATCGCTTGTCTGTTCTTGATACATCTA
 AAATAACAAAAATTACAGGCCAACCCAAAGAGGAAAGGGAATGTAGTA
 GCTATTATTGATACTGGCTTTGATATTAACCATGATATTTTTCGTTTAGA
 TAGCCCAAAAGATGATAAGCACAGCTTTAAACTAAGGCAGAAATTTGAGG
 AATTAAGCAAAAACATAATATCATTTATGGGAAATGGGTTAACGATAAG
 ATTGTTTTTGACATTAACCTACGCCAACCAATACAGAAACGGTGGCTGATAT
 TGCAGCAGCTATGAAAGATGGTTATGGGTGAGAGCAAGAAATATTTTGC
 ATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACCGTCCAGCA
 ATCAATAGTCTTCTTTAGAAGGTGCAGCGCCAAATGCTCAAGTCTTATT
 AATGGGTATTTCCAGATAAAATTGATTCGGACAAATTTGGAGAAGCATATG
 CTAAAGCAATCATAGACGCTGTTAATCTAGGAGCAAAAACGATTAATATG
 AGCCTGGGAAAAACCGCTGATTCTTAATTGCTCTCAATGATAAAGTTAA
 ATTAGCACTTAAATTAGCTTTCTGAGAAGGGCGTTGCAATTGTTGGGCTG
 CCGGAAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACCATTTATCACT
 AATCCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTT
 GAGTGTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAAGA
 CAACCTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTCTCTAAACCT
 TTTGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGGTGCAAA
 AAAGATTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAATTGAGCG
 TGGTGGTGGACTTGATTTTATGACTAAAACTCACTCATGCTACAAATCAG
 GTGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTT
 CTAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGG
 CGAGCGTATAAAAACTCTCAAGTCAGTTAACATTAAACAGAGTTTGTg
 AAGTAGTTGATAGCCAGGTGGCAATCGTATGCTGGAAACATCAAGTTGG
 GCGGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCTGGCTT
 TGAAATTTATCTTCAACCTATAAATCAATCACTAAACCAATGTCTGGTA
 CAAGTATGGCTTCAACCATGTTGAGGATTAATGACAATGCTTCAAAGT
 CATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATTGCT
 AGAATTGTCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTG
 AAGAGGATAAGGCGTTTTATTACCACGTCAGCAAGGTGCAGGTGTAGTT
 GATGCTGAAAAAGCTATCCAGGCTCAATATTATGTTACTGGAACCGATGG
 CAAAGTTAAAAATTAACTCTCAAACGAGAGGGAGATAAATTTGATATCAG
 TTACAATTCATaaACTTGTAGAAGGTGTCAAAGAATTGTATTATCAAGCT
 AATGTAGCaaCAGAAACAGTAAATaaAGGTAATTTGCCCTTaaCCaCA
 AGCCTTGTCTAGATACATTTGGCAGaaAGTaaATTCTTcGTGATAAAGAAA
 CACAAGTTcGATTTACTATcTGATGCTAGTCAATTTAGTCAGAAATTAAAA
 GAACAGATGGCAAAATGGTTATTCTTGAAGGTTTGTACGTTTAAAGA
 AGCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTTA
 ATGGTGATTTTGGCAACTcACAAGCACTTGAACACCGATTTATAAGACG
 CTTTCTAAAGGTAGTTCTACTATAaaCCAAATGATACAACTCATAAAGA
 CCAATTGGAGTACAATGAATCAGCTCCTTTTGAAGCAACACTATACTG
 CCTTGTTTAAACAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAT
 GGTGGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAATATTTTAGG
 AACTTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTGGAAAGAG
 ATGCAGCGAATAATCCATATTTTGCATTTCTCCAATAAAGATGGAAAT
 AGGGACGaaATCACTCCCCAGGCaACTTCTTAAGAAATGTTAAGGATAT
 TTCTGCTCAAGTCTTAGATCAAAATGGAATGTTATTTGGCAAAGTAAGG
 TTTTACCATCTTATCGTAAAAATTTCCATAATaATCCAAAGCAAGTGAT
 GGTCAATTATCGTATGGATGCTCTTCACTGGAGTGGTTTAGATAAGGATGG
 CAAAGTTGTAGCAGATGGTTTATACTTATCGCTTACGTTACACACCAG
 TAGCAGAGGAGCAAAATAGTCAGGAGTCAGACTTTAAAGTTCAAGTAAGT
 ACTAAGTCACCAATCTTCCCTTACGAGCTCAGTTTGATGAAACTAATCG
 AACATTAAAGCTTAGCCATGCTTAAGGAAAGTAGTTATGTTCTCATATC
 GTTTACAATTAGTTTATCTCATGTGTGTAAGATGAAGAAATATGGGGAT
 GAGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACT
 TCCTAAACCGGTTAAGATAGGAGAGAGTGAGGTTGCGGTAGACCCCTAAGG
 CCTTGACACTTGTGTGGAAGATAAAGCTGTAATTTTGCAACGGTAAAA
 TTGTCTGACCTCTTGAATAAGGCAGTAGTATCAGACAAAGAAAACGCTAT
 AGTAATTTCTAACAGTTTCAAAATATTTTGATAACTTGAAAGAAAGAACCTA
 TGTTTATTTCTAAAGAAGGAAAAGTAGTAAACAAGAAATCTAGAAGAAATA
 ACATTAGTTAAGCCTCAAACTACAGTTACTACTCAATCATTTGTCTAAAGA
 AATAACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATA
 GTAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

AACCATACC

SEQ ID NO. 4409

STRAIN CJB110

GAGGAGCAAGAATTAAAAACCAAGAGCAATCACCTGTAA
 TTGCTAAATGTTGCTCAACAGCCATCGCCATCGGTAACACTAATATTGTT
 GAAAAAATCATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCGAAAGAAAT
 GGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAATTTATGAAG
 AGTTATCTAAAAACCTTGATACGTCTAATWGGGGGCTGATCTTGAAGAA
 GAATATCCCTCTAAACAGAGACCAACCAATAAAGAAAGCAATGTAGT
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCGTATGAAG
 AGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTTTTGATACATCTAAA
 ATAACAAAATTGCAAGCCATAACCCAAAGAGGAAAGGAAATGTAGTAGC
 TATTATTGATCTGGCTTTGATATTAAACCATGATTTTTTCGTTTAGATA
 GCCCAAAGATGATAAGCACAGCTTTAAACTTAAAGCAGAATTCGAGGAA
 CTAAAGCAAAACATAATATCACTTTATGGGAATGGGTAAACGATAAGAT
 TGTTTTTGCACATAACTACGCCAACAAATACAGAAACGGTGGCTGATATTG
 CAGCAGCTATGAAAGATGGTTATGGGTGAGAAGCAAGAAATATTTTCGAT
 GGTACACACGTTGCTGGTATTTTTGTAGGTAAATAGTAAACGTCAGCAAT
 CAATGGTCTTTCTTTAGAGGTGCGCGCAATGCTCAAGTCTTATTA
 TGCGTATTCAGATAAAATTGATTGCGGCAAAATTTGGAGAAGCATATGCT
 AAAGCAATCACAGACGCTCTTAATCTAGGAGCAAAACGATTAAATATGAG
 CCTTGGAAAAACAGCAGATTCTTAATTCACCTCAATGATAAAGTTAAAT
 TAGCACTTAAATTAGCTTCTGAGAAGGGCGTTGCAAGTTGTTGTTGGCTGCC
 GGAATGAAGGTGCAATTTGGTATGGATTATAGCAAAACATTATCAACTAA
 TCTGACTACGGTACGGTTAATAGTCCAGCTATTTCTGAAGATACTTTGA
 GTGTTGCTAGCTATGAATCACTTAAACTATCAGTGAGGTGCTTGAACA
 ACTATTGAAGGTAAAGTTAGTTAAGTTGCGGATTGTGACTTCTAAACCTTT
 TGACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTTATGGTGCAAAAA
 AAGACTTTGAAGGTAAAGGACTTTAAAGGTAAAGATTGCATTAATTTAGCGT
 GGTGGTGCACTTGAATTTATGACTAAAATCACTCATGCTACAAATGCAGG
 TGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTT
 TAATTCCTTACCGTGAATTACCTGTGGGGTTATTAGTAAAGTAGATGGC
 GAGCGTATAAAAAATACITCAAGTCAGTTAACATTTAACCAAGTTTGA
 AGTAGTTGATAGCCAAAGGTGGCAATCGTATGCTGGAACCAATCAAGTGGG
 CGGTGACAGCTGAAGGAGCAATCAAGCCGTGATGTAACAGCTTCTGGCTTT
 GAAATTTTATTTCAACCTATAATAATCAATACCAAAACAAATGTCTGGTAC
 AAGTAGGCTTCAACCATGTTGCAAGGATTAATGCAATGCTTCAAAATC
 ATTTGGCTGAGAAATATAAAGGGATGAATTTAGATTCTAAAAAATGCTA
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
 AGAGGATTAAGCGTTTATTCAACAGCTCAGCAAGGTGCGAGGTGATGTTG
 ATGCTGAAAAAGCTATCCAAGCTCAATATTTATGTTACTGGAACAGATGGC
 AAAGCTAAAAATTAATCTCAACGAGTGGGAGATAAATTTGATATCACAGT
 TACAATTCATAAATTTGTAAGGTGTCAGGAATTTGATTTATCAAGCTA
 ATGTAGCAACAGAACCAAGTAAATAAAGTAAATTTGCCCTTAAACCAAC
 CCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTTGTGATAAAGAAAC
 ACAAGTTGATTTACTATGATGCTAGTCAATTTAGTCAGAAATTAAGAG
 AACAGATGGCAAAATGGTTATTTCTAGAGGTTTTGTACGTTTAAAGAA
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTGTAGGATTTAA
 TGGTGATTTTGCAGACTACAGCACTTGAACACCGGATTTATAAGACGC
 TTTCTAAAGGTAGTCTCTACTATAAACCAATGATACAACTCATAAGAC
 CAATTTGGAGTACAATGAATCAGCTCTTTTGAAGCAACAACTATACCTGC
 CTGTTTAACCAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAAAATG
 GTGGGAGTTAGAATTAGCACCGGAGAGTCCAAAAAGAAATTTATTTAGGA
 ACTTTTGAGAATAAGGTTGAGGATAAAACAAATTCATCTTTTGGAAAGAGA
 TGCAGCAATAATCCATATTTTGCCATTTCTCCAAATAAAGATGGAATA
 GGGATGAATCACTCCCGAGCAACTTTCTTAAGAAATGTTAAGGATATT
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGT
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAGTGATG
 GTCATTTATCGTATGGATGCCCTTCAGTGGAGTGGTTTAgATAAGGATGGC
 AAAGTTGTAGCAGATGGTTTTTATACTTATCGCCTACGTTACACACCAGT
 AGCAGAAAGGAGCAATAGTCAGGAGTCAGCTTTAAAGTTCAAGTAAGTA
 CTAAGTCACCAATCTTCTTTACTAGCTCAGTTTGATGAAACTAATCGA
 ACATTAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTCATATATCG
 TTTACAATTAGTTTATCTCATGTTGTAAAAGATGAAGAAATATGGGGATG
 AGACTTCTTACCATTATTTCCATATAGATCAAGAAGGTAAAGTGACACTT
 CCTAAAAACGGTTAAGATAGGAGAGAGTGGGTTGAGTAGACCTTAAGGC
 CTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTTGCAACGGTAAAT
 TGTCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAAACGCTATA
 GTAATTTCTAACAGTTTCAATATTTTGATAACTTGAAAAAAGAACTAT
 GTTTATTTCTAAAGAAGGAAAGTAGTAAACAAGAACTAGAAAGAAATAA
 CATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTTGTCTAAAGAA
 ATAATAAATCAGGAAATGAGAAAGTCTCACTCTACAAACAATAATAG
 TAGCAGAGTAGCTAAGATCATATCACCTAAACATAACGGGGATTCTGTTA
 ACCATACC

SEQ ID NO. 4410

STRAIN 1169NT

GAGGAGCAAGAATTAAAAACCAAGAGCAATC

ACCTGTAATTTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACACTA
 ATATTGTTGAAAAACATCTGTAAACAGCTGCTTCTGCTAGTAATACAGCG
 AAAGAAATGGGTGATACATCTGTAAAAAATGACAAAACAGAAGATGAAT
 ATTAGAAGAGTTATCTAAAAACCTTGATACGCTAATATGGGGGCTGATC

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

TTGAAGAAGAAATATCCCTCTAAACCAGAGACAACCAACAATAAGGAAAGC
 AATGTAGTAACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGC
 ATATGAAGAGGTGAAGCCAAAAGCAAGTCATCGCTTGCTGTTCTTGATA
 CATCTAAATAACAAATTTGCAAGCCATAACCCAAAGAGGAAAGGAAAT
 GTAGTAGCTATTATTGATACTGGCTTTGATATTAAACCATGATATTTTCG
 TTTAGATAGCCCAAAAGATGATAAGCACAGCTTTAAAAATAAGGCAGAAT
 TCGAGGAATTAAGCAAAACATAATATCATTATGGGAAATGGGTTAAC
 GATAAGATTGTTTTTGCACATAAAGTACGCCAACATACAGAAACGGTGGC
 TGATATTGCAGCAGCTATGAAAGATGGTTATGGTTGAGAGCAAAAGAAAT
 TTTCCGATGGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAACGT
 CCAGCAATCAATGGTCTTCTTTAGAGGTGCAGCGCCAAATGCTCAAGT
 CTTATTATGGCTATTCCAGATAAAATGATTTCGGACAAATTCGGAGAAG
 CATATGCTAAAGCAATCACAGACGCTGTTAATCTAGGAGCTAAACGATT
 AATATGAGTATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAA
 AGTTAAATTAGCACTTAAATTAGCTTCTGAGAGGGCGTTGAGTTGTTG
 TGGCTGCGGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACCGTTA
 TCAACTAATCTGACTACGGTACGGTAAATAGTCCAGCTATTTCTGAAGA
 TACTTTGAGTGTGCTAGCTATGAATCACTTAAACATCAGTGAAGTGG
 TTGAACAACATATTGAAGGTAAAGTTAGTTAAGTTCGCCATTGCGATTCT
 AAACCTTTTACAAAGGTAAAGCCTACGATGTGGTTTATGCCAATTATGG
 TGCAAAAAAGACTTTGAAGGTAAAGACTTTAAAGGTAAAGTTGCATTAA
 TTGAGCGTGGTGGTGGACTTGATTTATGACTAAATCACTCATGCTACA
 AATGCAGGTGTGTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGG
 AAATTTTCTAATTCCTTACCGTGAATTACCTGTGGGGTTTATTAGTAAAG
 TAGATGGCGAGCGTATAAAAAATACCTCAAGTCAGTTAAACATTTAACCAg
 AGATTTGAAGTAGTTGATAGCCAAAGTGGCAATCGTATGCTGGAACCAATC
 aAGTTGGGGCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAAACAGCTT
 CTGGCTTCGAATTTATTTCTTCTCaaCCTATAATAATCAATCAACCAATG
 TCTGGTACAAGTATGGCTTCCACCATGTTGCAGGATTAATGACAATGCT
 TCAAGTCATTGGCTGAGaAATATAAGGGATGAATTTAGATTCTAAaAA
 AATTGCTAGAAATTTCTAAAAACATCCCTCATGAGCTCAGCAACAGCATT
 TATAGTGAAGAGGATAAGGCGTTTTATTCAACAGTCAGCAAGGTCAGG
 TGATGTTGATGCTGAAAAAGCTATCCAAGCTCAATATTATGTTACTGGAA
 ACGATGGCAAGCTAAATTAATCTCAACAGAGTGGGAGATAAATTTGAT
 ATCAGCTTACATTCATAAACTTGTAGAAGGTGTCAAAGAATTGTATTA
 TCAAGCTAATGTAGCAACAGAACAGTAAATAAAGGTAAATTTGCCCTTA
 AACCAAGCCTTGCTAGATACTAATTGGCAGAAAGTAATTTCTTcGTAT
 AAAGAAACACAAGTTGATTTACTATTGATGCTAGTCAATTTAGTcAGAA
 ATTAAAAAGAACAGATGGCAAATGGTTATTTCTTAgAAGGTTTGTACGTT
 TTAAGAAGCTAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTA
 GGAATTTAATGGTGATTTTGGAGCTTACAAGCACTTGAACACCGATTTA
 TAAGACGCTTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAATC
 ATAAAGCAATTTGGAGTATAATGAATCAGCTCCTTTTGAAAGCAACAAC
 TATATGCTGCTTTAAACACAATCAGCGTCTTGGGGCTATGTTGATATGT
 CaAAAAATGGTGGGAGTTAGAATTAGCACCGGAGAGTcCAAAAGAAATTA
 TTTTAGGAACCTTTGAGAATAAGGTTGAGGATAAAACAATTCATCTTTTG
 GAAAGAGATGCAGCGAATAATCCATATTTTGCCATTTCTCCAATAAAGA
 TGGAAATAGGGATGAAATCACTCCCAAGGCAACTTTCTTAAGAAATGTTA
 AGGATATTTCTGCTCAAGTTCTAGATCAAAATGGAAATGTTATTGGCAA
 AGTAAGGTTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCA
 AGTGATGGTCATTATCGTATGGATGCCCTTCAGTGGAGTGGTTAgATA
 AGGATGGCAAGTTGTAGCAGATGGTTTTTACTTATCGCTTACGTTAC
 ACACAGTAGCAGAAGGAGCAATAGTCAGGAGTCAGACTTTAAAGTTCA
 AGTAAGTACTAAGTCACCAATCTTCTTCAAGAGCTCAGTTTGATGAaA
 CTAATCGAACATTAAAGCTTAGCCATGCCTAAGGGAAGTAGTTATGTTCT
 ATATATCGCTACCAATTAGTTTATCTCATGTTGTAAAGATGAAGAATA
 TGGAGATGAGACTTCTACTATTATTTCCATATAGATCAAGAAGGTAAAG
 CGACACTTCTTAAACCGGTTAAGATAGGAGAGAGTGAGTTGCAGTAGAC
 CCTAAGGCCCTTGACACTTGTGTGGAAGATAAAGCTGGTAATTTGCGCaC
 GGTAAATTTGCTGACCTCTTGAATAAGGCAGTAGTATCAGAGAAAGAAA
 ACGCTATAGTAATTTCTAACAGTTTCAAATATTTTGATAACTTGAAAAAA
 GAACCTATGTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAACTTAGA
 AGAaATAATATTAGTTAAGCCGCaCACTACAGTTACTACTCaATCATTGT
 CTAAGAATAAATACTAAATCAGGAAATGAGAAAGTCTCACTTCTACAAAC
 AATAATAGTAGTAGTAGCTAAAATCATATCACCTTAAACATAATGGGGA
 TTCGTTTAAACATACC

SEQ ID NO. 4411

STRAIN JM9130013

GAGGAGCAAGAATTAACCAAGAGCAATCACCTGTAA
 TTGCTAATGTTGCTCAACAGCCATCGCCATCGGTAACTACTAATACTGTT
 GAAAAAATCATCTGTAAAGCTGCTTCTGCTAGTAAATACAGCGAAAGAAAT
 GGGTGATACATCTGTAATAAATGACAAAACAGAAAGATGAATATTAGAAg
 AGTTATCTAAAAACCTTGATACGTCTAATTTGGGGGCTGATCTGAAGAA
 GAATATCCCTCTAAACAGAGACAACCAACAATAAAGAAAGCAATGTAGT
 AACAAATGCTTCAACTGCAATAGCACAGAAAGTTCCCTCAGCATATGAAG
 AGGTGAAGCCAGAAAGCAAGTCATCGCTTGCTGTTCTTGATACATCTAAA
 ATAAACAAATTAACAAGCCATAACCAAGAGGAAAGGGAAATGTAGTAGC
 TATTATTGATACCTGGCTTGATATTAAACATGATATTTTCGTTTAGATA
 GCCCAAGAGATGATAAGCACAGCTTAAACTAAGACAGAATTTGAGGAA
 TTAAAGCAAAACATAATATCATTATGGGAAATGGGTTAACGATAAGAT
 TGTTTTTGCACATAACTACGCCAACATACAGAAACGGTGGCTGATATTG
 CAGCAGCTAGAAAGATGGTTATGGTTAGAGCAAGCAAGAAATTTTCGCAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

GGTACACACGTTGCTGGTATTTTGTAGGTAATAGTAAACGTCAGCAAT
 CAATGGTCTTCTTTAGAGGTCAGCGCCAAATGCTCAAGTCTTATTA
 TGCGTATCCAGATAAAATTGATTCGGACAAATTGGTGAAGCATATGCT
 AAAGCAATCACAGACGCTGTTAATCTAGGAGCAAAAACGATTAAATAGAG
 TATTGAAAAACAGCTGATTCTTTAATTTGCTCTCAATGATAAAGTTAAAT
 TAGCACTTAAATTAGCTTCTGAGAAAGGCGTTCAGTTGTTGGCTGCC
 GGAAATGAAGGCGCATTTGGTATGGATTATAGCAAAACATTATCAACTAA
 TCCTGACTACGGTACGGTTAATAGTCCAGCTATTCTGAAGATACTTTGA
 GTGTTGCTAGCTATGAATCACTTAAAACTATCAGTGAGGTCGTTGAAACA
 ACTATTGAAGGTAAGTTAGTTAAGTTGCCGATTGTGACTTCTAAACCTTT
 TGACAAAGGTAAGGCTACGATGTGGTTTATGCCAATTATGGTGCAAAAA
 AAGACTTTGAAGGTAAGGACTTTAAAGGTAAGATTGCATTAAATGAGCGT
 GGTGGTGGACTTGATTATGACTAAAATCACTCATGTACAAATGACAGG
 TGTTGTTGGTATCGTTATTTTAAACGATCAAGAAAAACGTGGAAATTTTC
 TAATTCCTTACCGTGAATTACCTGTGGGGATTATTAGTAAAGTAGATGGC
 GAGCGTATAAAAAATACTTCAAGTCAGTTAACATTTAACCCAGAGTTTGA
 AGTAGTTGATAGCAAGGTCGTAATCGTATGCTGGAACAAATCAAGTTGGG
 GCGTGACAGCTGAAGGAGCAATCAAGCCTGATGTAACAGCTTCGCGCTTT
 GAAATTTATTTCTCAACCTATAATAATCAATACCAAAACATGCTCGGTAC
 AAGTATGGCTTACCACATGTTGACGAGTAAATGACAAATGCTTCAAGTC
 ATTTGGCTGAGAAATATAAAGGGAATGAATTTAGATTCTAAAAAATTGCTA
 GAATTTGCTAAAAACATCCTCATGAGCTCAGCAACAGCATTATATAGTGA
 AGAGGATAAGGCGTTTATTCCACACGTCAGCAAGGTCAGGTTAGTTG
 ATGCTGAAAAAGCTATCCAAAGCTCAATATTATATTCTGGAACGATGGC
 AAAGCTAAAATTAATCTCAACGAATGGGAGATAAATTTGATATCACAGT
 TACAATTCATAAATCTGTAGAAGGTGTCAAGAAATGTATTATCAAGCTA
 ATGTAGCAACAGAACAGTAAATAAAGGTAATTTGCCCTTAACCCACAA
 GCCTTGCTAGATACTAATTTGGCAGAAAGTAATTTCTTGTGATAAAGAAC
 ACAAGTTTCGATTACTATTGATGCTAGTCAATTTAGTCAGAAATTAAGAG
 AACAGATGGCAATGGTTATTTCTTGAAGGTTTGTACGTTTAAAGAA
 GCCAAGGATAGTAATCAGGAGTTAATGAGTATTCCTTTTGTAGGATTAA
 TGGTGAATTTTGGCACTTACAAGCACTTGAACACCCGATTATAAGACGC
 TTTCTAAAGGTAGTTTCTACTATAAACCAATGATACAACCTATAAGAC
 CAATTTGAGTACAATGAATCAGCTCCTTTTGAAGCAACAACTATACTGC
 CTTGTTAAACAAATCAGCGTCTTGGGGCTATGTTGATTATGTCAAAATG
 GTGGGAGTTAGAAATAGCACCCGAGAGTCCAAAAAGAAATTTATTTAGGA
 ACTTTTGAGAAATAGGTTGAGGATAAAACAAATTCATCTTTTGGAAGAGA
 TGCAGGAAATATCCATATTTGCCATTTCTCCAAATAAGATGGAATA
 GGCACGAATCACTCCCGAGCAACTTTCTTAAGAAATGTTAAGGATATT
 TCTGCTCAAGTTCTAGATCAAAATGGAATGTTATTTGGCAAGTAAGGT
 TTTACCATCTTATCGTAAAAATTTCCATAATAATCCAAAGCAAGTGATG
 GTCAATTATCGTATGGATGCTCTTCAAGTGGAGTGGTTTAGATAAGGATGGC
 AAAGTTGTAGCAGATGGTTTATATCTATCGCTTACGTTACACACCACT
 AGCAGAAGGAGCAAAATAGTCAGGAGTCAGACTTAAAGTACAAGTAAGTA
 CTAAGTCACCAAAATCTTCTTACGAGCTCAGTTTGTGAACTAATCGA
 ACATTAAAGCTTAGCCATGCCTAAGGAAAGTAGTTATGTTCTACATATCG
 TTTACAATTAGTTTATCTCATGTTGTAAAGATGAAGAAATAGGGGATG
 AGACTTCTTACCATTTATTTCCATATAGATCAAGAAGGTAAGTGACACTT
 CCTAAAAACGGTTAAGATAGGAGAGTGAAGTTGCGGTAGACCCCTAAGGC
 CTGTGACCTTGTGTGAAGATAAAGCTGGTAATTTGCGCAACGGTAAAT
 TGTCTGATCTCTGAATAAGGCAGTAGTATCAGAGAAAGAAACGCTATA
 GTAATTTCTAACAGTTTCAAAATTTTGTAACTTGAAGAAAGAAACCTAT
 GTTTATTTCTAAAAAGAAAAAGTAGTAAACAAGAATCTAGAAGAAATAA
 TATTAGTTAAGCCGCAAACTACAGTTACTACTCAATCATTGTCTAAAGAA
 ATAACATAATCAGGAAATGAGAAAGTCTCACTTCTACAAACAATAATAG
 TAGCAGAGTAGCTAAGATCATATCACTTAAACATAACGGGATTTCTGTTA
 ACCATACC

PRETTY of: /biotmp/msa183564.2{*} May 13, 2003 03:28 ...

	1	50
msa183564.2{147_COH1}	-----	-----
msa183564.2{147_M732}	-----	-----
msa183564.2{147_M781}	-----	-----
msa183564.2{147_2603}	gtggataaac atcactcaaa aaaggctatt tttaaggttaa cacttataac	
msa183564.2{147_JM9130013}	-----	-----
msa183564.2{147_18RS21}	-----	-----
msa183564.2{147_090}	-----	-----
msa183564.2{147_CJB110}	-----	-----
msa183564.2{147_A909}	-----	-----
msa183564.2{147_H36B}	-----	-----
msa183564.2{147_1169NT}	-----	-----
Consensus	*****	*****

	51	100
msa183564.2{147_COH1}	-----	GAGGAGCAAG
msa183564.2{147_M732}	-----	GAGGAGCAAG
msa183564.2{147_M781}	-----	GAGGAGCAAG
msa183564.2{147_2603}	aactagtatt ttattaatgc atagcaatca agtgaatgca	GAGGAGCAAG
msa183564.2{147_JM9130013}	-----	GAGGAGCAAG
msa183564.2{147_18RS21}	-----	GAGGAGCAAG
msa183564.2{147_090}	-----	GAGGAGCAAG
msa183564.2{147_CJB110}	-----	GAGGAGCAAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_A909}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_H36B}	-----	-----	-----	-----	GAGGAGCAAG
msa183564.2{147_1169NT}	-----	-----	-----	-----	GAGGAGCAAG
Consensus	*****	*****	*****	*****	*****
101					
msa183564.2{147_COH1}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M732}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_M781}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_2603}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_JM9130013}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_18RS21}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_090}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_CJB110}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_A909}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_H36B}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
msa183564.2{147_1169NT}	AATTAAAAA	CCAAGAGCAA	TCACCTGTAA	TTGCTAATGT	TGCTCAACAG
Consensus	*****	*****	*****	*****	*****
151					
msa183564.2{147_COH1}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M732}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_M781}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_2603}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_JM9130013}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_18RS21}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_090}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_CJB110}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_A909}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_H36B}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
msa183564.2{147_1169NT}	CCATCGCCAT	CGGTAACCTAC	TAATATGTGT	GAAAAAACAT	CTGTAAcAgC
Consensus	*****	*****	*****	*****	*****
201					
msa183564.2{147_COH1}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M732}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_M781}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_2603}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_JM9130013}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_18RS21}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_090}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_CJB110}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_A909}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_H36B}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
msa183564.2{147_1169NT}	TGCTTCTGCT	AGTAATACAG	tGAAAGAAAT	GGGTGATACA	TCTGTAAAAA
Consensus	*****	*****	*****	*****	*****
251					
msa183564.2{147_COH1}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M732}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_M781}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_2603}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_JM9130013}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_18RS21}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_090}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_CJB110}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_A909}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_H36B}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
msa183564.2{147_1169NT}	ATGACAAAAC	AGAAGATGAA	TTATTAGAAG	AGTTATCTAA	AAACCTTGAT
Consensus	*****	*****	*****	*****	*****
301					
msa183564.2{147_COH1}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M732}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_M781}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_2603}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_JM9130013}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_18RS21}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_090}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_CJB110}	ACGTCTAATw	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_A909}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_H36B}	ACGTCTAATt	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
msa183564.2{147_1169NT}	ACGTCTAATA	TGGGGGCTGA	TCTTGAAGAA	GAATATCCCT	CTAAACCAGA
Consensus	*****	*****	*****	*****	*****
351					
msa183564.2{147_COH1}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M732}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_M781}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_2603}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_JM9130013}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_18RS21}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG
msa183564.2{147_090}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_CJB110}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_A909}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_H36B}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
msa183564.2{147_1169NT}	GACAACCAAC	AATAAaGAAA	GCAATGTAGT	AACAAATGCT	TCAACTGCAA
Consensus	*****	*****	*****	*****	*****
401					450
msa183564.2{147_COH1}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M732}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_M781}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGtC	AgAAAGCAAG
msa183564.2{147_2603}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_JM9130013}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_18RS21}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_090}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_CJB110}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_A909}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_H36B}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
msa183564.2{147_1169NT}	TAGCACAGAA	AGTTCCTCA	GCaTATGAAG	AGGTGAAGcC	AgAAAGCAAG
Consensus	*****	*****	**-----	*****-	*-----
451					500
msa183564.2{147_COH1}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M732}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_M781}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_2603}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_JM9130013}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_18RS21}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TaCAAGCCAc
msa183564.2{147_090}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_CJB110}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_A909}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_H36B}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
msa183564.2{147_1169NT}	TCATCgCTTG	CTGTTcTTGA	TACATCTAAA	ATAACAAAAT	TgCAAGCCAc
Consensus	*****	*****	*****	*****	*-----
501					550
msa183564.2{147_COH1}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_M732}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_M781}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_2603}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_JM9130013}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_18RS21}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_090}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_CJB110}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_A909}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_H36B}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
msa183564.2{147_1169NT}	AACCCAAAGA	GGAAAGGGAA	ATGTAGTAGC	TATTATTGAT	ACTGGCCTTG
Consensus	*****	*****	*****	*****	*****
551					600
msa183564.2{147_COH1}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M732}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_M781}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_2603}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_JM9130013}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_18RS21}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_090}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_CJB110}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_A909}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_H36B}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
msa183564.2{147_1169NT}	ATATTAAACCA	TGATATTTT	CGTTTAGATA	GCCCAAAAGA	TGATAAGCAC
Consensus	*****	*****	*****	*****	*****
601					650
msa183564.2{147_COH1}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M732}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_M781}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_2603}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_JM9130013}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_18RS21}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_090}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_CJB110}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_A909}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_H36B}	AGCTTTAAAA	cTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
msa183564.2{147_1169NT}	AGCTTTAAAA	aTAaggCAGA	ATTtGAGGAA	TTAAAAGCAA	AACATAATAT
Consensus	*****	-***-****	***-*****	*****	*****
651					700
msa183564.2{147_COH1}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M732}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_M781}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_2603}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_JM9130013}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_18RS21}	CACCTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_090}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_CJB110}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_A909}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_H36B}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
msa183564.2{147_1169NT}	CACCTTATGGG	AAATGGGTTA	ACGATAAGAT	TGTTTTTGCA	CATAACTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M732}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_M781}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_2603}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_JM9130013}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_18RS21}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_090}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_CJB110}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_A909}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_H36B}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
msa183564.2{147_1169NT}	CCAACAATAC	AGAAACGGTG	GCTGATATTG	CAGCAGCTAT	GAAAGATGGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_M732}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_M781}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_2603}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_JM9130013}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_18RS21}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_090}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_CJB110}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_A909}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_H36B}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
msa183564.2{147_1169NT}	TATGGGTCAG	AAGCAAAGAA	TATTTTGCAT	GGTACACACG	TGCTGGTAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_M732}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_M781}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_2603}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_JM9130013}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_18RS21}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_090}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_CJB110}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_A909}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_H36B}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
msa183564.2{147_1169NT}	TTTTGTAGGT	AATAGTAAAC	GTCCAGCAAT	CAATAGTCTT	CTTTAGAAAG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M732}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_M781}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_2603}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_JM9130013}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_18RS21}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_090}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_CJB110}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_A909}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_H36B}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
msa183564.2{147_1169NT}	GTGCAGCGCC	AAATGCTCAA	GTCTTATTAA	TGCGTATTCC	AGATAAAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_M732}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_M781}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_2603}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_JM9130013}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_18RS21}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_090}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_CJB110}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_A909}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_H36B}	GATTTCGGACA	AATTTGGtGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
msa183564.2{147_1169NT}	GATTTCGGACA	AATTTGGaGA	AGCATATGCT	AAAGCAATCA	cAGACGCTGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M732}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_M781}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	ccTgGGAAAA	ACgGcTGATT
msa183564.2{147_2603}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_JM9130013}	TAATCTAGGA	GCaAAAACGA	TTAATATGAG	taTtGGAAAA	ACaGcTGATT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_18RS21}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
msa183564.2{147_090}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcGATT
msa183564.2{147_CJB110}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcGATT
msa183564.2{147_A909}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcGATT
msa183564.2{147_H36B}	TAATCTAGGA	GCaAAAACGA	TAAATATGAG	ccTtGGAAAA	ACaGcGATT
msa183564.2{147_1169NT}	TAATCTAGGA	GCTAAAACGA	TAAATATGAG	taTtGGAAAA	ACaGcTGATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M732}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_M781}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_2603}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_JM9130013}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_18RS21}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_090}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_CJB110}	CTTTAATTGC	aCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_A909}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_H36B}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
msa183564.2{147_1169NT}	CTTTAATTGC	tCTCAATGAT	AAAGTTAAAT	TAGCACTTAA	ATTAGCTTCT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_M732}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_M781}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_2603}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
msa183564.2{147_JM9130013}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
msa183564.2{147_18RS21}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
msa183564.2{147_090}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_CJB110}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_A909}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_H36B}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GtGCATTGG
msa183564.2{147_1169NT}	GAGAAGGCGC	TTGCAGTTGT	TGTGGCTGCC	GGAAATGAAG	GcGCATTGG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M732}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_M781}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_2603}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_JM9130013}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_18RS21}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_090}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_CJB110}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_A909}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_H36B}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
msa183564.2{147_1169NT}	TATGGATTAT	AGCAAACCaT	TATCAACTAA	TCCTGACTAC	GGTACGGTTA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M732}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_M781}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_2603}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_JM9130013}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_18RS21}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_090}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_CJB110}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_A909}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_H36B}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
msa183564.2{147_1169NT}	ATAGTCCAGC	TATTTCTGAA	GATACITTTGA	GTGTTGCTAG	CTATGAATCA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M732}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_M781}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_2603}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_JM9130013}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_18RS21}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_090}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_CJB110}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_A909}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_H36B}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
msa183564.2{147_1169NT}	CTTAAAACTA	TCAGTGAGGT	CGTTGAAACA	ACTATTGAAG	GTAAGTTAGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M732}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_M781}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_2603}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_JM9130013}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_18RS21}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_090}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_CJB110}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_A909}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_H36B}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
msa183564.2{147_1169NT}	TAAGTTGCCG	ATTGTGACTT	CTAAACCTTT	TGACAAAGGT	AAGGCCTACG
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M732}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_M781}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_2603}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_JM9130013}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_18RS21}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_090}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_CJB110}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_A909}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_H36B}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
msa183564.2{147_1169NT}	ATGTGGTTTA	TGCCAATTAT	GGTGC..AAA	AAAGATTTTG	AAGGTAAGGA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M732}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_M781}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_2603}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_JM9130013}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_18RS21}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_090}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_CJB110}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_A909}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_H36B}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
msa183564.2{147_1169NT}	CTTTAAAGGT	AAGATTGCAT	TAATTGAGCG	TGGTGGTGGA	CTTGATTTTA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_M732}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_M781}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_2603}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_JM9130013}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_18RS21}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_090}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_CJB110}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_A909}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_H36B}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
msa183564.2{147_1169NT}	TGACTAAAAT	CACATCATGCT	ACAAATGCAG	GTGTTGTTGG	TATCGTTAAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M732}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_M781}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_2603}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_JM9130013}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_18RS21}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_090}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_CJB110}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_A909}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_H36B}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
msa183564.2{147_1169NT}	TTTAACGATC	AAGAAAAACG	TGGAATTTT	CTAATTCCTT	ACCGTGAATT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M732}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_M781}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_2603}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_JM9130013}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_18RS21}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_090}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_CJB110}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_A909}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_H36B}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
msa183564.2{147_1169NT}	ACCTGTGGGG	gTTATTAGTA	AAGTAGATGG	CGAGCGTATA	AAAAATACCT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M732}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_M781}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTGG	AAGTAGTTGA	TAGCCAAGGT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_2603}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_JM9130013}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_18RS21}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_090}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_CJB110}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_A909}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_H36B}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
msa183564.2{147_1169NT}	CAAGTCAGTT	AACATTTAAC	CAGAGTTTG	AAGTAGTTGA	TAGCCAAGGT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M732}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_M781}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_2603}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_JM9130013}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_18RS21}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_090}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_CJB110}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_A909}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_H36B}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
msa183564.2{147_1169NT}	GGCAATCGTA	TGCTGGAACA	ATCAAGTTGG	GGCGTGACAG	CTGAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M732}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_M781}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_2603}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_JM9130013}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_18RS21}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_090}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_CJB110}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_A909}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_H36B}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
msa183564.2{147_1169NT}	AATCAAGCCT	GATGTAACAG	CTTCTGGCTT	tGAAATTTAT	TCTTCAACCT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M732}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_M781}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_2603}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_JM9130013}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_18RS21}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_090}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_CJB110}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_A909}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_H36B}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
msa183564.2{147_1169NT}	ATAATAATCA	ATACCAAACA	ATGTCTGGTA	CAAGTATGGC	TTCAACCAT
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M732}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_M781}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_2603}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_JM9130013}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_18RS21}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_090}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_CJB110}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_A909}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_H36B}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
msa183564.2{147_1169NT}	GTTGCAGGAT	TAATGACAAT	GCTTCAAAGT	CATTGGCTG	AGAAATATAA
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M732}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_M781}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_2603}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_JM9130013}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_18RS21}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_090}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_CJB110}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_A909}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_H36B}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
msa183564.2{147_1169NT}	AGGGATGAAT	TTAGATTCTA	AAAAATTGCT	AGAATTGTCT	AAAAACATCC
Consensus	*****	*****	*****	*****	*****
msa183564.2{147_COH1}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT
msa183564.2{147_M732}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTAT

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M781}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_2603}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_JM9130013}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_18RS21}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_090}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_CJB110}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_A909}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_H36B}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
msa183564.2{147_1169NT}	TCATGAGCTC	AGCAACAGCA	TTATATAGTG	AAGAGGATAA	GGCGTTTTAT
Consensus	*****	*****	*****	*****	*****
1901					
msa183564.2{147_COH1}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M732}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_M781}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_2603}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_JM9130013}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_18RS21}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_090}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_CJB110}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_A909}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_H36B}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
msa183564.2{147_1169NT}	TCACCACGTC	AGCAAGGTGC	AGGTGTAGTT	GATGCTGAAA	AAGCTATCCA
Consensus	*****	*****	*****	*****	*****
1951					
msa183564.2{147_COH1}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M732}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_M781}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_2603}	AGCTCAATAT	TATaTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_JM9130013}	AGCTCAATAT	TATaTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_18RS21}	AGCTCAATAT	TATaTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_090}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_CJB110}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_A909}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_H36B}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
msa183564.2{147_1169NT}	AGCTCAATAT	TATgTTACTG	GAACCGATGG	CAAAGtTAAA	ATTAATCTCA
Consensus	*****	***-*****	*****	*****-****	*****
2001					
msa183564.2{147_COH1}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M732}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_M781}	AACGAgagGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_2603}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_JM9130013}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_18RS21}	AACGAatGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_090}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_CJB110}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_A909}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_H36B}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
msa183564.2{147_1169NT}	AACGAggGGG	AGATAAAATT	GATATCACAG	TTACAATTCA	TAAACTTGTA
Consensus	*****-****	*****	*****	*****	*****
2051					
msa183564.2{147_COH1}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M732}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_M781}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_2603}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_JM9130013}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_18RS21}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_090}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_CJB110}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_A909}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_H36B}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
msa183564.2{147_1169NT}	GAAGGTGTCA	AAGAATTGTA	TTATCAAGCT	AATGTAGCAA	CAGAACAAGT
Consensus	*****	*****	*****	*****	*****
2101					
msa183564.2{147_COH1}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M732}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_M781}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_2603}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_JM9130013}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_18RS21}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_090}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_CJB110}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_A909}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_H36B}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
msa183564.2{147_1169NT}	AAATAAAGGT	AAATTTGCC	TTAAACCACA	AGCCTTGCTA	GATACTAATT
Consensus	*****	*****	*****	*****	*****
2151					
msa183564.2{147_COH1}	GGCAGAAAGT	AATTCCTCGT	GATAAAGAAA	CACAAGTTCG	ATTACTATT
2200					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_M732}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_M781}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_2603}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_JM9130013}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_18RS21}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_090}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_CJB110}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_A909}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_H36B}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
msa183564.2{147_1169NT}	GGCAGAAAGT AATTCTTCGT GATAAAGAAA CACAAGTTCG ATTTACTATT	
Consensus	*****	*****
msa183564.2{147_COH1}	2201 GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	2250
msa183564.2{147_M732}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_M781}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_2603}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_JM9130013}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_18RS21}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_090}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_CJB110}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_A909}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_H36B}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
msa183564.2{147_1169NT}	GATgCTAGTC AATTTAGTCA GAAATTAAAA GAACAGATGG CAAATGGTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2251 TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	2300
msa183564.2{147_M732}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_M781}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_2603}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_JM9130013}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_18RS21}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_090}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_CJB110}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_A909}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_H36B}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
msa183564.2{147_1169NT}	TTTCTTAGAA GGTITTTGAC GTTTTAAAGA AGCcAAGGAT AGTAATCAGG	
Consensus	*****	*****
msa183564.2{147_COH1}	2301 AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	2350
msa183564.2{147_M732}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_M781}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_2603}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_JM9130013}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_18RS21}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_090}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_CJB110}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_A909}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_H36B}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
msa183564.2{147_1169NT}	AGTTAATGAG TATTCCTTTT GTAGGATTTA ATGGTGATTT TGCGAaCTTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2351 CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	2400
msa183564.2{147_M732}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_M781}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_2603}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_JM9130013}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_18RS21}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_090}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_CJB110}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_A909}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_H36B}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
msa183564.2{147_1169NT}	CAAGCACTTG AAACACCGAT TTATAAGACG cTTTCTAAAG GTAGTTTCTA	
Consensus	*****	*****
msa183564.2{147_COH1}	2401 CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	2450
msa183564.2{147_M732}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_M781}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_2603}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_JM9130013}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_18RS21}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_090}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_CJB110}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_A909}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_H36B}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
msa183564.2{147_1169NT}	CTATAAACCA AATGATACAA CTCATAAAGA CCAATTGGAG TAcAATGAAT	
Consensus	*****	*****

2451

2500

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_COH1}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M732}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_M781}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_2603}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_JM9130013}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_18RS21}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_090}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_CJB110}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_A909}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_H36B}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
msa183564.2{147_1169NT}	CAGCTCCITT	TGAAAGCAAC	AACTATACTG	CCTTGTAAAC	ACAATCAGCG
Consensus	*****	*****	*****	*****	*****
2501					
msa183564.2{147_COH1}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M732}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_M781}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_2603}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_JM9130013}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_18RS21}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_090}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_CJB110}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_A909}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_H36B}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
msa183564.2{147_1169NT}	TCITGGGGCT	ATGTTGATTA	TGTCAAAAAT	GGTGGGGAGT	TAGAATTAGC
Consensus	*****	*****	*****	*****	*****
2551					
msa183564.2{147_COH1}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M732}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_M781}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_2603}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_JM9130013}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_18RS21}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_090}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_CJB110}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_A909}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_H36B}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
msa183564.2{147_1169NT}	ACCGGAGAGT	CCAAAAAGAA	TTATTTTAGG	AACTTTTGAG	AATAAGGTTG
Consensus	*****	*****	*****	*****	*****
2601					
msa183564.2{147_COH1}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M732}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_M781}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_2603}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_JM9130013}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_18RS21}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_090}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_CJB110}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_A909}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_H36B}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
msa183564.2{147_1169NT}	AGGATAAAAC	AAATTCATCT	TTGGAAAGAG	ATGCAGCGAA	TAATCCATAT
Consensus	*****	*****	*****	*****	*****
2651					
msa183564.2{147_COH1}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M732}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_M781}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_2603}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_JM9130013}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_18RS21}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_090}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_CJB110}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_A909}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_H36B}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
msa183564.2{147_1169NT}	TTTGCCATTT	CTCCAAATAA	AGATGGAAAT	AGGGACGAAA	TCACTCCCCA
Consensus	*****	*****	*****	*****	*****
2701					
msa183564.2{147_COH1}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M732}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_M781}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_2603}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_JM9130013}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_18RS21}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_090}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_CJB110}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_A909}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_H36B}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
msa183564.2{147_1169NT}	GGCAACTTTC	TTAAGAAATG	TTAAGGATAT	TTCTGCTCAA	GTTCTAGATC
Consensus	*****	*****	*****	*****	*****
2750					

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		2751					2800
msa183564.2{147_COH1}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_M732}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_M781}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_2603}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_JM9130013}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_18RS21}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_090}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_CJB110}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_A909}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_H36B}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
msa183564.2{147_1169NT}		AAAAATGGAAA	TGTTATTGG	CAAAGTAAGG	TTTTACCATC	TTATCGTAAA	
Consensus		*****	*****	*****	*****	*****	
		2801					2850
msa183564.2{147_COH1}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_M732}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_M781}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_2603}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_JM9130013}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_18RS21}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_090}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_CJB110}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_A909}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_H36B}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
msa183564.2{147_1169NT}		AAITTCCTATA	ATAATCCAAA	GCAaAGTGAT	GGTCATTATC	GTATGGATGC	
Consensus		*****	*****	***-*****	*****	*****	
		2851					2900
msa183564.2{147_COH1}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_M732}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_M781}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_2603}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_JM9130013}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_18RS21}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_090}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_CJB110}		tcTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_A909}		ccTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_H36B}		ccTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
msa183564.2{147_1169NT}		ccTTCAGTGG	AGTGGTTTAG	ATAAGGATGG	CAAAGTTGTA	GCAGATGGTT	
Consensus		--*****	*****	*****	*****	*****	
		2901					2950
msa183564.2{147_COH1}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_M732}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_M781}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_2603}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_JM9130013}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_18RS21}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_090}		TTTATACTTA	TCGccTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_CJB110}		TTTATACTTA	TCGccTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_A909}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_H36B}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
msa183564.2{147_1169NT}		TTTATACTTA	TCGctTACGT	TACACACCAG	TAGCAGAAGG	AGCAAATAGT	
Consensus		*****	***-*****	*****	*****	*****	
		2951					3000
msa183564.2{147_COH1}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_M732}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_M781}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_2603}		CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_JM9130013}		CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_18RS21}		CAGGAGTCAG	ACTTTAAAGT	aCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_090}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_CJB110}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_A909}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_H36B}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
msa183564.2{147_1169NT}		CAGGAGTCAG	ACTTTAAAGT	tCAAGTAAGT	ACTAAGTCAC	CAAAATCTCC	
Consensus		*****	*****	-*****	*****	*****	
		3001					3050
msa183564.2{147_COH1}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_M732}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_M781}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_2603}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_JM9130013}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_18RS21}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_090}		TTtActAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_CJB110}		TTtActAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_A909}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_H36B}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
msa183564.2{147_1169NT}		TTcACgAGCT	CAGTTTGATG	AAACTAATCG	AACATTAAGC	TTAGCCATGC	
Consensus		**--*****	*****	*****	*****	*****	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

		3051				3100
msa183564.2	{147_COH1}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_M732}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_M781}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_2603}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_JM9130013}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_18RS21}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_090}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_CJB110}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTtTACAATT	AGTTTTATCT
msa183564.2	{147_A909}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTcTACAATT	AGTTTTATCT
msa183564.2	{147_H36B}	CTAAGGaAAG	TAGTTATGTT	CCTACATATC	GTcTACAATT	AGTTTTATCT
msa183564.2	{147_1169NT}	CTAAGGaAAG	TAGTTATGTT	CCTATATATC	GTcTACAATT	AGTTTTATCT
Consensus		*****	*****	*****	*****	*****
		3101				3150
msa183564.2	{147_COH1}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_M732}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_M781}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_2603}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_JM9130013}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_18RS21}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_090}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_CJB110}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_A909}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_H36B}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	AccATTATTT
msa183564.2	{147_1169NT}	CATGTTGTAA	AAGATGAAGA	ATATGGgGAT	GAGACTTCTT	ActATTATTT
Consensus		*****	*****	*****	*****	*****
		3151				3200
msa183564.2	{147_COH1}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M732}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_M781}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_2603}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_JM9130013}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_18RS21}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_090}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_CJB110}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACg	GTTAAGATAG
msa183564.2	{147_A909}	CCATATAGAT	CgAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_H36B}	CCATATAGAT	CaAGAAGGTA	AAGtGACACT	TCCTAAAACa	GTTAAGATAG
msa183564.2	{147_1169NT}	CCATATAGAT	CaAGAAGGTA	AAGcGACACT	TCCTAAAACg	GTTAAGATAG
Consensus		*****	*****	*****	*****	*****
		3201				3250
msa183564.2	{147_COH1}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M732}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_M781}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_2603}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_JM9130013}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_18RS21}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_090}	GAGAGAGTGA	GGTTGCgGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_CJB110}	GAGAGAGTGA	GGTTGCcGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_A909}	GAGAGAGTGA	GGTTGCcGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_H36B}	GAGAGAGTGA	GGTTGCcGTA	GACCCTAAGa	CCTTGACACT	TGTTGTGGAA
msa183564.2	{147_1169NT}	GAGAGAGTGA	GGTTGCcGTA	GACCCTAAGg	CCTTGACACT	TGTTGTGGAA
Consensus		*****	*****	*****	*****	*****
		3251				3300
msa183564.2	{147_COH1}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_M732}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_M781}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_2603}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_JM9130013}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_18RS21}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_090}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_CJB110}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_A909}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_H36B}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
msa183564.2	{147_1169NT}	GATAAAGCTG	GTAATTTtGC	AACGGTAAAA	TGTCCTGAcC	TCTTGAATAA
Consensus		*****	*****	*****	*****	*****
		3301				3350
msa183564.2	{147_COH1}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M732}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_M781}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_2603}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_JM9130013}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_18RS21}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_090}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_CJB110}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA
msa183564.2	{147_A909}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACaTTTCA
msa183564.2	{147_H36B}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACaTTTCA
msa183564.2	{147_1169NT}	GGCAGTAGTA	TCAGAGAAAG	AAAACGCTAT	AGTAATTTCT	AACAgTTTCA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

Consensus	*****	*****	*****	*****	*****
	3351				3400
msa183564.2{147_COH1}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M732}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_M781}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_2603}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_JM9130013}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_18RS21}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_090}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_CJB110}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_A909}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_H36B}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
msa183564.2{147_1169NT}	AATATTTTGA	TAACITGAAG	AAAGAAcCTA	TGTTTATTTC	TAAAgAAGGa
Consensus	*****	*****	*****	*****	*****
	3401				3450
msa183564.2{147_COH1}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M732}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_M781}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_2603}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_JM9130013}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_18RS21}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_090}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_CJB110}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_A909}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_H36B}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
msa183564.2{147_1169NT}	AAAGTAGTAA	ACAAGAATCT	AGAAGAAATA	acATTAGTTA	AGCCcCAaAC
Consensus	*****	*****	*****	*****	*****
	3451				3500
msa183564.2{147_COH1}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M732}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_M781}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_2603}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_JM9130013}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_18RS21}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_090}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_CJB110}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_A909}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_H36B}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
msa183564.2{147_1169NT}	TACAGTTACT	ACTCAATCAT	TGTCTAAAGA	AATAACTaAA	TCAGGAAATG
Consensus	*****	*****	*****	*****	*****
	3501				3550
msa183564.2{147_COH1}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_M732}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_M781}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_2603}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_JM9130013}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_18RS21}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_090}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_CJB110}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_A909}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_H36B}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
msa183564.2{147_1169NT}	AGAAAGTCCT	CACCTTCTACA	AACAATAATA	GTAGcAGAGT	AGCTAaGATC
Consensus	*****	*****	*****	*****	*****
	3551				3600
msa183564.2{147_COH1}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M732}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_M781}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_2603}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_JM9130013}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_18RS21}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_090}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_CJB110}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_A909}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_H36B}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
msa183564.2{147_1169NT}	ATATCACCTA	AACATAAcGG	GGATTCTGTT	AACCATACC-	-----
Consensus	*****	*****	*****	*****	*****
	3601				3650
msa183564.2{147_COH1}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_M732}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_M781}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_2603}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_JM9130013}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_18RS21}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_090}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_CJB110}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_A909}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat
msa183564.2{147_H36B}	atcagataga	gcaacgaatg	gtctatttgg	tggtactttg	gcattgttat

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3651				3700
msa183564.2{147_COH1}	-----	-----	-----	-----	-----
msa183564.2{147_M732}	-----	-----	-----	-----	-----
msa183564.2{147_M781}	-----	-----	-----	-----	-----
msa183564.2{147_2603}	-----	-----	-----	-----	-----
msa183564.2{147_JM9130013}	-----	-----	-----	-----	-----
msa183564.2{147_18RS21}	-----	-----	-----	-----	-----
msa183564.2{147_090}	-----	-----	-----	-----	-----
msa183564.2{147_CJB110}	-----	-----	-----	-----	-----
msa183564.2{147_A909}	-----	-----	-----	-----	-----
msa183564.2{147_H36B}	-----	-----	-----	-----	-----
msa183564.2{147_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 4412

STRAIN 2603

VDKHHSSKAILKLTITLITTSILLMHSNQVNAEEQELKNQEQSPVIANVAQQPSPSVTTNTIV
 EKTSTVTAASANTAKEMGDTSVKNDKTEDELEELSKNLDTSNLGADLEEEYPSKPEITIN
 NKESNVVTNASTAIAQKVPAYEEVKEPKSSSLAVLDTSKITKLQAITQKQGNVVAIID
 TGFDINHDI FRLDSPKDDKHSFKTKTEFEELKAKHNITYGKWNVDKIVFAHNYANNNTETV
 ADIAAAMKDGYGSEAKNISHGTHVAGIFVGNKRPAINGLLLEGAAPNAQVLLMRIPDKI
 DSDKFGEAYAKAITDAVNLGAKTINMSIGKTADSLIALNDKVKLALKLAASEKGVAVVVAA
 GNEGAFGMDYSKPLSTNPDYGTVNSPAISEDTLSVASYESLKTISEVVETIEGKLVKLP
 IVTSKPFDKGKAYDVVYANYGAKKDFEGKDFGKIALIERGGGLDFMTKI THATNAGVVG
 IVIDQKQKGNFLIPYRELPGVIISKVDGERIKNTSSQLTFNQSFVVDQSQGNRMLEQ
 SSGVGTAEBAIKPDVTASGFIEYSSSTYNNQYQTMSTGSMASPHVAGLMTMLQSHLAEKYK
 GMLNLSKLLLELKNILMSSATALLYSEEDKAFYSPRQQGAGVVDAAEKAIQAQYYITGNDG
 KAKINLKRMGDKFDTITVTIHKLVGKELYQANVATEQVNGKGFALKPQALLDNTWQKV
 ILRDKETQVRFTIDASQFSQKLEQMGANGYFLEGFVRFEAKDSNQELMSIPFVGFGNDF
 ANLQALETPITYKTLKSGSFYKPNDTTHKDLQLEYNESAPFESNNYTALLTQSASWGYVDY
 VKNGGELELAPESPKRIILGTFFENKVEDKTIHLERDAANNPYFAISPNDGNGRDEITPQ
 ATFLRNVDKISAQVLDQNGNVIWQSKVLPSYRKNFHNPKQSDGHYRMDALQWGLDKDG
 KVVADGFTYRRLRYTPVAEGANSQESDFKVQVSTKSPNLPSRAQFDETNRTLSLAMPKES
 SYVPTYRLQLVLSHVVKDEEYGDDETSYHYFHIHQEGKVTLPKTVKIGESEVAVDPKALT
 VVEDKAGNFATVKLSDLLNKAVVSEKENAIVISNSFKYFDNLKKEPMFISKKEKVVNKNL
 EEIILVKPQTITVTQSLSKETKSGNEKVLSTNNSSRAKIIISPKHNGDSVNHTLPST
 SDRATNGLVGTLALSLSSLLLYLKPKTKNNKS

SEQ ID NO. 4413

STRAIN A909

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE
 LLEELSKNLDTSNLGADLEEEYPSKPEITINNKESNVVTNASTAIAQKVPAYEEVKEPKES
 SSLAVLDTSKITKLQAITQKQGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
 LKAKHNITYGKWNVDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
 TADSLIALNDKVKLALKLAASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
 DTLVASYESLKTISEVVETIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKRL.R.G
 L.R.DCIN.AWWT.FYD.NHSCYKCRCCWYRYF.RSRKTWKFSNSLP.ITCGGY..SRW
 RAYKKYFKSVNT.PEF.SS..PRWQSYAGTIKLGDRS.RSNQA.CNSFWL.NLFFNL..S
 IPNNVWYKGYFTTCCIRINDNASKSFG.EI.RDEFRF.KIARIV.KHPHELSNII..RG.
 GVLFTTSARCRC.S.CSYPSSILCYWKRWS.N.SQTSGR.I.YHSYNS.TCRRCORIV
 LSS.CSNRTSK.R.ICP.TTSLARY.LAESNSS..RNTSSIIY.F.SI.SEIKRTDGKWL
 FLRRFCTF.RSQQ..SGVNEYSFCRI.W.FCELTST.NTDL.DAF.R.FLL.TK.YNS.R
 PIGVQ.ISSF.KQQLYCLVNTISVLGLC.LCQKWGWVRISTGESKKNYFRNF.E.G.G.N
 NSSFGKRCSE.SIFCHFSK.RWK.G.NHSPGNFLKCC.GYFCSSSRSKWKCYLAK.GFTI
 LS.KFP..SKAK.WSLSYGCPSEWFR.GWQSCSRWFLYLSFTLHTSSRRSK.SGVRL.S
 SSKY.VTKSSFTSSV..N.SNIKLSHA.GK.LCSYISSTISFISCKKR.RIWR.DFLPLF
 PYRSRR.SDTS.NS.DRRE.GCSR.PDLTCCGR.SW.FRNGKIV.PLE.GSSIRERKRY
 SNF.QFQIF..LEKRTYVYF.RRKSSQESRRNSIS.AANYSSYIIV.RNNSIRK.ESP
 HFYKQ...QSS.DHRT.T.RGFC.PY

SEQ ID NO. 4414

STRAIN H36B

EEQELKNQEQSPVIANVAQQPSPSVTTNTVEKTSVTSASANTAKEMGDTSVKNDKTEDE
 LLEELSKNLDTSNLGADLEEEYPSKPEITINNKESNVVTNASTAIAQKVPAYEEVKEPKES
 SSLAVLDTSKITKLQAITQKQGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
 LKAKHNITYGKWNVDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
 NSKRPAINGLLLEGAAPNAQVLLMRIPDKIDSDKFGEAYAKAITDAVNLGAKTINMSLGK
 TADSLIALNDKVKLALKLAASEKGVAVVVAAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
 DTLVASYESLKTISEVVETIEGKLVKLPVITSKPFDKGKAYDVVYANYGAKKDFEGK
 FKGKIALIERGGGLDFMTKI THATNAGVVGIVIVNDQKQKGNFLIPYRELPGVIISKVDG
 ERIKNTSSQLTFNQSFVVDQSQGNRMLEQSSSGVGTAEBAIKPDVTASGFIEYSSSTYNNQ
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLSKLLLELKNILMSSATALLYSEEDK
 AFYSPRQQGAGVVDAAEKAIQAQYYITGNDGKAKINLKRVDKFDITVTIHKLVGKELY
 QANVATEQVNGKGFALKPQALLDNTWQKVIILRDKETQVRFTIDSSQFSQKLEQMGANGY
 FLEGFVRFEAKDSNQELMSIPFVGFGNDFANLQALETPITYKTLKSGSFYKPNDTTHK
 QLEYNESAPFESNNYTALLTQSASWGYVDYVKNGGELELAPESPKRIILGTFFENKVEDK
 TIHLERDAANNPYFAISPNDGNGRDEITPQATFLRNVDKISAQVLDQNGNVIWQSKVLPS
 YRKNFHNPKQSDGHYRMDALQWGLDKDGKVVADGFTYRRLRYTPVAEGANSQESDFKV
 QVSTKSPNLPSRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDDETSYHYF

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

HIDQEGKVTLPKTVKIGESEVAVDPKTLTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEELVKPQTIVTTQSLSKETITQSGNEKVL
TSTNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4415**STRAIN 18RS21**

EEQELKNQEQSPVIANVAQOPSPSVTNTVEKTSVTAASASNTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNGLADLEEEYPSKPETTTNNKESNVVTNASTAIAQKVPSAYEEVKPESK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETITIEGKLVKLPVITSKPFDDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDMTKITHTATNAGVVGIVIFNDQEKRGNFILPYRELPVGIISKVDG
ERIKNTSSQLTFNQSFVVDSDQGNRMLEQSSWGVTAEGA IKPDVTAAGCFEYISSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDSSKLLLELSKNILMSSATALYSEEDK
AFYSPRQOQAGVVDAAEKAIQAQYITGNDGKAKINLKRMDGKDFITVTIHLKVEGVKELY
YQANVATEQVNVKGFALKPQALLDTNWKVILRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGVFRFKEAKDSNQLMSIPFVGFNGDFANLQALETPITYKTSKGSFYYPNDTTHKD
QLEYNESAPFESNNYITALLTQSASWGYVDVYKNGGELELAPESPKRIILGTFFENKVEDKT
IHLLERDAANNPYFAISPNDGGRDEITPQATFLRNVDKISAQVLDQNGNVIWQSKVLP
YRKNPHNNPKQSDGHRMDALQWGLDKDGKVVADGFYTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSPRAQFDETNRITSLAMPKESYVPTYRLQLVLSHVVDKDEEYGDSTSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTTLVVEDKAGNFATVKLSDLLNKAVVSEKENAI
VTSNNFKYFDNLKKEPMFI SKKGVVNNKLEELILVKPQTIVTTQSLSKETITQSGNEKVL
TSTNNSSRVAKIISPKNHNGDSVNHT

SEQ ID NO. 4416**STRAIN M732**

EEQELKNQEQSPVIANVAQOPSPSVTNTIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNGLADLEEEYPSKPETTTNNKESNVVTNASTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETITIEGKLVKLPVITSKPFDDKGKAYDVVYANYGAKKILKVRT
LKVRILH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIGK.I.ILKNC.NCLKTSS.AQQOHIYVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPNHHKPC.ILIGRK.FFVKKHGFDDLMLVNLVRN.KNRWQMI
S.KVLYVLKPKRIVIRS..VFLD.DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT
NWSTNQLLKATTILPC.HNQRGLAMLIMSKMVG.S.N.HRRVQKELP.ELLRLRLRIKQ
FIFWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIVVWMLFSGVV.IRMAKL.QMVFILIAVYTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHLSLMKLIH.A.PCLRKVVMFLHIVYN.FYLM.LKMKNMGMRLLTIIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTIL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLLK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILITI

SEQ ID NO. 4417**STRAIN COH1**

EEQELKNQEQSPVIANVAQOPSPSVTNTIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNGLADLEEEYPSKPETTTNNKESNVVTNASTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETITIEGKLVKLPVITSKPFDDKGKAYDVVYANYGAKKILKVRT
LKVRILH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA
SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCFKVIWLRNIGK.I.ILKNC.NCLKTSS.AQQOHIYVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLETMAKLLISNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNLPNHHKPC.ILIGRK.FFVKKHGFDDLMLVNLVRN.KNRWQMI
S.KVLYVLKPKRIVIRS..VFLD.DLMVILRTYKHLKHFIRRFKVVSTINQMIQLIKT
NWSTNQLLKATTILPC.HNQRGLAMLIMSKMVG.S.N.HRRVQKELP.ELLRLRLRIKQ
FIFWKEMQRIIHLPLFLQIKMEIGTKSLPRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISIIIQSKVMVIVVWMLFSGVV.IRMAKL.QMVFILIAVYTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHLSLMKLIH.A.PCLRKVVMFLHIVYN.FYLM.LKMKNMGMRLLTIIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLLWKIKLVILQR.NCLTS.IRQ.YQRKKTIL.
.FLTVSNILIT.RKNLCLFLKKEK..TRI.KK.H.LSLKLQLLLNHCLLK.LNQEMRKSS
LLQTIIVAE.LRSYHLNITGILITI

SEQ ID NO. 4418**STRAIN M781**

EEQELKNQEQSPVIANVAQOPSPSVTNTIVEKTSVTAASASNTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNGLADLEEEYPSKPETTTNNKESNVVTNASTAIAQKVPSAYEEVKSEK
SSLAVLDTSKITKLQATTQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNNTETVADIAAAMKDGYGSEAKNILHGHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRI PDKIDSDKFGEAYAKAIDAVNLGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKTISEVVETITIEGKLVKLPVITSKPFDDKGKAYDVVYANYGAKKILKVRT
LKVRILH.LSVVVDLIL.LKSLMLQMQLVLSLFLTIKKNVEIF.FLTVNVLWGLLVK.MA

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

SV.KILQVS.HLTRVLK.LIAKVAIVCWNQVGA.QLKEQSSLM.QLLALKFILQPIIIN
TKQCLVQVWLHMLQD..QCCKVIWLRNKG.I.ILKNC.NCLKTSS.AQQOHYIVKRIR
RFIHHVSKVQV.LMLKKLSKLNIMLLETMAKLKLSNEREINLISQLQFINL.KVSKNCI
IKLM.QQNK.IKVNPLPLNHKPC.ILIGRK.FFVIKKHKFDLLMLVNLVRN.KNRWQMI
S.KVLYVLKKPRIVIRS..VFL.LDLMVILRTYKHLKHFIRFLKVVSTINQMIQLIKT
NWSTMNQLLLKATILPC.HNQLGAMLIMSKMVGS.N.HRRVQKELF.ELLRIRLRIKQ
IFPWKEMQRIIHLPLFQIKMEIGTKSLRQLS.EMLRIFLLKF.IKMEMLFGKVRFYHL
IVKISII IQSKVMVIIVWMLFSGVV.IRMAKL.QMVFLIAYVTHQ.QKEQIVRSQTLKF
K.VLSHQIFLHLSMLKLIH.A.PCLRKVMFLHIVYN.FYLM.LKMKMGMRLLTIIS
I.IKKVK.HFLKRLR.ERVRLR.TLRP.HLWIKILVILQR.NCLTS.IRQ.YORKKTL.
.FLTVSNILIT.RKNLCFLKKEK..TRI.KK.H.LSLKLQLLNHCLKK.LNQEMRKSS
LQTIIVAE.LRSYHLNITGILLTI

SEQ ID NO. 4419

STRAIN JM9130013

EEQELKNQEQSPVIANVAQQPSPSVTTNTEKTSVTAASANTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKTEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIIPDKIDSDFGEAYAKAITDAVNLAGAKTINMSIGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLPITVSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVDAEKAIQAQYYITGNDGKAKINLKRMDKFDITVTIHKLVGKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVLDRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS
YRKNFHNPKQSDGHYRMDALQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPSRAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDTSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNAKVVSEKENAI
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4420

STRAIN 090

EEQELKNQEQSPVIANVAQQPSPSVTTNTEKTSVTAASANTVKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIIPDKIDSDFGEAYAKAITDAVNLAGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLPITVSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVDAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVGKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVLDRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDTSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNAKVVSEKENAI
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4421

STRAIN CJB110

EEQELKNQEQSPVIANVAQQPSPSVTTNTEKTSVTAASANTAKEMGDTSVKNDKTEDE
LLEELSKNLDTSNLGADLEEYPSKPEPTNNKESNVVNTASTAIAQKVPSAYEEVKPESK
SSLAVFDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI.FRLDSPKDDKHSFKTKAEFEE
LKAKHNITYGKWVNDKIVFAHNYANNTETVADIAAAMKDGYGSEAKNISHGTHVAGIFVG
NSKRPAINGLLLEGAAPNAQVLLMRIIPDKIDSDFGEAYAKAITDAVNLAGAKTINMSLGK
TADSLIALNDKVKLALKLASEKGVAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
DTLSVASYESLKITSEVVETIIEGKLVKLPITVSKPFDKGKAYDVVYANYGAKKDFEGKD
FKGKIALIERGGGLDFMTKITHATNAGVVGIVIFNDQEKRGNFILPYRELPGVISKVDG
ERIKNTSSQLTFNQSFVVDSQGGNRMLEQSSWGVTAEAGIKPDVTASGFEIYSSTYNNQ
YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLD SKKLELSKNILMSSATALYSEEDK
AFYSPRQGGAGVDAEKAIQAQYYVTGNDGKAKINLKRVDKFDITVTIHKLVGKELY
YQANVATEQVNGKGFALKPQALLDTNWQKVLDRDKETQVRFTIDASQFSQKLKEQMANGY
FLEGFVRFEKAKDSNQELMSIPFVGFGNDFANLQALETPITYKLSKGSFYKPNDTTHKD
QLEYNESAPFESNNYTALLTQSASWGYYVDYVKNNGGELELAPESPKRIILGTFFENKVEDKT
IHLLERDAANNPYFAISPENKDGNRDEITPQATFLRNVDISAQVLDQNGNVIWQSKVLPS
YRKNFHNPKQSDGHYRMDAFQWSGLDKDGKVVADGFTYRLRYTPVAEGANSQESDFKV
QVSTKSPNLPLLAQFDETNRTLSLAMPKESYVPTYRLQLVLSHVVKDEEYGDTSYHYF
HIDQEGKVTLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLNAKVVSEKENAI
VISNSFKYFNLKKEPMFISKEGKVVKNLEEBITLVKPQTTVTTQSLSKETKSGNEKVL
TSTNNSSRVAKIISPKNHGDVSNHT

SEQ ID NO. 4422

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

STRAIN 1169NT

EEQELKNQEQSPVIANVAQQSPSVTTNI VEKTSVTAASANTAKEMGDTSVKNDKTEDE
 LLEELSKNLDTSNMGADLEEYPSKPETTNNKESNVVTINASTAIAQKVPSAYEEVKPKSK
 SSLAVLDTSKITKLQAITQRGKGNVVAIIDTGFDINHDI FRLDSPKDDKHSPFNKAEEFEE
 LKAKHNITYGKWNVDKIVFAHNNYANTTETVADIAAAMKDDGYGSEAKNISHGTHVAGIFVG
 NSKRPAINGLLLEGAAFNPAQVLLMRI PDKIDSDKFGEAYAKAITDAVNLGAKTINMSIGK
 TADSLIALNDKVKLALKLASEKGAVVVAAGNEGAFGMDYSKPLSTNPDYGTVNSPAISE
 DTLASVASYESLKTISEVVETITIEGKLVKLPVITVSKPFDKGAIDVYVANYGAKKDFEGKD
 FKQKIALIERGGGLDMFTKITHTATNAGVVGIVIFNDQEKRGNFILPYRELPGVVISKVDG
 ERKNTSSQLTFNQRFEVVDSSQGGNRMLEQSSWGVTAAGAIKPDVTASGFEEIYSSTYNNQ
 YQTMSTGSMASPHVAGLMTMLQSHLAEKYKGMNLDSSKLLLELSKNILMSSATALYSEEDK
 AFYSPPRQGGAGVVDAAEKAIQAQYVVTGNDGKAKINLKRVDGKFDITVTIHKLVEGVKELY
 YQANVATEQVNGKGFALKPQALLDTNWQKVIILRDKETQVRFTIDASQFSQKLKEQMANGY
 FLEGFVRPFKEAKDSNQBLSIPFVGFGNGDFASLQALETPIYKTLKSGSFYYPNDTTHKD
 QLEYNESAPPFESSNYTALLTQSSASWGYVDVYKNGGELELAPESPRIILGTFFENKVEDKT
 IHLERDAANNPYFAISPNDGGRDEITPQATFLRNVKDISAQVLDQNGNVIWQSKVLPS
 YRKNFHNPNKQSDGHYRMDALQWGLDKDGKVVADGFYTYRLRYTPVABGANSQESDPKV
 QVSTKSPNLPSPRAQFDETNRTLSLAMPKGSYVPIYRLQVLVSHVVKDEYGDSTSYYP
 HLDQEGKATLPKTVKIGESEVAVDPKALTIVVEDKAGNFATVKLSDDLKAVVSEKENAI
 VISNSFKYFDNLKKEPMFISKKEKVVNKNLEELILVKPHTTITVTSLSKEITKSGNEKVL
 TSTNNSSRVAKIISPKNHGSVNHNT

PRETTY of: /biotmp/msa209368.2{*} February 10, 2003 02:09 ..

	1	50
msa209368.2{147_COH1}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M732}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_M781}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_18RS21}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_2603}	vdkhhskkai lkltlittsi llmhsngvna	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_JM9130013}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_090}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_CJB110}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_1169NT}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_H36B}	-----	EEQELKNQEQ SPVIANVAQQ
msa209368.2{147_A909}	-----	EEQELKNQEQ SPVIANVAQQ
Consensus	*****	*****

	51	100
msa209368.2{147_COH1}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M732}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_M781}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_18RS21}	PSPSVTtNtV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_2603}	PSPSVTtNtV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_JM9130013}	PSPSVTtNtV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_090}	PSPSVTtNiV EKTsvTaASA SNTvKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_CJB110}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_1169NT}	PSPSVTtNiV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_H36B}	PSPSVTtNtV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
msa209368.2{147_A909}	PSPSVTtNtV EKTsvTaASA SNTaKEMGDT SVKNDKTEDE	LLEELSKNLD
Consensus	*****	*****

	101	150
msa209368.2{147_COH1}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKseSK
msa209368.2{147_M732}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKseSK
msa209368.2{147_M781}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKseSK
msa209368.2{147_18RS21}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_2603}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_JM9130013}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_090}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_CJB110}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_1169NT}	TSNmGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpkSK
msa209368.2{147_H36B}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
msa209368.2{147_A909}	TSNlGADLEE EYPSKPETTNNKESNVVTINA STAlAQKVPS	AYEEVKpeSK
Consensus	***-*****	*****

	151	200
msa209368.2{147_COH1}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M732}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_M781}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_18RS21}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_2603}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_JM9130013}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_090}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_CJB110}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_1169NT}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_H36B}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
msa209368.2{147_A909}	SSLAVLDTSK ITKLQAtQR GKGNNVVAIID TGFDINHDI FRLDSPKDDKH	
Consensus	*****	*****

	201	250
msa209368.2{147_COH1}	SFKtKaEFEE LKAKHNITYG KWNVDKIVFA HNYANNTETV ADIAAAMKDG	

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_M732}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_M781}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_18RS21}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_2603}	SFKtKtEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_JM9130013}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_090}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_CJB110}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_1169NT}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_H36B}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
msa209368.2{147_A909}	SFKtKaEFEE	LKAKHNITYG	KWVNDKIVFA	HNYANNTETV	ADIAAAMKDG
Consensus	*****-****	*****	*****	*****	*****
msa209368.2{147_COH1}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M732}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_M781}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_18RS21}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_2603}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_JM9130013}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_090}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_CJB110}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_1169NT}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_H36B}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
msa209368.2{147_A909}	YGSEAKNIiH	GTHVAGIFVG	NSKRPAInSL	LLEGAAPNAQ	VLLMRIPDKI
Consensus	*****-*	*****	*****-*	*****	*****
msa209368.2{147_COH1}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M732}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_M781}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_18RS21}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_2603}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_JM9130013}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_090}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_CJB110}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_1169NT}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_H36B}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
msa209368.2{147_A909}	DSDKFGGEAYA	KAIiDAVNlG	AKTINMSlGK	TADSLIALND	KVKLALKLAS
Consensus	*****	***-*****	*****-*	*****	*****
msa209368.2{147_COH1}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M732}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_M781}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_18RS21}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_2603}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_JM9130013}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_090}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_CJB110}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_1169NT}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_H36B}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
msa209368.2{147_A909}	EKGVAVVVAA	GNEGAFGMDY	SKPLSTNPdY	GTvNSPAISE	DTLSVASYES
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M732}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_M781}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKilkvrt
msa209368.2{147_18RS21}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_2603}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_JM9130013}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_090}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_CJB110}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_1169NT}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_H36B}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKdfegkd
msa209368.2{147_A909}	LKTISeVVET	TIEGKLvKlP	IVTSKPFdKG	KAYDVVYANY	GAKKrl.r.g
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	lkvrhlh.lsv	vvdlil.lks	lmlgmqvllv	slfltkknv	eiF.fltny
msa209368.2{147_M732}	lkvrhlh.lsv	vvdlil.lks	lmlgmqvllv	slfltkknv	eiF.fltny
msa209368.2{147_M781}	lkvrhlh.lsv	vvdlil.lks	lmlgmqvllv	slfltkknv	eiF.fltny
msa209368.2{147_18RS21}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_2603}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_JM9130013}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_090}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_CJB110}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_1169NT}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_H36B}	fkqkialier	ggglldfntki	thatnagvvg	ivifndqekr	gnFlipyrel
msa209368.2{147_A909}	l.r.dcin.a	wwwt.fyd.n	hscykrcrcw	yyrf.rsrkt	wkFsnslp.i
Consensus	-----	-----	-----	-----	-----

501

550

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M732}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_M781}	lwGllvk.ma	sv.Kilqvs.	hltrvlk.li	akvaivcwnn	qvga.qlkeq
msa209368.2{147_18RS21}	pvGiiskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_2603}	pvGiiskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_JM9130013}	pvGiiskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_090}	pvGviskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_CJB110}	pvGviskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_1169NT}	pvGviskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_H36B}	pvGviskvkd	eriKntssql	tfngsfvvd	sqgggnrmleq	sswgvttaega
msa209368.2{147_A909}	tcGgy..srw	rayKkyfksv	ni..pef..ss.	.prwqsyagt	iklgrds.rs
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M732}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_M781}	sslm.qllal	kfilqpiiin	tkqclvqvwl	hhmlqd..qc	fkviwlrnk
msa209368.2{147_18RS21}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_2603}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_JM9130013}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_090}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_CJB110}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_1169NT}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_H36B}	ikpdvtasgf	eiyssstynnq	yqtmagtsma	sphvaglmntm	lqshlaekyk
msa209368.2{147_A909}	nqa.cnsfwl	.nlffnl..s	ipnnvwykyg	fttccrindn	asksfg.ei.
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	g.i..ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M732}	g.i..ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_M781}	g.i..ilknc.	nclktss.aq	qghyivkrir	rflhhvskvq	v.lmlkKlSk
msa209368.2{147_18RS21}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_2603}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_JM9130013}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_090}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_CJB110}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_1169NT}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_H36B}	gmnlidskkl	elsknilmss	atalyseedk	afysprqgga	gvvdaeKaiq
msa209368.2{147_A909}	rdefrf.kia	riv.khphel	nsii...rg.	gvlfettsarc	rscs.c.Ksyp
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M732}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_M781}	lnimlletma	klklisnere	inlisqlqfi	nl.kvsknci	iklm.qgnk.
msa209368.2{147_18RS21}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_2603}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_JM9130013}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_090}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_CJB110}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_1169NT}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_H36B}	aqyyitgndg	kakinlkrmg	dkfditvtih	klvegkely	yqanvateqv
msa209368.2{147_A909}	ssilcywkrw	qs.n.sqtsg	r.i.yhsyns	.tccrcqriv	lss.csnrts
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmv
msa209368.2{147_M732}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmv
msa209368.2{147_M781}	ikvnlplnhk	pc.iligrk.	ffvikkhkfd	lllmlvnlvr	n.Knrwqmv
msa209368.2{147_18RS21}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_2603}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_JM9130013}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_090}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_CJB110}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_1169NT}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_H36B}	nkqkfalkpq	alldtnwqkv	ilrdketqvr	ftidasqfsq	klKegmangy
msa209368.2{147_A909}	k.r.icp.tt	slary.laes	nss..rntss	iyf.f.si.s	eiKrtgdgkw
Consensus	*****	*****	*****	*****	*****
msa209368.2{147_COH1}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M732}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_M781}	s.kvlyvlkk	privirs..v	fl1.dlmvil	rtykhkhkrf	irrfkvvst
msa209368.2{147_18RS21}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_2603}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_JM9130013}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_090}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_CJB110}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_1169NT}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_H36B}	flegfvrkfe	akdsngelms	ipfvfgngdf	anlqaletpi	yktlsgsfy
msa209368.2{147_A909}	flrrfctf.r	sgg..sgvne	ysfcrl.w.f	celtat.ntd	l.daf.r.fl
Consensus	*****	*****	*****	*****	*****

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

msa209368.2{147_COH1}	inqmiqlikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M732}	inqmiqlikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_M781}	inqmiqlikt	nwstmnglll	kattilpc.h	nqrlgamlim	skmvgs.n.h
msa209368.2{147_18RS21}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_2603}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_JM9130013}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_090}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_CJB110}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_1169NT}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_H36B}	ykpnndtthkd	qleynesapf	esnnytalit	qsaswgyvdy	vknggelela
msa209368.2{147_A909}	l.tk.yns.r	pigvq.issf	.kqglyclvn	tisvlglc.l	cqkwwgvriss
Consensus	-----	-----	-----	-----	-----

msa209368.2{147_COH1}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M732}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_M781}	rrvqKelf.e	llrirlrikq	fifwkemqri	ihilpflqik	meigtkslpr
msa209368.2{147_18RS21}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_2603}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_JM9130013}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_090}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_CJB110}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_1169NT}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_H36B}	pespKriilg	tfenkvedkt	ihlllerdaan	npyfaispnk	dgnrdeitpq
msa209368.2{147_A909}	tgesKknyfr	nf.e.g.g.n	nssfgkrcse	.sifchfsk.	rwk.g.nhsp
Consensus	-----	-----	-----	-----	-----

msa209368.2{147_COH1}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiiliqs	kvmvliivwml
msa209368.2{147_M732}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiiliqs	kvmvliivwml
msa209368.2{147_M781}	qls.emlrif	llkf.ikmem	lfgkvrfyhl	ivkisiiliqs	kvmvliivwml
msa209368.2{147_18RS21}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_2603}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_JM9130013}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_090}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_CJB110}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_1169NT}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_H36B}	atflrnvkdi	saqvldqngn	viwqskvlps	yrknfhnnpk	qsdghyrmda
msa209368.2{147_A909}	gnflkkc.gy	fcssrsrskwk	cylak.gfti	ls.kfp..sk	ak.wslsygc
Consensus	-----	-----	-----	-----	-----

msa209368.2{147_COH1}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M732}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_M781}	fsgvv.irma	kl.qmvFili	ayvthq.qke	qivrsqtlkf	k.vlshqifl
msa209368.2{147_18RS21}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_2603}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_JM9130013}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_090}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_CJB110}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_1169NT}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_H36B}	lqwsqldkdq	kvvadgFyty	rlrytpvaeg	ansqesdfkv	qvstksnplp
msa209368.2{147_A909}	psvewfr.gw	qscsrwFlly	sftlhtsarr	sk.sgvrl.s	ssky.vtkss
Consensus	-----	-----	-----	-----	-----

msa209368.2{147_COH1}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_M732}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_M781}	helslmkllie	h.a.pclrkv	vmflhivyn.	fyml.Kmkn	mgmrl1tiis
msa209368.2{147_18RS21}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_2603}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_JM9130013}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_090}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_CJB110}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_1169NT}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_H36B}	sraqfdetnr	tlslampkes	syvptyrlql	vlshvvKdee	ygdetsyhyf
msa209368.2{147_A909}	ftssv..n.s	niklsha.gk	.lcsyissti	sfisccKr.r	iwr.dflplf
Consensus	-----	-----	-----	-----	-----

msa209368.2{147_COH1}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.ncelts.ir
msa209368.2{147_M732}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.ncelts.ir
msa209368.2{147_M781}	i.ikkvk.hf	lkrlr.ervr	lr.tlrlp.hl	lwkiklvilq	r.ncelts.ir
msa209368.2{147_18RS21}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_2603}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_JM9130013}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_090}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_CJB110}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_1169NT}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_H36B}	hidqegkvtl	pktkvigese	vavdpkaltl	vvedkagnfa	tvklsdllnk
msa209368.2{147_A909}	pyrsrr.sdt	s.ns.drre.	gcsrp.dldt	ccgr.sw.fr	ngkiv.ple.
Consensus	-----	-----	-----	-----	-----

Table 44: Comparative Sequences relating to SAG0416 (strain info highlighted in BOLD)

	1101		1150
msa209368.2{147_COH1}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_M732}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_M781}	q.yqrkktl. .fltvsnili t.rKnlclfl kkeK..tri. kk.h.lslkl		
msa209368.2{147_18RS21}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqgt		
msa209368.2{147_2603}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqgt		
msa209368.2{147_JM9130013}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqgt		
msa209368.2{147_090}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt		
msa209368.2{147_CJB110}	avvsekenai visnsfkyfd nlkKesmfis kegKvvknkl eeitlvkpqt		
msa209368.2{147_1169NT}	avvsekenai visnsfkyfd nlkKepmfis kkeKvvknkl eeilvlpqgt		
msa209368.2{147_H36B}	avvsekenai visnsfkyfd nlkKepmfis kegKvvknkl eeilvlpqgt		
msa209368.2{147_A909}	gssirerkry snf.qfqif. .leKrtvyvf .rrKsskqes rrnsis.aan		
Consensus	-----	---*-----	-----
	1151		1200
msa209368.2{147_COH1}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_M732}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_M781}	qlllnhclkk .lngemrkss llqtiivae. lrsyhlnitg illti-----		
msa209368.2{147_18RS21}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_2603}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhTlpst		
msa209368.2{147_JM9130013}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_090}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_CJB110}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_1169NT}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_H36B}	tvttqslske itksgnekvl tstnnssrv akiispkhng dsvnhT-----		
msa209368.2{147_A909}	ysyysiiv.r nnsirk.espf hfykq...qs s.dhit.t.r gfc.py-----		
Consensus	-----	-----	-----*****
	1201		1233
msa209368.2{147_COH1}	-----	-----	---
msa209368.2{147_M732}	-----	-----	---
msa209368.2{147_M781}	-----	-----	---
msa209368.2{147_18RS21}	-----	-----	---
msa209368.2{147_2603}	edratnglfv gtlallsl1 lylpkpktkn nsk		
msa209368.2{147_JM9130013}	-----	-----	---
msa209368.2{147_090}	-----	-----	---
msa209368.2{147_CJB110}	-----	-----	---
msa209368.2{147_1169NT}	-----	-----	---
msa209368.2{147_H36B}	-----	-----	---
msa209368.2{147_A909}	-----	-----	---
Consensus	*****	*****	***

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)**SEQ ID NO. 4501****STRAIN 2603**

ATGAAAAAGATTAGAAAAAGTTTAGGACTTCTACTATGTTGCTTTTATAGGATTGGTACAA
 TTAGCGTTTTTTCCGGTAGCCAGTGTAATGCTGATACCCCTAATCAACTAACAATCACA
 CAGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGGACTGTG
 ACTGACAACTTAAAAGTTGATTATTGAGCCAAATGACAGATAGCGAATTGAACCGAAG
 TATAAGAGTATCTTGACTTCTCCTACTGATACTAATGGTCAGACAAAGATAGCACTCCCA
 AATGGTTTCGTACTTTGGTCGTCTTATAAGCTGATCAAAGCGTTTCAACAATAGTACCT
 TTTTATATTGAATTACAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGA
 AAAGTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGATAAAGAAA
 AGGCTATCCGGAGTAATATTGTATTATACGATAACCAGAATCAGCCAGTTGCTTTAAA
 AATGGACGATTACGACCGATCAAGATGGGATTACTTCATTAGTAACTGATGATAAGGGA
 GAAATTGAGGTTGAAGGTTTATTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTA
 ACTGGTTACCGTATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAG
 GAAGTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCATCACAA
 CCGCTTTTCCACATCTATTCTTCTTAAACAGGAATGATTATTGGTGGAGGACTGACA
 ATTCTTGGTTGTATTATTTGGGAATTTTGTATTCTTTTAAAGAAAACATAAAATAGC
 AAATCTGAAGAAACGATACAGTA

SEQ ID NO. 4502**STRAIN 090**

GATACCCCTAATCAACTAACAATCACAC
 AGATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTA
 TGGACTGTGACTGACAACTTAAAAGTTGATTATTAGGCCAAATGACAGATA
 TAGCGAATTGAACAGAGTATAAGAGTATCTTGACTTCTCCTACTGATA
 CTAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGT
 CTTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGA
 ATTACAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGAA
 AAGTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAG
 ATAAAGAAAAGGCTATCAGGAGTAATTTGTATTATACGATAACAGAA
 TCAGCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGA
 TTACTTCATTAGTAAGTATGATGATAAGGGAGAAATTGAGGTTGAAGGTTTA
 TTACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCG
 TATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGG
 AAGTAgAGGTAAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAA
 CCAATCAACCG

SEQ ID NO. 4503**STRAIN H36B**

GATACCCCTAATCAACTAACAATCACACAGA
 TAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATGG
 ACTGTGACTGACAACTTAAAAGTTGATTATTAGGCCAAATGACAGATAG
 CGAATTGAACAGAGTATAAGAGTATCTTGACTTCTCCTACTGATACTA
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT
 TATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAATT
 ACCAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGAAAAG
 TTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGATA
 AAGAAAAGGCTwTCCGGAGTAATTTGTATTATACGATAACCAAGATCA
 GCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATTA
 CTTTATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATTA
 CCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTAT
 ATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG
 TAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACCA
 TCACAACCGC

SEQ ID NO. 4504**STRAIN 18RS21**

GATACCCCTAATCAACTAACAATCACACAG
 ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
 GACTGTGACTGACAACTTAAAAGTTGATTATTAGGCCAAATGACAGATA
 GCCAATTGAACAGAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 ATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTGCT
 TTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAAT
 TACCAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGAAAA
 GTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGAT
 AAAGAAAGGCTATCCGGAGTAATTTGTATTATACGATAACCAAGATC
 AGCCAGTTTCGCTTTAAAAATGGACGATTTACGACCGATCAAGATGGGATT
 ACTTCATTAGTAAGTATGATAAGGGAGAAATTGAGGTTGAAGGTTTATT
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGAAG
 GTAGAGGTAGAAAACGAAAAGAACTCCTCCACCAACAAATCCTAAACC
 ATCAACACC

SEQ ID NO. 4505**STRAIN CJB110**

GATACCCCTAATCAACTAACAATCACACA
 GATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTAT
 GGACTGTGACTGACAACTTAAAAGTTGATTATTAGGCCAAATGACAGAT
 AGCGAATTGAACAGAGTATAAGAGTATCTTGACTTCTCCTACTGATACT
 TAATGGTCAGACAAAGATAGCACTCCCAAATGGTTTCGTACTTTGGTCGTG
 CTTATAAAGCTGATCAAAGCGTTTCAACAATAGTACCTTTTATATTGAA
 TTACCAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGAAA
 AGTTGAAACAGGCCGATTAAAACCTATTAAATATACAAAAGAAGGAAAGGA

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

TAAAGAAAAGGCTaTCAGGAGTAATATTTGTATTATACGATAACCAAGAT
 CAGCCAGTTTCGCTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT
 TACTTCATTAGTAAGTATGATGATAAGGGAGAAATGAGGTTGAAGGTTTAT
 TACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTaCCGT
 ATATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA
 AGTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAAC
 CATCACAAACC

SEQ ID NO. 4506

STRAIN 1169NT

GATACCCCTAATCAACTAACATCACACAG

ATAGGACTTCAGCCAAATACTACAGAGGAGGGGATTTCTTATCGTTTATG
 GACTGTGACTGACAACTTAAAGTTGATTATTAGGCGAAATGACAGATA
 GCGAATTGAACCAAGTATAAGAGTATCTTGACTTCTCTACTGATACT
 AATGGtCagaCAAAAGATAGCACTCCCAATGGTTTCGTACTTTGGTTCGTGC
 TTATAAAGCTGATCAAGCGTTTCAACAATAGTACCTTTTATATGAAT
 TACCAGATGATAAGTTATCAAAATCAATTACAGATAAATCCTAAGCGAAAA
 GTTGAACAGGCCGATTAAAACTTATTAATATACAAAGAGGAAAGAT
 AAAGAAAAGGCTATCAGGAGTAATATTTGTATTATACGATAACCAAGATC
 AGCCAGTTTCGCTTTAAAAATGGACGATTTCAGCCGATCAAGATGGGAT
 ACTTCATTAGTAAGTATGATAAGGAGAAATGAGGTTGAAGGTTTAT
 ACCTGGTAAGTATATTTTCGAGAAGCAAAAGCACTAACTGGTTACCGTA
 TATCTATGAAGGATGCTGTAGTTGCTGTAGTTGCTAATAAAACACAGGA
 GTAGAGGTAGAAAACGAAAAAGAACTCCTCCACCAACAAATCCTAAACC
 ATCACAAACC

PRETTY of: /biotmp/msa184750.2{*} May 13, 2003 06:23 ..

	1				50
msa184750.2{150_090}	-----	-----	-----	-----	-----
msa184750.2{150_1169NT}	-----	-----	-----	-----	-----
msa184750.2{150_CJB110}	-----	-----	-----	-----	-----
msa184750.2{150_18RS21}	-----	-----	-----	-----	-----
msa184750.2{150_2603}	atgaaaaaga	ttagaaaaag	tttaggactt	ctactatggt	gctttttagg
msa184750.2{150_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa184750.2{150_090}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_1169NT}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_CJB110}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_18RS21}	-----	-----	-----	-----	---GATACCC
msa184750.2{150_2603}	attggtacaa	ttagcgtttt	tttcggtagc	cagtgtaaat	gctGATACCC
msa184750.2{150_H36B}	-----	-----	-----	-----	---GATACCC
Consensus	*****	*****	*****	*****	*****
	101				150
msa184750.2{150_090}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_1169NT}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_CJB110}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_18RS21}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_2603}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
msa184750.2{150_H36B}	CTAATCAACT	AACAATCACA	CAGATAGGAC	TTCAGCCAAA	TACTACAGAG
Consensus	*****	*****	*****	*****	*****
	151				200
msa184750.2{150_090}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_1169NT}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_CJB110}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_18RS21}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_2603}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
msa184750.2{150_H36B}	GAGGGGATTT	CTTATCGTTT	ATGGACTGTG	ACTGACAACT	TAAAAGTTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa184750.2{150_090}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_1169NT}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_CJB110}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_18RS21}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_2603}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
msa184750.2{150_H36B}	TTTATTGAGC	CAAATGACAG	ATAGCGAATT	GAACCAGAAG	TATAAGAGTA
Consensus	*****	*****	*****	*****	*****
	251				300
msa184750.2{150_090}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_1169NT}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_CJB110}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_18RS21}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_2603}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
msa184750.2{150_H36B}	TCTTGACTTC	TCCTACTGAT	ACTAATGGTC	AGACAAAGAT	AGCACTCCCA
Consensus	*****	*****	*****	*****	*****
	301				350

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184750.2{150_090}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_1169NT}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_CJB110}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_18RS21}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_2603}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
msa184750.2{150_H36B}	AATGGTTCGT	ACTTTGGTTCG	TGCTTATAAA	GCTGATCAAA	GCGTTTCAAC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	351	400			
msa184750.2{150_1169NT}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_CJB110}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_18RS21}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_2603}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
msa184750.2{150_H36B}	AATAGTACCT	TTTTATATTG	AATTACCAGA	TGATAAGTTA	TCAAATCAAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	401	450			
msa184750.2{150_1169NT}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_CJB110}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_18RS21}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_2603}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
msa184750.2{150_H36B}	TACAGATAAA	TCCTAAGCGA	AAAGTTGAAA	CAGGCCGATT	AAAACTTATT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	451	500			
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_1169NT}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_CJB110}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCaG	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_18RS21}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTaTCcG	GAGTAATATT
msa184750.2{150_H36B}	AAATATACAA	AAGAAGGAAA	GATAAAGAAA	AGGCTwTCcG	GAGTAATATT
Consensus	*****	*****	*****	*****_--*	*****
msa184750.2{150_090}	501	550			
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_1169NT}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_CJB110}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_18RS21}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
msa184750.2{150_H36B}	TGTATTATAC	GATAACCAGA	ATCAGCCAGT	TCGCTTTAAA	AATGGACGAT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	551	600			
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_1169NT}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_CJB110}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_18RS21}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
msa184750.2{150_H36B}	TTACGACCGA	TCAAGATGGG	ATTACTTCAT	TAGTAACTGA	TGATAAGGGA
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	601	650			
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_1169NT}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_CJB110}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_18RS21}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
msa184750.2{150_H36B}	GAAATTGAGG	TTGAAGGTTT	ATTACCTGGT	AAGTATATTT	TTCGAGAAGC
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	651	700			
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_1169NT}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_CJB110}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_18RS21}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
msa184750.2{150_H36B}	AAAAGCACTA	ACTGGTTACC	GTATATCTAT	GAAGGATGCT	GTAGTTGCTG
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	701	750			
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_1169NT}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_CJB110}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_18RS21}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
msa184750.2{150_H36B}	TAGTTGCTAA	TAAAACACAG	GAAGTAGAGG	TAGAAAACGA	AAAAGAACT
Consensus	*****	*****	*****	*****	*****
msa184750.2{150_090}	751	800			
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CCg-----	-----
msa184750.2{150_1169NT}	CCTCCACCAA	CAAATCCTAA	ACCATCACAA	CC-----	-----

Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

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msa184750.2{150_CJB110} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_18RS21} CCTCCACCAA CAAATCCTAA ACCATCACAA CC-----
msa184750.2{150_2603} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgCtttttc cacaatcatt
msa184750.2{150_H36B} CCTCCACCAA CAAATCCTAA ACCATCACAA CCgC-----
Consensus *****

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801 850

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} tcttcctaaa acaggaatga ttattggtgg aggactgaca attcctggtt
msa184750.2{150_H36B} -----
Consensus *****

```

851 900

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} gtattatttt gggaattttg tttatccttt taagaaaaac taaaaatagc
msa184750.2{150_H36B} -----
Consensus *****

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901 924

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msa184750.2{150_090} -----
msa184750.2{150_1169NT} -----
msa184750.2{150_CJB110} -----
msa184750.2{150_18RS21} -----
msa184750.2{150_2603} aaatctgaaa gaaacgatac agta
msa184750.2{150_H36B} -----
Consensus *****

```

SEQ ID NO. 4507**STRAIN 2603**

MKKIRKSLGGLLCCFLGLVQLAFFSVASVNADTPNQLTITQIGLQPNTEEGISYRLWTV
 TDNLKVDLLSQMTDSELNQKYKSILTSPTDTNGQTKIALPNGSYFGRAYKADQSVSTIVP
 FYIELPDDKLSNQLQINPKRKVETGRLKLIK YTKEGKIKKRLSGVIFVLVDNQNPVRFK
 NGRFTTDDGITSVLVDDKGEIEVEGLLPKYIFREAKALTGYRISMKDAVVAVVANKTQ
 EVEVEKEKTPPPTNPKPSQPLFPQSFLPKTGMIGGGLTILGCI ILGILFI FLRKTRNS
 KSERNDTV

SEQ ID NO. 4508**STRAIN 090**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTKEGKIKKRLSGVIFVLVDNQNPVRFKNGRFTTDDGITSVLVDDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

SEQ ID NO. 4509**STRAIN H36B**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTKEGKIKKRLSGVIFVLVDNQNPVRFKNGRFTTDDGITSVLVDDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

SEQ ID NO. 4510**STRAIN 18RS21**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTKEGKIKKRLSGVIFVLVDNQNPVRFKNGRFTTDDGITSVLVDDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

SEQ ID NO. 4511**STRAIN 1169NT**

DTPNQLTITQIGLQPNTEEGISYRLWTVTDNLKVDLLSQMTDSELNQKYKSILTSPTDT
 NGQTKIALPNGSYFGRAYKADQSVSTIVPFYIELPDDKLSNQLQINPKRKVETGRLKLIK
 YTKEGKIKKRLSGVIFVLVDNQNPVRFKNGRFTTDDGITSVLVDDKGEIEVEGLLPKG
 YIFREAKALTGYRISMKDAVVAVVANKTQEVENEKETPPPTNPKPSQ

PRETTY of: /biotmp/msa184868.2{*} May 13, 2003 06:25 ..

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1 50
msa184868.2{150_090} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_2603} mkkirkslgl llccflglvq laffsvasvn aDTPNQLTIT QIGLQPNTE
msa184868.2{150_H36B} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_1169NT} ----- -DTPNQLTIT QIGLQPNTE
msa184868.2{150_18RS21} ----- -DTPNQLTIT QIGLQPNTE
Consensus *****

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51 100

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msa184868.2{150_090} EGISYRLWTV TDNLKVDLLS QMTDSELNQK YKSILTSPTD TNGQTKIALP

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Table 45: Comparative Sequences relating to SAG1404 (strain info highlighted in BOLD)

msa184868.2{150_2603}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNQK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_H36B}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNQK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_1169NT}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNQK	YKSILTSPTD	TNGQTKIALP
msa184868.2{150_18RS21}	EGISYRLWTV	TDNLKVDLLS	QMTDSELNQK	YKSILTSPTD	TNGQTKIALP
Consensus	*****	*****	*****	*****	*****
101					
msa184868.2{150_090}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_2603}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_H36B}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_1169NT}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRCLKLI
msa184868.2{150_18RS21}	NGSYFGRAYK	ADQSVSTIVP	FYIELPDDKL	SNQLQINPKR	KVETGRCLKLI
Consensus	*****	*****	*****	*****	*****
151					
msa184868.2{150_090}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_2603}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_H36B}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_1169NT}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
msa184868.2{150_18RS21}	KYTKEGKIKK	RLSGVIFVLY	DNQNQPVRFK	NGRFTTDQDG	ITSLVTDDKG
Consensus	*****	*****	*****	*****	*****
201					
msa184868.2{150_090}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_2603}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_H36B}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_1169NT}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
msa184868.2{150_18RS21}	EIEVEGLLPG	KYIFREAKAL	TGYRISMKDA	VVAVVANKTQ	EVEVENEKET
Consensus	*****	*****	*****	*****	*****
251					
msa184868.2{150_090}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_2603}	PPPTNPKPSQ	plfpqsfllpk	tgmiigggt	ilgciilgil	fiflrktkns
msa184868.2{150_H36B}	PPPTNPKPSQ	p-----	-----	-----	-----
msa184868.2{150_1169NT}	PPPTNPKPSQ	-----	-----	-----	-----
msa184868.2{150_18RS21}	PPPTNPKPSQ	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
301					
msa184868.2{150_090}	-----	-----	-----	-----	-----
msa184868.2{150_2603}	kserndtv	-----	-----	-----	-----
msa184868.2{150_H36B}	-----	-----	-----	-----	-----
msa184868.2{150_1169NT}	-----	-----	-----	-----	-----
msa184868.2{150_18RS21}	-----	-----	-----	-----	-----
Consensus	*****	-----	-----	-----	-----

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

SEQ ID NO. 4601

STRAIN A909

TGACAAATATTTTACCCAACTGGTTTAGAGCAAGCAGGTGTAACATATTTACCTTT
 CTCACCGAATAATATCAGTGAGGATTTAGAGATTATTGCAGGAAATGCTTTTCGTCCAGA
 TAACATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCATTTTAAACGATATCATGA
 ATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTGGGGCACATGGAAA
 AACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATTACAGACACTTCTTTCTCT
 AATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTGTGTTTGAAGCTGA
 TGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCAATTATTACCAATATTGA
 TTTTGACCATCTGATTATTTACAGGCCCTAGAGGACGTATTCAATGCCTTTAATGACTA
 TGCTAAGCAAGTTCAAAAAGGTTTATTATTATGGAGAAGATCCAAAACCTTCATGAAAT
 CACTTCTGAGGCACCAATATATTATTGGTTTGAAGATTCAAATGATTTTATAGCAAA
 AGACATCACTCGAAGCTGTTAATGGTTCTGACTTTAAGGTTTCTATAACCAAGAAAGAAAT
 TGGTCAGTTTCATGTACCGATACGGTAAACATAATATCTTAAATGCAACTGCTGTTAT
 TGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGCATTGAAGACATT
 TTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACGATCTGTCATTATTGATGA
 CTTTGGCTCACCATCTCTACTGAGATTATTGCGACATTAGATGCTGCTCGACAAAAATACCC
 GTCAAAAGAAATTTGATGCTAATTTTCCAACCGCATACGTTCACTCGTACGATAGCTCTTTT
 AGACGAATTTGCGCCCTTGAGTCAAGCGGATAGCGTTTATCTCGCTCAAAATATATGG
 TTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGAAGATTAGCTGCTAAGATTGT
 CAAACACTCAGATTATTAGTGACAGTCGAAAATGTCTCGCCTTTACTCAATCATGATATGTC
 TGTCTATGTCCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCTCTTTGAAGAATT
 ATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4602

STRAIN 1169NT

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACTGGTTTAGAGCAAGC
 AGGTGTAACATATATACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGC
 AGGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTA
 TCATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGG
 TGTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAA
 TATTACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
 TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
 CTCAAATTATACCAANTATTGATTTTGACCATCTGATTATTTTACAGGCCCTAGAGGACGT
 ATTCAATGCCCTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGA
 AGATCCAAAACCTTCATGAATTCACCTTCTGAGGCACCAATATATTATTATGGTTTGAAGA
 TTCAAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT
 TTTCTATAACCAAGAAAGAAATTTGGTCAGTTTCATGTACCGATACGGTAAACATAATAT
 CTTAAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGT
 AGCTGAGCATTGAAGACATTTTACAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA
 CGATACCTGTCATTATTGATGACTTTGCTCACCATCTTACTGAGATTATTGCGACATTAGA
 TGCTGCTCGACAAAAATACCCGTCAAAAGAAATTTGATGCTAATTTTCCAACCGCATACGTT
 CACTCGTACGATAGCTCTTTTACAGCAATTTGCCATGCTTGGTCAAGCGGATAGCGT
 TTATCTCGCTCAAAATATGCTGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGA
 AGATTAGCTGCTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGTCTCGCC
 TTACTCAATCATGATATATGCTGCTATGCTTTATGGGTGCTGGAGACATTCAATTGTA
 TGAGCGCTCTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4603

STRAIN 090

AAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACCCAACTGGTTTAGAGCAAGCA
 GGTGTAACATATATACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCA
 GGAAATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
 CATTTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGT
 GTAGCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
 ATTACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
 TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
 TCAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCCCTAGAGGACGTA
 TTCATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAA
 GATTCAAAACCTTCATGAATTCACCTTCTAAGGCACCAATATATTATTATGGTTTGAAGAT
 TCAATGATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGT
 TTCTATAACCAAGAAAGAAATTTGGTCAGTTTCATGTACCGATACGGTAAACATAATAT
 TTAATGCAACTGCTGTTTATGCTAACCCTTTACATAATGGGAATTGATATGGCATTAGTA
 GCTGAGCATTGAAGACATTTTACAGGGGTAAACGTCGTTTACTGAGAAGATTATTGAC
 GATACTGTCATTATTGATGACTTTGCTCACCATCTTACTGAGATTATTGCGACATTAGAT
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTTGATGCTAATTTTCCAACCGCATACGTT
 ACTCGTACGATAGCTCTTTTACAGCATTTTGCCATGCTTTGAGTCAAGCGGATAGCGTT
 TATCTTGTCTCAAAATATGCTGTTCTGCTAGAGAAGTAGATAATGGTGAAGGTAGA
 GATTTAGCTGCTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGTCTCGCC
 TTACTCAATCATGATATATGCTGCTATGCTTTATGGGTGCTGGAGACATTCAATTGTAT
 GAGCGCTCTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4604

STRAIN H36B

AAAAGCAGGCTCTAGTGACGTTGACAAATATTATTTTACTCAACGTCGTTTAGAGCAAGCAGGT
 ATAACATATATACCTTTCTCACCAGAATAATATCAGTGAGGATTTAGAGATTATTGCAAGG
 AATGCTTTTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATCAT
 TTTAAACGATATCATGAATTTCTCGGAGATTATTATGCGTCAGTTCACTAGTCTAGGTGTA
 GCTGGGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATT
 ACAGACACTTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATAC
 TTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACTCA
 ATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCCCTAGAGGACGTTATTC
 AATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTTATGGAGAAGAT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

CCAAAACCTTCATGAAATCACTTCTGAGGCACCAATATATTATTATGGTTTGAAGATTCA
AATGATTTTATAGCAAAAGATATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTC
TATAACCAAGAAGAAATGGTCAGTTTACGTAACCATACGATACGGTAAACATAATATCTTA
AATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCT
GAGCATTGGAAGACATTTTCAGGGGTAACCGTCTGTTTACTGAGAAAATTATTGACGAT
ACTGTCATTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGATGCT
GCTCGACAAAATATCCCGTCAAAAGAAATGTAGCTATTTTCCAACCGCATACGTTCACT
CGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTGTAGTCAAGCGGATAGCGTTTAT
CTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGAT
TTAGTCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCTTTA
CTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTATGAG
CGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4605

STRAIN 18RS21

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCA
GGTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA
GGAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
CATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
ATTACAGACACTTCTTTCTAATGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
TACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
TCAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTA
TTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA
GATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGAT
TCAAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATAT
TTAAATGCAACTGCTGTTATTTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
GCTGAGCATTGGAAGACGTTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGAC
GATACTGTCTATTATTTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGAT
GCTGCTCGACAAAATATCCCGTCAAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTT
ACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGTT
TATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
GATTTAGTCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCT
TTACTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTAT
GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4606

STRAIN M732

AAAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
TAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
TTACAGACACTTCTTTCTAATTTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
ACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATACT
CAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTT
TCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAAG
ATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGATT
CAAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTT
TTCTATAACCAAGAAGAAATTTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATATCT
TAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAG
CTGAGCATTGGAAGACATTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACG
ATACTGTCTATTATTTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGCATTAGATG
CTGCTCGACAAAATATCCCGTCAAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTTCA
CTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGTT
ATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
ATTAGTCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCT
TACTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTATG
AGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4607

STRAIN M781

AAAGCAGGCTCTAGTGACGTTGACAAATATTTTACCACCGTGGTTTAGAGCAAGCAG
GTGTAACCTATATACCTTTCTCACCGAATAATATCAGTGAGGATTAGAGATTATTGCA
GAAATGCTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTATC
ATTTTAAACGATATCATGAATTTCTCGGAGATTTTATGCGTCAGTTCACTAGTCTAGGT
GTAGCTGGGGCAGATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAAT
TATTACAGACACTTCTTTCTAATTTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAA
TTACTTTGTGTTTGAAGCTGATGAATACGAACGTCATTTTATGCCGTACCATCCAGAATA
TCAATTATTACCAATATTGATTTTGACCATCTGATTATTTTACAGGCTTAGAGGACGTT
ATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGA
AGATCCAAAACCTTCATGAATCACTTCTGAGGCACCAATATATTTATGGTTTGAAGA
TTCAAAATGATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGT
TTTCTATAACCAAGAAGAAATTTGGTCAGTTTTCATGTACAGCATACGGTAAACATAATAT
CTTAAATGCAACTGCTGTTTATTTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGT
AGCTGAGCATTGGAAGACATTTTCAGGGGTAAAGCGTCGTTTACTGAGAAGATTATTGA
CGATACTGTCTAATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGA
TGCTGCTCGACAAAATATCCCGTCAAAAGAAATTTAGTAGCTATTTTCCAACCGCATACGTT
CACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTGGAGTCAAGCGGATAGCGT
TTATCTCGCTCAAAATATATGGTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGA
AGATTAGTCTGCTAAGATTGTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCC
TTTACTCAATCATGATAATGCTGTCTATGCTTTATGGGTGCTGGAGACATTCAATTGTAT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

TGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4608

STRAIN CJB110

AAAAAGCAGGCTCTAGTGACGTTGACAAATATATTTTACCCAACGTGGTTAGAGCAAGCA
 GGTGTAACATAATACCTTTCTCACGGAATAATATCAGTGAGGATTAGAGATTATTGCA
 GGAAATGCTTTTCTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTAT
 CATTTTAAACGATATCATGAATTTCTCGGAGATTATGCGTCAGTTCACTAGTCTAGGT
 GTAGCTGGGGCACATGGAACCTCAACGACAGGTTATTAGCTCATGTTTAAAAAAT
 ATTACAGACACTTCTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAAT
 TACTTTGTGTTGAAGCTGATGAATACGACGTCATTTATGCCGTACCATCCAGAATAC
 TCAATTATTACCAATATGATTGTTGACCATCTGATTATTTACAGGCCCTAGAGGACGTA
 TTCAATGCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAGAA
 GATTCAAACTTTCATGAATCACTTCAAGGCACCAATATATATTATGTTTGAAGAT
 TCAATGATTTTATAGCAAAAGACATCACTCGAAGCTGTTAATGGTTCTGACTTTAAGGTT
 TTCTATAACCAAGAGAAATGGTCAAGTTTCACTACGAGCATACGGTAAACATAATATC
 TTAATGCAACTGCTGTTTATTGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTA
 GCTGAGGATTGGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAGATTATTGAC
 GATACTGTCAATTATGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGAT
 GCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCAACCCGCATACGTTT
 ACTCGTACGATAGCTCTTTTAGACGATTTTGCCCATGCTTTGAGTCAAGCGGATAGCGTT
 TATCTTGCTCAAAATATGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAA
 GATTAGCTGCTAAGATTGTTCAAACTCAGATTAGTGACAGTCGAAAATGTCTCGCCT
 TTACTCAATCATGATAATGCTGCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTAT
 GAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4609

STRAIN JM9130013 (reverse complement)

GTTCAAAAAGCAGGCTCTAGTGACGTTGACAAATATATTTTACTCAACGTGGTTTGA
 GCAAGCAGGTATACCTATATTAACCTTTCTCACGGAATAATATCAGTGAGGATTAGAGAT
 TATGTCAGGAATGCTTTTCTCGTCCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAA
 GGGCTATCATTTTAAACGATATCATGAATTTCTCGGAGATTATGCGTCAGTTCACTAG
 TCTAGGTGATAGCTGGGGCACATGGAACCTCAACGACAGGTTATTAGCTCATGTTT
 AAAAAATATTACAGACACTTCTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAA
 TGCTAATTACTTTTGTGTTTGAAGCTGATGAATACGAACTGCTTTTATGCCGTACCATCC
 AGAATACCTAATATTAACCAATATTGATTTTGACCATCCTGATTATTTACAGGCCCTAGA
 GGAGCTATTCAATGCTTTTAAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTA
 TGGAGAAGATCCAAACTTCATGAATCACTTCTGAGGCACCAATATATATTATGTTT
 TGAAGATTCAATGATTTTATAGCAAAAGATATCACTCGAAGCTGTTAATGGTTCTGACTT
 TAAGGTTTCTTATAACCAAGAGAAATGGTCAAGTTTCACTACGAGCATACGGTAAACCA
 TAATATCTTAAATGCAACTGCTGTTATTGCTAACCTTTACATAATGGGAATTGATATGGC
 ATTAGTAGCTCAGCATTTGAAGACATTTTCAAGGGTAAAACGTCGTTTACTGAGAAAT
 TATTGACGATACCTGCTATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGAC
 ATTAGATGCTGCTCGACAAAAATACCCGTCAAAAGAAATTGTAGCTATTTTCCAACCGCA
 TACGTTCACTCGTACGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGA
 TAGCGTTTATCTCGCTCAAAATATGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAA
 GGTAGAAGATTAGCTGCTTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGT
 CTCGCCCTTACTCAATCATGATAATGCTGCTATGCTTTTATGGGTGCTGGAGACATTCA
 ATTGTATGAGCGCTCTTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4610

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTGACAAATATATTTTACCCAACGTGGTTAGAGCAAGCAGGTGTAA
 CTATATTACCTTTCTCACGGAATAATATCAGTGAGGATTAGAGATTATTGTCAGGAATG
 CTTTTCGTCAGATACATGAAGAGTTGGCTTATGTTATTGAAAAGGGCTCATTTTAA
 AACGATATCATGAATTTCTCGGAGATTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
 GGGCACATGGAACCTCAACGACAGGTTATTAGCTCATGTTTAAAAAATATTACAG
 ACACCTCTTTCTTAATTGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG
 TGTTGAAGCTGATGAATACGAACTGCTTTTATGCCGTACCATCCAGAATACTCAATTA
 TTACCAATATTGATTTTGACCATCCTGATTATTTTACAGGCCCTAGAGGACGTAATCAATG
 CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCAATTATGGAAGATCCAA
 AACCTCATGAATCACTTCTGAGGCACCAATATATATTATGTTTGAAGATTCAATG
 ATTTTATAGCAAAAGACATCACTCGAAGCTTAAATGGTTCTGACTTTAAGGTTTCTATA
 ACCAAGAAGAAATGGTCAAGTTTCACTGACGATACGGTAAACATAATATCTTAAATG
 CAAGTCTGTTTATGCTAACCTTTACATAATGGGAATTGATATGGCATTAGTAGCTGAGC
 ATTTGAAGACATTTTCAAGGGTAAAGCGTCGTTTACTGAGAAGATTATTGACGATACCT
 TCATTATTGATGACTTTGCTCACCATCCTACTGAGATTATTGCGACATTAGATGCTGCTC
 GACAAAAATACCCGTCAAAAGAAATGTAGCTATTTTCCAACCGCATACGTTCACTCGTA
 CGATAGCTCTTTTAGACGAATTTGCCCATGCTTTGAGTCAAGCGGATAGCGTTTATCTCG
 CTCAATATATTGTTTCTGCTAGAGAAGTAGATAATGGTGAGGTGAAGGTAGAAGATTAG
 CTGCTAAGATTGTCAAACTCAGATTATTAGTGACAGTCGAAAATGTCTCGCCTTACTCA
 ATCATGATAATGCTGCTATGCTTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
 CTTTGAAGAATTATTAGCTAACCTAACTAAAAATACACAA

SEQ ID NO. 4611

STRAIN 2603

atgtcaaaaacttatcattttattgggtattaaaggatccggaatgagtgccctagcactg
 atgcttcacataaatgggacataaacgtccaaggaagtgacgttgacaaatattatttacc
 caacgtgggttagagcaagcaggtgtaactatattacctttctcaccgaataatcagc
 gaggatttagagattattgcaggaatgcttttctgctccagataacaatgaagagttggct
 tatgttatggaaaagggtatcaatttaaacgataatgaattttctcgagattttatg
 cgtcagttcaactagtcaggtgtagctggggcacatggaaaaacctcaacgacaggttta
 ttagctcatgttttaaaaatattacagacacttctttcctaattggagatgggtacagga

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

cgtgggtctgctaattactttgtgttgaagctgatgaatacgaacgtcatttt
 atgccgtaccatccagaataactcaattattaccaatattgattttgaccatcctgattat
 tttacaggcttagaggacgtattcaatgcctttaatgactatgctaagcaagttcaaaaa
 gggtttattcatttatggagaagatccaaaacttcatgaaatcacttctgaggcaccaata
 tattattatgggttttgaagattcaaatgattttatagcaaaagacatcactcgaactgtt
 aatgggtctgacttttaagggtttctataaccaagaagaatttggtcagtttcatgtacca
 gcatacggtaaaacataatatttaaatgcaactgctgttattgctaaccctttacataatg
 ggaatttgatattggcatttagtagctgagcatttgaagacgttttcaggggtaagcgtcgt
 ttactgagaagattattgacgatactgtcattattgatgactttgctcaccatcctact
 gagattattgcgacatttagatgctgctcgacaaaaataccggtcaaaagaattttagct
 attttccaacccgatacgttcaactcgtacgatactgtttagacgaatttgcccatgcc
 ttgagtcaagcggatagcgtttatctcgctcaaatatattggttctgctagagaagtagat
 aatgggtgaggtgaaggttagaagatttagctgctaagatttgtcaaacactcagatttagtg
 acagtgcgaattgtctcgcttactcaatcatgataatgctgtctatgtctttaggggt
 gctggagacattcaattgtatgagcgtcttttgaagaattatttagtaacctaaactaaa
 aatacacia

SEQ ID NO. 4612

STRAIN COH1 reverse complement

CAGGCTCTAGTGACGTTGACAAATATATTTTACCCCAACGTGGTATTAGAGCAAGCAGGTGTAA
 CTATATTACTCTTCTCACCGAATAATATCAGTGAGGATTATGAGATTATTCAGGAAATG
 CTTTTCGTCAGATAACAATGAAGAGTTGGCTTATGTTATTGAAAAGGCTATCATTTTA
 AACGATATCATGAATTTCTCGGAGATTTATGCGTCAGTTCACTAGTCTAGGTGTAGCTG
 GGGCACATGGAAAAACCTCAACGACAGGTTTATTAGCTCATGTTTAAAAAATATACAG
 ACACCTCTTTCTTAATGGAGATGGTACAGGACGTGGTTCTGCTAATGCTAATTACTTTG
 TGTTTGAAGCTGTATGAATGACGAGTCAATTTATGCGGTACCATCCAGAATACTCAATTA
 TTACAATATTGATTGACCATCTGATTATTTACAGGCTTAGAGGACGTATTCAATG
 CCTTTAATGACTATGCTAAGCAAGTTCAAAAAGGTTTATTCATTTATGGAGAAGATCCAA
 AACITCATGAATACACTTCTGAGGCACCAATATATTTATTTGTTTGAAGATTCAAATG
 ATTTTATAGCAAAAGACATCACTCGAACTGTTAATGGTTCTGACTTTAAGGTTTCTATA
 ACCAAGAAGAAATGGTCAGTTTATGTAACGACATACGGTAAACATAATATCTTAAATG
 CACTGCTGTTTATGCTAACCTTTACATAATGGGAATTTGATATGGCATTAGTAGCTGAGC
 ATTTGAAGACATTTTCAGGGGTAAAGCGTCTGTTTACTGAGAAGATTATTGACGATACTG
 TCATTTATGATGACTTTGCTCACCATCTACTGAGATTATTGCGACATTAGATGCTGCTC
 GACAAAAATACCCGTCAAAAGAAATTTGTAGCTATTTTCCAACCGCATACGTTCACTCGTA
 CGATAGCTCTTTTAGACGAATTTGCCCATGCGCTTGAAGTCAAGCGGATAGCGTTTATCTCG
 CTCAAATATATGCTTCTAGAGAAGTAGATAATGGTGAGGTGAAGTGAAGAATTTAG
 CTGCTAAGATTGTCAAACACTCAGATTATTAGTGACAGTGCAAAAATGCTCTCGCTTTACTCA
 ATCATGATAATGCTGTCTATGCTCTTTATGGGTGCTGGAGACATTCAATTGTATGAGCGCT
 CTTTGAAGAATTTATAGCTAACCTAACCTAAAAATACACAA

PRETTY of: /biotmp/msa56524.2{*} November 26, 2002 08:06 ..
 PRETTY of: /biotmp/msa253045.2{*} January 31, 2003 03:51 ..

	1		50
msa253045.2{157_090}	-----	-----	-----
msa253045.2{157_CJB110}	-----	-----	-----
msa253045.2{157_H36B}	-----	-----	-----
msa253045.2{157_JM9130013}	-----	-----	-----
msa253045.2{157_1169NT}	-----	-----	-----
msa253045.2{157_A909}	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----
msa253045.2{157_M732}	-----	-----	-----
msa253045.2{157_M781}	-----	-----	-----
msa253045.2{157_18RS21}	-----	-----	-----
msa253045.2{157_2603}	atgtcaaaaa	cttatcattt	tattgggtatt
Consensus	*****	*****	*****
	51		100
msa253045.2{157_090}	-----	-----	-----
msa253045.2{157_CJB110}	-----	-----	-----
msa253045.2{157_H36B}	-----	-----	-----
msa253045.2{157_JM9130013}	-----	-----	-----
msa253045.2{157_1169NT}	-----	-----	-----
msa253045.2{157_A909}	-----	-----	-----
msa253045.2{157_COH1}	-----	-----	-----
msa253045.2{157_M732}	-----	-----	-----
msa253045.2{157_M781}	-----	-----	-----
msa253045.2{157_18RS21}	-----	-----	-----
msa253045.2{157_2603}	cctagcactg	atgcttcac	aaatgggacA
Consensus	*****	*****	*****
	101		150
msa253045.2{157_090}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_CJB110}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_H36B}	tTGACAAATA	TTATTTTACt	CAACGTGGTT
msa253045.2{157_JM9130013}	tTGACAAATA	TTATTTTACt	CAACGTGGTT
msa253045.2{157_1169NT}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_A909}	-TGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_COH1}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_M732}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_M781}	tTGACAAATA	TTATTTTACc	CAACGTGGTT
msa253045.2{157_18RS21}	tTGACAAATA	TTATTTTACc	CAACGTGGTT

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_2603}	tTGACAAATA	TTATTTTAcc	CAACGTGGTT	TAGAGCAAGC	AGGTgTAACT
Consensus	*****	*****	*****	*****	*****
	151				200
msa253045.2{157_090}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_CJB110}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_H36B}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_JM9130013}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_1169NT}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_A909}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_COH1}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M732}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_M781}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_18RS21}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
msa253045.2{157_2603}	ATATTACCTT	TCTCACCgAA	TAATATCAGT	GAGGATTTAG	AGATTATTGC
Consensus	*****	*****	*****	*****	*****
	201				250
msa253045.2{157_090}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_CJB110}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_H36B}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_JM9130013}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_1169NT}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_A909}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_COH1}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M732}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_M781}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_18RS21}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
msa253045.2{157_2603}	AGGAAATGCT	TTTCGTCCAG	ATAACAATGA	AGAGTTGGCT	TATGTTATTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa253045.2{157_090}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_CJB110}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_H36B}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_JM9130013}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_1169NT}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_A909}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_COH1}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M732}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_M781}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_18RS21}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
msa253045.2{157_2603}	AAAAGGGCTA	TCAtTTTAAa	CGATATCATG	AATTTCTCGG	AGATTTTATG
Consensus	*****	*****	*****	*****	*****
	301				350
msa253045.2{157_090}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_CJB110}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_H36B}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_JM9130013}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_1169NT}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_A909}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_COH1}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M732}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_M781}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_18RS21}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
msa253045.2{157_2603}	CGTCAGTTCA	CTAGTCTAGG	TGTAGCTGGG	GCACATGGAA	AAACCTCAAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa253045.2{157_090}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_CJB110}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_H36B}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_JM9130013}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_1169NT}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_A909}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_COH1}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M732}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_M781}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_18RS21}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
msa253045.2{157_2603}	GACAGGTTTA	TTAGCTCATG	TTTTAAAAAA	TATTACAGAC	ACTTCCTTCC
Consensus	*****	*****	*****	*****	*****
	401				450
msa253045.2{157_090}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_CJB110}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_H36B}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_JM9130013}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_1169NT}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_A909}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_COH1}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M732}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_M781}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCTG	CTAATGCTAA	TTACTTTGTG

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_18RS21}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCCTG	CTAATGCTAA	TTACTTTGTG
msa253045.2{157_2603}	TAATTGGAGA	TGGTACAGGA	CGTGGTTCCTG	CTAATGCTAA	TTACTTTGTG
Consensus	*****	*****	*****	*****	*****
	451				500
msa253045.2{157_090}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_CJB110}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_H36B}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_JM9130013}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_1169NT}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_A909}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_COH1}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M732}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_M781}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_18RS21}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
msa253045.2{157_2603}	TTTGAAGCTG	ATGAATACGA	ACGTCATTTT	ATGCCGTACC	ATCCAGAATA
Consensus	*****	*****	*****	*****	*****
	501				550
msa253045.2{157_090}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_CJB110}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_H36B}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_JM9130013}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_1169NT}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_A909}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_COH1}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M732}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_M781}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_18RS21}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
msa253045.2{157_2603}	CTCAATTATT	ACCAATATTG	ATTTTGACCA	TCCTGATTAT	TTTACAGGCc
Consensus	*****	*****	*****	*****	*****
	551				600
msa253045.2{157_090}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_CJB110}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_H36B}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_JM9130013}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_1169NT}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_A909}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_COH1}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M732}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_M781}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_18RS21}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
msa253045.2{157_2603}	TAGAGGACGT	ATTCAATGCT	TTTAATGACT	ATGCTAAGCA	AGTTCAAAAA
Consensus	*****	*****	*****	*****	*****
	601				650
msa253045.2{157_090}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTaA
msa253045.2{157_CJB110}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTaA
msa253045.2{157_H36B}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_JM9130013}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_1169NT}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_A909}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_COH1}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M732}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_M781}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_18RS21}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
msa253045.2{157_2603}	GGTTTATTCA	TTTATGGAGA	AGATcCAAAA	CTTCATGAAA	TCACCTCTgA
Consensus	*****	*****	*****	*****	*****
	651				700
msa253045.2{157_090}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_CJB110}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_H36B}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_JM9130013}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_1169NT}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_A909}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_COH1}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M732}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_M781}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_18RS21}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
msa253045.2{157_2603}	GGCACCAATA	TATTATTATG	GTTTGAAGA	TTCAAATGAT	TTTATAGCAA
Consensus	*****	*****	*****	*****	*****
	701				750
msa253045.2{157_090}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_CJB110}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_H36B}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_JM9130013}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_1169NT}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_A909}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_COH1}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC
msa253045.2{157_M732}	AAGAcATCAC	TCGAACGTGT	AATGGTTCCTG	ACTTTAAGGT	TTTCTATAAC

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M781}	AAGACATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_18RS21}	AAGACATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
msa253045.2{157_2603}	AAGACATCAC	TCGAACGTGT	AATGGTTCTG	ACTTTAAGGT	TTTCTATAAC	
Consensus	****-****	*****	*****	*****	*****	
751						800
msa253045.2{157_090}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_CJB110}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_H36B}	CAAGAAGAAA	TTGGTCAGTT	TCACGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_JM9130013}	CAAGAAGAAA	TTGGTCAGTT	TCACGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_1169NT}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_A909}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_COH1}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M732}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_M781}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_18RS21}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
msa253045.2{157_2603}	CAAGAAGAAA	TTGGTCAGTT	TCATGTACCA	GCATACGGTA	AACATAATAT	
Consensus	*****	*****	****-****	*****	*****	
801						850
msa253045.2{157_090}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_CJB110}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_H36B}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_JM9130013}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_1169NT}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_A909}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_COH1}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M732}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_M781}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_18RS21}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
msa253045.2{157_2603}	CTTAAATGCA	ACTGCTGTTA	TTGCTAACCT	TTACATAATG	GGAATTGATA	
Consensus	*****	*****	*****	*****	*****	
851						900
msa253045.2{157_090}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_CJB110}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_H36B}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_JM9130013}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_1169NT}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_A909}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_COH1}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_M732}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_M781}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACaT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_18RS21}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCTG	
msa253045.2{157_2603}	TGGCATTAGT	AGCTGAGCAT	TTGAAGACgT	TTTCAGGGGT	AAAaCGTCTG	
Consensus	*****	*****	*****	*****	***-****	
901						950
msa253045.2{157_090}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_CJB110}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_H36B}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_JM9130013}	TTTACTGAGA	AaATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_1169NT}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_A909}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_COH1}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M732}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_M781}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_18RS21}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
msa253045.2{157_2603}	TTTACTGAGA	AgATTATTGA	CGATACTGTC	ATTATTGATG	ACTTTGCTCA	
Consensus	*****	*-*****	*****	*****	*****	
951						1000
msa253045.2{157_090}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_CJB110}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_H36B}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_JM9130013}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_1169NT}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_A909}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_COH1}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M732}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_M781}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_18RS21}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
msa253045.2{157_2603}	CCATCCTACT	GAGATTATTG	CGACATTAGA	TGCTGCTCGA	CAAAAATACC	
Consensus	*****	*****	*****	*****	*****	
1001						1050
msa253045.2{157_090}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_CJB110}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_H36B}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_JM9130013}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_1169NT}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_A909}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	
msa253045.2{157_COH1}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG	

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_M732}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_M781}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_18RS21}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
msa253045.2{157_2603}	CGTCAAAAGA	AATTGTAGCT	ATTTTCCAAC	CGCATACGTT	CACCTCGTACG		
Consensus	*****	*****	*****	*****	*****		
msa253045.2{157_090}	1051	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT	1100
msa253045.2{157_CJB110}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_H36B}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_JM9130013}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_1169NT}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_A909}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_COH1}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M732}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_M781}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_18RS21}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
msa253045.2{157_2603}	ATAGCTCTTT	TAGACGAaTT	TGCCCATGcC	TTGAGTCAAG	CGGATAGCGT		
Consensus	*****	*****_**	*****	*****	*****	*****	*****
msa253045.2{157_090}	1101	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG	1150
msa253045.2{157_CJB110}	TTATCTtGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_H36B}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_JM9130013}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_1169NT}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_A909}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_COH1}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M732}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_M781}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_18RS21}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
msa253045.2{157_2603}	TTATCTcGCT	CAAATATATG	GTTCTGCTAG	AGAAGTAGAT	AATGGTGAGG		
Consensus	*****_***	*****	*****	*****	*****	*****	*****
msa253045.2{157_090}	1151	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG	1200
msa253045.2{157_CJB110}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_H36B}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_JM9130013}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_1169NT}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_A909}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_COH1}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M732}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_M781}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_18RS21}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
msa253045.2{157_2603}	TGAAGGTAGA	AGATTTAGCT	GCTAAGATTG	TCAAACACTC	AGATTTAGTG		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa253045.2{157_090}	1201	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT	1250
msa253045.2{157_CJB110}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_H36B}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_JM9130013}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_1169NT}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_A909}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_COH1}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M732}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_M781}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_18RS21}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
msa253045.2{157_2603}	ACAGTCGAAA	ATGTCFCGCC	TTTACTCAAT	CATGATAATG	CTGTCTATGT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa253045.2{157_090}	1251	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT	1300
msa253045.2{157_CJB110}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_H36B}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_JM9130013}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_1169NT}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_A909}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_COH1}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M732}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_M781}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_18RS21}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
msa253045.2{157_2603}	CTTTATGGGT	GCTGGAGACA	TTCAATTGTA	TGAGCGCTCT	TTTGAAGAAT		
Consensus	*****	*****	*****	*****	*****	*****	*****
msa253045.2{157_090}	1301	TATTAGCTAA	CCTAACTAAA	AATACACAA			1329
msa253045.2{157_CJB110}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_H36B}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_JM9130013}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_1169NT}	TATTAGCTAA	CCTAACTAAA	AATACACAA				
msa253045.2{157_A909}	TATTAGCTAA	CCTAACTAAA	AATACACAA				

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253045.2{157_COH1}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M732}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_M781}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_18RS21}	TATTAGCTAA	CCTAACTAAA	AATACACAA
msa253045.2{157_2603}	TATTAGCTAA	CCTAACTAAA	AATACACAA
Consensus	*****	*****	*****

SEQ ID NO. 4613**STRAIN A909 frame: 2**

DKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHFKRYHE
 FLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANANYFVFEAD
 EYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGEDPKLHEI
 TSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVI
 ANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDAARQKYP
 SKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIV
 KHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4614**STRAIN 1169NT frame: 2**

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDA
 ARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4615**STRAIN 090 FRAME:1**

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DSKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDA
 ARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4616**STRAIN H36B frame: 2**

KAGSSDVKYYFTQRGLEQAGITILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDA
 ARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4617**STRAIN 18RS21 frame: 1**

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDA
 ARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4618**STRAIN M732 frame: 2**

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKHNIL
 NATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIATLDA
 ARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4619**STRAIN JM9130013 frame: 2**

FKKAGSSDVKYYFTQRGLEQAGITILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEK
 GYHFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSAN
 ANYFVFEADEYERHFMYPHYEYSIITNIDFDHPDYFTGLEDVFNAFNDYAKQVQKGLFIY
 GEDPKLHEITSEAPIYYGFEEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAYGKH
 NILNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDDTVIIDDFAHHPTEIAT
 LDAARQKYPSEKEIVAIQFPHFTFTRTIALLDEFahalSQADSVYLAQIYGSAREVDNGEVK
 VEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTNTQ

SEQ ID NO. 4620**STRAIN M781 frame: 1**

KAGSSDVKYYFTQRGLEQAGVTILPFPSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVLNITDTSFLIGDGTGRGSANAN

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE
 DPKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTEIIATLD
 AARQKYPSEKIVAIIFQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4621

STRAIN CJB110 frame: 3

KAGSSVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGY
 HFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVKNITDTSFLIGDGTGRGSANAN
 YFVFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGE
 DSKLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHN
 LNATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTEIIATLD
 AARQKYPSEKIVAIIFQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVE
 DLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4622

STRAIN 2603 frame: 1

MSKTYHFIGIKGSGMSALALMLHQMGNHVQGSVDKYYFTQRGLEQAGVTILPFSPNNIS
 EDLEIIAGNAFRPDNNEELAYVIEKGYQFKRYHEFLGDFMRQFTSLGVAGAHGKTSTTGL
 LAHVKNITDTSFLIGDGTGRGSANANYFVFEADEYERHFMPYHPEYSIIITNIDFDHPDY
 FTGLEDFVNAFNDYAKQVQKGLFIYGEDPKLHEITSEAPIYYYGFEDSNDFIAKDITRTV
 NGSDFKVFYNQEEIGQFHVPAKGKHNILNATAVIANLYIMGIDMALVAEHLKTFSGVKRR
 FTEKIIDTVIIDFAHHPTEIIATLDAARQKYPSEKIVAIIFQPHFTFTRTIALLDFAHA
 LSQADSVYLAQIYGSAREVDNGEVKVEDLAAKIVKHSDLVTVENVSPLLNHDNAVYVFMG
 AGDIQLYERSFEELLANLTKNTQ

SEQ ID NO. 4623

STRAIN COH1 frame: 3

GSSVDKYYFTQRGLEQAGVTILPFSPNNISEDLEIIAGNAFRPDNNEELAYVIEKGYHF
 KRYHEFLGDFMRQFTSLGVAGAHGKTSTTGLLAHVKNITDTSFLIGDGTGRGSANANYF
 VFEADEYERHFMPYHPEYSIIITNIDFDHPDYFTGLEDFVNAFNDYAKQVQKGLFIYGEDP
 KLHEITSEAPIYYYGFEDSNDFIAKDITRTVNGSDFKVFYNQEEIGQFHVPAKGKHNILN
 ATAVIANLYIMGIDMALVAEHLKTFSGVKRRFTEKIIDTVIIDFAHHPTEIIATLDAAR
 QKYPSEKIVAIIFQPHFTFTRTIALLDFAHALSQADSVYLAQIYGSAREVDNGEVKVEDL
 AAKIVKHSDLVTVENVSPLLNHDNAVYVFMGAGDIQLYERSFEELLANLTKNTQ

PRETTY of: /biotmp/msa56635.2{*} November 26, 2002 08:08 ..

	1		50
msa253220.2{157_090}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_CJB110}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_1169NT}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_18RS21}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M732}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_M781}	-----	-----kag	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_COH1}	-----	-----g	ssdvDKYYFT QRGLEQAGvT
msa253220.2{157_H36B}	-----	-----kag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_JM9130013}	-----	-----fkkag	ssdvDKYYFT QRGLEQAGiT
msa253220.2{157_2603}	msktyhfigi	kgsgmsalal	mlhqmghnvq gsdvDKYYFT QRGLEQAGvT
msa253220.2{157_A909}	-----	-----	DKYYFT QRGLEQAGvT
Consensus	*****	*****	-----*****
	51		100
msa253220.2{157_090}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_CJB110}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_1169NT}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_18RS21}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_M732}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_M781}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_COH1}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_H36B}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_JM9130013}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
msa253220.2{157_2603}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYqFK RYHEFLGDFM
msa253220.2{157_A909}	ILPFSPNNIS	EDLEIIAGNA	FRPDNNEELA YVIEKGYhFK RYHEFLGDFM
Consensus	*****	*****	*****_**
	101		150
msa253220.2{157_090}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_CJB110}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_1169NT}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_18RS21}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_M732}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_M781}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_COH1}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_H36B}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_JM9130013}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_2603}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
msa253220.2{157_A909}	RQFTSLGVAG	AHGKTSTTGL	LAHVKNITD TSFLIGDGTG RGSANANYFV
Consensus	*****	*****	*****
	151		200
msa253220.2{157_090}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY FTGLEDFVNA FNDYAKQVQK

Table 46: Comparative Sequences relating to SAG1615 (strain info highlighted in BOLD)

msa253220.2{157_CJB110}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_1169NT}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_18RS21}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M732}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_M781}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_COH1}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_H36B}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_JM9130013}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_2603}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
msa253220.2{157_A909}	FEADEYERHF	MPYHPEYSII	TNIDFDHPDY	FTGLEDVFNA	FNDYAKQVQK
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_CJB110}	GLFIYGEDsK	LHEITskAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_1169NT}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_18RS21}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_M732}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_M781}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_COH1}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_H36B}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_JM9130013}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_2603}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
msa253220.2{157_A909}	GLFIYGEDpK	LHEITseAPI	YYYGFEDSND	FIKADITRTV	NGSDFKVFYN
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_CJB110}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_1169NT}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_18RS21}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M732}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_M781}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_COH1}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_H36B}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_JM9130013}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_2603}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
msa253220.2{157_A909}	QEEIGQFHVP	AYGKHNILNA	TAVIANLYIM	GIDMALVAEH	LKTFSGVKRR
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_CJB110}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_1169NT}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_18RS21}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M732}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_M781}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_COH1}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_H36B}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_JM9130013}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_2603}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
msa253220.2{157_A909}	FTEKIIDDTV	IIDDFAHHT	EIIATLDAAR	QKYSKEIVA	IFQPHTFTRT
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_CJB110}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_1169NT}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_18RS21}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M732}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_M781}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_COH1}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_H36B}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_JM9130013}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_2603}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
msa253220.2{157_A909}	IALLDdFAHA	LSQADSVYLA	QIYGSAREVD	NGEVKVEDLA	AKIVKHSIDL
Consensus	*****	*****	*****	*****	*****
msa253220.2{157_090}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_CJB110}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_1169NT}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_18RS21}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M732}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_M781}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_COH1}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_H36B}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_JM9130013}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_2603}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
msa253220.2{157_A909}	TVENVSPLL	HDNAVYVFMG	AGDIQLYERS	FEELLANLTK	NTQ
Consensus	*****	*****	*****	*****	*****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)**SEQ ID NO. 4701****STRAIN A909**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4702**STRAIN H36B**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4703**STRAIN 18RS21**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4704**STRAIN M732**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4705**STRAIN COH1**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT
 TATAAAGGTAATTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 AGCCGTTAAGGAAAAAAGCGGAGAAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAATTTCTCAGACGAGGATACCTGCTAAAAAAGAA
 GATAAGGCTCCTGAAACAAAAGTAGAAGATATTGTCAITGATTATAAAGA
 AAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4706**STRAIN M781**

TATTTTAAACAACAAAAAGGAAAAGAGC
 TAAGGAAAAATGCAGAAAAATTTCTATGGAGAATATAAAGAAAATCCAGAA
 GAATATCATCAAATAGCTAAAGATAAAGCAAGTGAATATTCAAATTTAGC
 TGTGATACITTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGA
 CAACAGAGGATATCGTCTCAGCCGTTAAGGAAAAAAGCGGAGAAGTAGTT
 GACTTTGCTAATGATTTTGTCAATCAAGCTAAATCAAATTTCTCAGACGA
 GGATACCTGCTAAAAAAGAGATAAGGCTCCTGAAACAAAAGTAGAAGATA
 TTGTCAITGATTATAAAGAAAACACAGAAGATAAAGAAAAA

SEQ ID NO. 4707**STRAIN 2603**

tatTTTTaacaacaaaaaaggaaaagagctaaggaaaaatgcagaaaa
 attctatggagaatataaagaaaatccagaagaatcatcaaataagcta
 aagataaagcaagtgaatattcaaatttagctgttgatacttttaagat
 tataaaggtaaatTTGAATCAGGTGAATTGACAACAGAGGATATCGTCTC
 agccgttaaggaaaaaagcggagaagtagttgactttgctaatgattttg
 tcaatcaagctaaatcaaaattctcagacgaggatactgctaaaaaagaa
 gataaggctcctgaacaaaaagtagaagatattgtcattgattataaaga
 aaacacagaagataaagaaaaa

SEQ ID NO. 4708**STRAIN 090**

TATTTTAAACAACAAAAAGGAAAAGAGCTAAGGAAAAATGCAGAAAA
 ATTCTATGGAGAATATAAAGAAAATCCAGAAGAATATCATCAAATAGCTA
 AAGATAAAGCAAGTGAATATTCAAATTTAGCTGTTGATACITTTAAAGAT

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

TATAAAGGTTAAATTGAATCAGGTGAATTGACACAGAGGATATCGTCTC
 AGCCCGTTAAGGAAAAAGCGGAGAGTAGTTGACTTTGCTAATGATTTTG
 TCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATCTGCTAAAAAGAA
 GATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTGATTATAAAGA
 AAACACAGAAGATAAGAAAA

SEQ ID NO. 4709

STRAIN CJB110

TATTTTAAACAAAAAGGAAAAAGGCTAAGGAAAA
 ATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCAT
 CAAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATA
 TTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAGG
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC
 TAAAAAGAAGATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG
 ATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4710

STRAIN 1169NT

TATTTTAAACAAAAAGGAAAAAGGCTAAGGAAAA
 AATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCA
 TCAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATA
 CTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAG
 GATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGC
 TAATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGATGAGGATACTG
 CTAAAAAGAAAAATAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATT
 GATTATAAAGAAAAACAGAAGATAAAGAAAA

SEQ ID NO. 4711

STRAIN JM9130013

TATTTTAAACAAAAAGGAAAAAGGCTAAGGAAAA
 ATGCAGAAAAATTTCTATGGAGAATATAAGAAAAATCCAGAAGATATCAT
 CAAATAGCTAAAGATAAAGCAAGTGAATATTTCAAATTTAGCTGTTGATA
 TTTTAAAGATTATAAAGGTAATTTGAATCAGGTGAATTGACACAGAGG
 ATATCGTCTCAGCCGTAAAGGAAAAAGCGGAGAAGTAGTTGACTTTGCT
 AATGATTTTGTCAATCAAGCTAAATCAAAATTTCTCAGACGAGGATACTGC
 TAAAAAGAAGATAAAGGCTCTGAAACAAAAAGTAGAAGATATTGTCATTG
 ATTATAAAGAAAAACAGAAGATAAAGAAAA

PRETTY of: /biotmp/msa68511.2{*} January 22, 2003 05:47 ..

	1	50
msa68511.2{164_090}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_18RS21}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_2603}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_A909}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_CJB110}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_COH1}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_H36B}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_JM9130013}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_M732}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_M781}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
msa68511.2{164_1169NT}	TATTTTAA	CAACAAAAAGGAAAAAGAGCTAAGGAAAA
Consensus	*****	*****
	51	100
msa68511.2{164_090}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_18RS21}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_2603}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_A909}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_CJB110}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_COH1}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_H36B}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_JM9130013}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_M732}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_M781}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
msa68511.2{164_1169NT}	ATTCTATGGA	GAATATAAAG AAAATCCAGA AGAATATCAT CAAATAGCTA
Consensus	*****	*****
	101	150
msa68511.2{164_090}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_18RS21}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_2603}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_A909}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_CJB110}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_COH1}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_H36B}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_JM9130013}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_M732}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_M781}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
msa68511.2{164_1169NT}	AAGATAAAGC	AAGTGAATAT TCAAAATTTAG CTGTTGATAC TTTTAAAGAT
Consensus	*****	*****

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

	151		200
msa68511.2{164_090}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_18RS21}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_2603}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_A909}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_CJB110}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_COH1}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_H36B}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_JM9130013}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M732}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_M781}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
msa68511.2{164_1169NT}	TATAAAGGTA	AATTTGAATC	AGGTGAATTG
Consensus	*****	*****	*****
	201		250
msa68511.2{164_090}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_18RS21}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_2603}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_A909}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_CJB110}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_COH1}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_H36B}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_JM9130013}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M732}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_M781}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
msa68511.2{164_1169NT}	AGCCGTTAAG	GAAAAAAGCG	GAGAAGTAGT
Consensus	*****	*****	*****
	251		300
msa68511.2{164_090}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_18RS21}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_2603}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_A909}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_CJB110}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_COH1}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_H36B}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_JM9130013}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M732}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_M781}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
msa68511.2{164_1169NT}	TCAATCAAGC	TAAATCAAAA	TTCTCAGACG
Consensus	*****	*****	*****
	301		350
msa68511.2{164_090}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_18RS21}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_2603}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_A909}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_CJB110}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_COH1}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_H36B}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_JM9130013}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M732}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_M781}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
msa68511.2{164_1169NT}	GATAAGGCTC	CTGAAACAAA	AGTAGAAGAT
Consensus	*****	*****	*****
	351		372
msa68511.2{164_090}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_18RS21}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_2603}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_A909}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_CJB110}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_COH1}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_H36B}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_JM9130013}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M732}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_M781}	AAACACAGAA	GATAAAGAAA	AA
msa68511.2{164_1169NT}	AAACACAGAA	GATAAAGAAA	AA
Consensus	*****	*****	**

SEQ ID NO. 4712

STRAIN 2603

YFLITTKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL
 TTEDIVSAVKEKSGEVDFDFVNDQAKSKFSDDEDATKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4713

STRAIN A909 frame: 1

YFLITTKGKELRKNAEKFYGEYKENPEEYHQIAKDKASEYSLNLAVDTFKDYKGFESGEL
 TTEDIVSAVKEKSGEVDFDFVNDQAKSKFSDDEDATKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4714

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

STRAIN H36B frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4715
 STRAIN 18RS21 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4716
 STRAIN M732 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4717
 STRAIN COH1 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4718
 STRAIN M781 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4719
 STRAIN 090 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4720
 STRAIN CJB110 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4721
 STRAIN 1169NT frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKENKAPETKVEDIVIDYKENTE
 DKEK

SEQ ID NO. 4722
 STRAIN JM9130013 frame: 1
 YFLTTKKGKELRKNAEKIFYGEYKENPEEYHQIAKDKASEYSNLAVDTFKDYKGGKFESGEL
 TTEDIVSAVKEKSGEVVDFANDFVNQAKSKFSEDTAKKEDKAPETKVEDIVIDYKENTE
 DKEK

PRETTY of: /biotmp/msa68746.2(*) January 22, 2003 05:54 ..

	1		50
msa68746.2{164_090}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_1169NT}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_18RS21}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_2603}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_A909}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_CJB110}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_COH1}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_H36B}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_JM9130013}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M732}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
msa68746.2{164_M781}	YFLTTKKGKE	LRKNAEKIFYG EYKENPEEYH QIAKDKASEY SNLAVDTFKD	
Consensus	*****	*****	*****
	51		100
msa68746.2{164_090}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_1169NT}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_18RS21}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_2603}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_A909}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_CJB110}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_COH1}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_H36B}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_JM9130013}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M732}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	
msa68746.2{164_M781}	YKGFESGEL	TTEDIVSAVK EKSSEVVDF NDFVNQAKSK FSDEDTAKKE	

Table 47: Comparative Sequences relating to SAG0739 (strain info highlighted in BOLD)

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Consensus *****
msa68746.2{164_090} 101 dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_1159NT} nKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_18RS21} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_2603} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_A909} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_CJB110} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_COH1} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_H36B} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_JM9130013} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M732} dKAPETKVED IVIDYKENTE DKEK
msa68746.2{164_M781} dKAPETKVED IVIDYKENTE DKEK
Consensus *****

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Table 48: Comparative Sequences relating to SAG1474

SEQ ID NO: 4801

STRAIN 2603

aatagtagtgagacaagtgccttcagtagttcctactacaaatactatcgt
 tcaaactaatgacagtaaatcctaccgcaaaatttgatcagaatcaggac
 aatctgtaaatagggtcaagtaaaaccagataattctgcggcgcttacaaca
 gtgacacgcctcatcatatttcagctccagatgctttaaaacaactca
 atcaagtcctgctgcttgagagtacttctactaagttactgaagagactt
 acaaacacaaaagatgggtcaagatttagccaacatgggtgagaagtgggtcaa
 gttagtagtgaggaaactcggttaatatggcatacagataatttgctaaaga
 aaacccatctttaaatgcagtcattactactagacgccaagaagctattg
 aagaggctagaaaacttaagataccaatcagccggttttaggtgttccc
 ttgtagtagcaaggggttagggcacagatttaaagggtgggtgaaccaataa
 tgggttgatctatgcagatggaaaaattagcacatttgacagtagctatg
 tcaaaaaataataagatttaggatttattatttttaggacaaacgaacttt
 ccagagtattgggtggcgtaataataacagattctaaattatacgggtctaac
 gcataatccttgggatcttgctcataatgctgggtggtctcttctgggtgaa
 gtgcagcagccattgctagcgaatgacgccaattgctagcggtagtgat
 gctgggtgggttctatccgtattccatctcttggacgggttggtaggttt
 aaaaccaacaagaggattgggtgagtaataaaaagccagattcgtagta
 cagcagttcatctttccattactaagtcattagagacgcagaaaacatta
 ttaacttatctaaagaaaagcgatcaaacgctagtagtcaagtaagattt
 aaaatctttaccaattgcttatactttgaaatcaccaatgggaacagaag
 tttagcaagatgctaaaaacgctatttaggacaacgctcacattcttaaga
 aaacaaggattcaagtaacagagatagacttaccatttgatggtagagc
 ataatgctgattattcaacctgggtattggcatgggaggagcttttt
 caacaattgaaaaagacttaaaaaaacatgggtttactaaagaagacggt
 gatcctattacttgggcagttcatggtatttatcaaaattcagataaaggc
 tgaacttaagaaatctattatggaagcccaaaaacataggtgattatc
 gtaaggcaatggagaagcttcacaagcaatttccatcttcttatcgcca
 acgacgcgaagtttagccctctaataacagatccatagtaacagagga
 agataaaaagagcgatttataatatggaaaacttgagccaagaagaagaa
 ttgctctctttaatcgccagtgaggagcctatggtgctagaacacctttt
 acacaaattgctaataatgacaggaactccagctatcagtagtcccgactta
 ctatctgagtagtgggttaccatagggagcagtagttaatggcaggtgcaa
 actatgatatgggtatttaattaaatttgcaacttctttgaaaaacatcat
 gggttttaattgtaaatggcaagaataatagataaagaagtgaaccatc
 tactggcctaataacagcctaactaactccctctttaaagctcattcatcat
 tagtaaaattagaagaaaattcacagttactcaagtagtcatctctctaaa
 aatggatgaaatcgctctgttaaaaataaacatccgtaattggcatatca
 aaaagca

SEQ ID NO: 4802

STRAIN 090

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAA
 ATACTATCGTTCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCA
 GAATCAGGACAATCTGTAATAGGTCAAGTAAACCAGATAATTTCTCGGC
 GCTTACAACAGTTGACACGCCTCATCATATTTAGCTCCAGATGCTTTAA
 AAACAACCTCAATCAAGTCTGTCGTGAGAGTACTTCTACTAAGTTAACT
 GAAGAGACTTACAACAAAAAGATGGTAAAGATTAGCCAACATGGTGAG
 AAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATATGGCATAAGATATTA
 TTGCTAAAGAAAAACCCATCTTTAAATGCACTCATTTACTACTAGACGCCAA
 GAAGCTTATTGAAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGCTTTT
 AGGTGTTCCCTTTGTTAGTCAAGGGGTTAGGGCACAGTATTAAAGTGGTG
 AAACCAATAATGGCTTGATCTATGCAGATGGAATAATTAGCACATTTGAC
 AGTAGCTATGTCAAAAAATATAAAGATTAGGATTTATTATTTTAGGACA
 AACGAACCTTCCAGAGTATGGGTGGCGTAATAAACAGATTCTAAATTAT
 ACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTGGTGGCTCT
 TCTGGTGGAAGTGACGAGCCATTGCTAGCGGAATGACGCCAATTGCTAG
 CGGTAGTGATGCTGCTGTTCTATCCGTATTCCATCTTCTGGACGGGCT
 TGGTAGGTTTAAACCAACAAGAGGATTGGTGAGTAATGAAAGCCAGAT
 TCGTATAGTACAGCAGTTCAATTTCCATTAACTAAGTCATCTAGAGACGC
 AGAAACATTATTAATCTATCTAAAGAAAAGCGATCAACCGCTAGTATCAG
 TTAATGATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCAATG
 GGAACAGAAGTTAGTCAAGATGCTAAAAACGCTATTATGGACAACGCTCAC
 ATTCTTAAGAAAAAAGGATTCAAAGTAACAGAGATAGACTTACCAATTG
 ATGGTAGAGCATTAAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGA
 GGAGCTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTACTAA
 AGAAGACGTTGATCCTATTACTTTGGGCAGTTCAATGTTATTTATCAAAAT
 CAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAAACATATG
 GATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTTCTATTTT
 CTTATCGCCAACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATG
 TAACAGAGGAAGATAAAGAGCGATTATAATATGGAACCTTGAGCCAA
 GAAGAAGAATTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAG
 AACACCTTTTACACAAATGCTAATATGACAGGACTCCAGCTATCAGTA
 TCCCCACTTACTTATCTGAGTCTGGTTTACCCTAGGGACGATGTTAATG
 CGAGGTGCAAACTATGATATGGTATTAATTAAATTTGCAACTTTCTTTGA
 AAAACATCATGGTTTAAATGTTAATGGCAAGAATAATAGATAAAGAAG
 TGAACCATCTACTGGCCTAATACAGCCTACTAATCCCTCTTTAAAGCT
 CATTCATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATC
 TATCTCTAAAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAA
 TGGCATATCAAAAAGCA

SEQ ID NO: 4803

Table 48: Comparative Sequences relating to SAG1474

STRAIN A909

TACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAAT
 TTGTATCAGAATCAGGACAATCTGTAATAGGTCAAGTAAACAGATAAT
 TCTGCGGCGCTTACAACAGTTGACACGCTCATCATATTTAGCTCCAGA
 TGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTTGAGAGTACTTCTACTA
 AGTTAATCTGAAGAGACTTACAACAAAAAGATGGTCAAGATTAGCCAAC
 ATGGTGAGAAAGTGGTCAAGTTACTAGTGAGGAACTCGTTAATATGGCATA
 CGATATTATTGCTAAAGAAAACCCATCTTTAAATGCAGTCATTACTACTA
 GACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATACCAATCAG
 CCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACAGTATTAA
 AGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAAATTAGCA
 CATTTGACAGTAGCTATGTCAAAAAATATAAGATTAGGATTATATTATT
 TTAGGACAAACGAACCTTCCAGAGTATGGGTGGCGTAATATAACAGATT
 TAAATTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCATAATGCTG
 GTGGCTCTTCTGGTGAAGTGACAGCCATTGCTAGCGGAATGACGCCA
 ATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTCATCTTCTTG
 GACGGGCTTGGTAGGTTTAAAAACCAACAGAGGATTGGTGAGTAATGAAA
 AGCCAGATTCTATAGTACAGCAGTTCATTTCCATTAACTAAGTCATCT
 AGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAAGCGATCAACGCT
 AGTATCAGTTAATGATTAAAAATCTTACCAATTGCTTATACCTTGAAT
 CACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAACGCTATTATGGAC
 AAGCTCACaTTCTTAAAGAAAACAAGGATTCAAGTAACAGAGATAGACTT
 ACCAATTGATGGTAGAGCATTATGCGTGATTATCAACCTTGGCTATTG
 GCAATGGGAGGAGCTTTTTCAACAATTGAAAAAGACTTAAAAAACATGGT
 TTTACTAAAGAAGACGTTGATCCTATTACTTGGGCAGTTCATGTTATTTA
 TCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAAGCCCAAA
 AACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAAGCAATTT
 CCTATTTCTTATCGCCAACGACCGCAAGTTAGCCCCCTCTAATAACAGA
 TCCATATGTaACAGAGGAAGATAAAAGAGCGATTATTAATATGAAAACT
 TGAGCCAAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGGAGCCATG
 TTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGACTCCCAGC
 TATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGA
 TGTTAATGGCAGGTGCAAACTATGATATGTTAATTAAATTTGCAACT
 TTCTTTGAAAAACATCATGGTTTTAATGTTAAATGGCAAAGAATAATAGA
 TAAAGAAGTGAAACCATCTACTGGCCCTAATACAGCCTACTAATCCCTCT
 TTAAAGCTCATTTCATCATAGTAAATTTAGAAGAAAATTCACAAGTTACT
 CAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAAAATAAACC
 ATCCGTAATGCGATATCAAAAAGCA

SEQ ID NO: 4804

STRAIN COH1

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAAT
 ACTATCGTTCAAACCTAATGACAGTAATCCTACCGCAAAATTTGCATCAGA
 ATCAGGCAATCTGTAATAGGTCAAGTAAACAGCTAATCTGCGGCGC
 TTACAACAGTTGACACGCTCATATTTAGCTCCAGATGCTTTAAAAACA
 ACTCAATCAAGTCCTGTCTGTTGAGAGTCTTCTACTAAGTTAACTGAAGA
 GACATACAAACAAAAAGATGGTCAAGATTAGCCAACATGGTGAGAAGTG
 GTCAGTTTACTAGTGAGGAACCTCGTCAATATGGCATACGATATTATCGCT
 AAAGAAAACCCATCTTTAAATGCAAGTCAATCTACTAGACGCCAAGAAGC
 CATTGAAGAGGCTAGAAAACTTAAAGATACTAATCAGCCGTTTTTAGGTG
 TTCCCTTGTAGTCAAGGGGTTAGGGCACAGTATTAAAGGTGGTGAACCC
 AATAATGGCTTGATCTATGCAGATGGAAAAATTAGCACATTTGACAGTAG
 CTATGTCAAAAAATATAAGATTAGGATTATTATTTTAGGACAAACGA
 ATTTTCCAGATATGGGTGGCGTAATATAACAGACTCTAAATATATACGGT
 CCAACGCATAATCCTTGAATCTTGCTCATAACGCTGGTGGCTCTTCTGG
 TGGAAAGTGACAGCAGTATTGCTAGCGGAATGACGCCAATTGCTAGCGGCA
 GTGATGCTGGTGGTCTATCCGTATTCATCTTCTGGACGGGCTTAGTA
 GGTTTAAACCAACAAAGAGGATTGGTGAGTAATGAAAAGCCAGATTGTA
 TAGTACAGCAGTTTCTTTCCATTAACTAAGTCACTAGAGACGAGAAA
 CATTTGTTAACTTACCTAAAGAAAAGCGATCAACGCTAGTATCAGTTAAT
 GATTTAAATCTTTACCAATTGCTTATACTTTGAAATCACCATTGGGAAC
 AGAAGTTAGTCAAGATGCTAAAAATGCTATTATGGACAACGTCACATCT
 TAAGAAAACAAGGATTCAAAGTGACAGAGATAGATTACCAATTGATGGT
 AGAGCAITTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGC
 TTTTTCAACAATTGAAAAAGACTTAAAAAACATGGTTTTACTTAAAGAAG
 ACGTTGATCCCATTAATTTGGGCAGTTCATGTTATTATCAAAATTCAGAT
 AAGGCTGAACCTTAAGAAATCTATTGTGAAGCCCAAAACATATGGATGA
 TTATCGTTAAGGCAATGGAGAAGCTTCACAAGCAATTCCTATTTCTTAT
 CGCCAACGACCGCAAGTTTAGCCCTCTAATAACAGATCCATATGTAACA
 GAGAAAGATAAAGAGCGATTATTAATATGGAAGAACTTGAGCCAAGAAGA
 AAGAATTGCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACAC
 CTTTACACCAATTGCTAATATGACAGGACTCCCAGCTATCAGTATCCCG
 ACTTACTTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGG
 TGCAAACTATGATATGGTATTAAATTTGCAACTTTCTTTGAAAAAC
 ATCATGGTTTTAATGTTAATGGCAAAGAATAATAGATAAAGAAGTGAAA
 CCATCTGCTGACCTAATACAGCCTACTAATCTCCCTCTTTAAAGCTCATT
 ATCATTAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCT
 CTAAGAAATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCA
 TATCAAAAGCA

SEQ ID NO: 4805

STRAIN M732

TCAGTAGCTCCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCC

Table 48: Comparative Sequences relating to SAG1474

TACCGCAAAATTGTCATCAGAATCAGGACAACTCTGTAATAGGTCAAGTAA
 AACCGCTAATCTGCGGCGCTTACAACAGTTGACACGCTCATATTTCA
 GCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGAGTCC
 TTCTACTAAGTTAACTGAAGAGACATACAAACAAAAGATGGTCAAGATT
 TAGCCAACATGGTGAGAGTGGTCAAGTTACTAGTGAGGAACCTGTCAT
 ATGGCATACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAGTCAT
 TACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACCTAAAGATA
 CTAATCAGCCGTTTTTAGGTGTTCCCTTGTTAGTCAAGGGGTTAGGGCAC
 AGTATTAAGAGTGGTGAAACCAATTAATGGCTTGATCTATGCAGATGGAAA
 AATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTAGGAT
 TTATTATTTTAGGACAAACGAATTTCCAGAGTATGGTGGCGTAATATA
 ACAGACTCTAAATTATACGGTCAACGCATTAATCCTTGGGATCTTGGCTCA
 TAACGCTGGTGGCTCTTCTGGTGGAAGTGACAGCAGTATGCTAGCGGAA
 TGACGCCAATTGCTAGCGGCGATGCTGGTGGTTCATCCGTTATCCCA
 TCTTCTTGGACGGGCTTAGTAGGTTTAAACCAACAAGAGGATTGGTGAG
 TAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTTCTTTCCATTAACTA
 AGTCATCTAGAGACGCAGAAACATTTGTTAACTTACCTAAAGAAAAGCGAT
 CAAACGCTAGTATCAGTTAATGATTTAAAACTTTTACCAATTGCTTATAC
 TTTGAAATCACCATTGGGAACAGAAGTTAGTCAAGATGCTAAAAATGCTA
 TTATGGACAACGTCACATTTCTTAAGAAAACAAGGATTCAAAGTGACAGAG
 ATAGATTTTACCAATTGATGGTAGAGCATTAATGCGTGATTATTCAACCTT
 GGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTAAAAA
 AACATGGTTTTTACTAAAGAAGACGTTGATCCCATTTACTGGGCGAGTTTCA
 GTTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTGTGGA
 AGCCCAAAACATATGGATGATTATCGTAAGCAATGGAGAAGCTTCCACA
 AGCAATTTCTATTTCTTATCGCCAAACGACCGCAAGTTTAGCCCTCTA
 AATACAGATCCATATGTTACAGAGAAAGATAAAAGAGCGATTATATAAT
 GGAAAACCTTGAGCCAGAAGAAGAAATGCTCTCTTAAATCGCCAGTGGG
 AGCTATGTTGGGTAGAACACCTTTTACACCAATTGCTAATATGACAGGA
 CTCCCGCTATCAGTATCCGCACTTACTTATCTGAGTCTGGTTTACCCAT
 AGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAAT
 TTGCAACTTTCTTTGAAAACATCATGGTTTAAATGTTAAATGGCAAAGA
 ATAATAGATAAAGAAGTGAAACCATCTGCTGACCTAATACAGCCTACTAA
 CTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCAC
 AAGTTACTCAAGTATCTATCTCTAAAAAATGGATGAAATCGTCTGTTAAA
 AATAAACCATCCGTAATGTCATATCAAAAAGCA

SEQ ID NO: 4806

STRAIN 18RS21

AATAGTACTGAGACAAGTGCTTCAGTAGTTCCTACTACAAATACTATCGT
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGTATCAGAATCAGGAC
 AATCTGTAATAGGTCAAGTAAACCAGATAATCTGCGGCGCTTACAACA
 GTTGACAGCCCTCATCATATTTAGCTCCAGATGCTTTAAAAACAACCTCA
 ATCAAGTCTCTGTTGAGAGTACTTCTACTAAGTTAACTGAAGAGACTT
 ACAAAACAAAAGATGGTCAAGATTTAGCCCAACATGGTGAGAAGTGGTCAA
 GTTACTAGTGAGGAACCTCGTTAATATGGCATACGATATTATTGCTAAAGA
 AAACCCATCTTTAAATGCAGTCATTACTACTAGACGCCAAGAGCTATTG
 AAGAGGCTAGAAAACTTAAAGATACCAATCAGCCGTTTTTAGGTGTTCC
 TTGTTAGTCAAGGGTTAGGGCACAGTATTAAAGTGGTGAAACCAATAA
 TGGCTTGATCTATGCAGATGGAAAAATTAGCACATTGACAGTAGCTATG
 TCAAAAAATATAAAGATTAGGATTTATTTATTTTAGGACAAACGAACCTT
 CCAGAGTATGGTGGCGTAAATATAACAGATTCTAAATTATACGGTCTAAC
 GCATAATCCTTGGGATCTTGGCTATAATGCTGGTGGCTCTTCTGGTGGAA
 GTGCAGCAGCCATTGCTAGCGGAATGACGCCAATTGCTAGCGGTAGTGAT
 GCTGGTGGTTCTATCCGTATTCATCTTCTTGGACGGGCTTGGTAGGTTT
 AAAACCAACAGAGGATTGGTGAGTAATGAAAAGCCAGATTCTGTATAGTA
 CAGCAGTTTCAATTTCCATTAACTAAGTCATCTAGAGACGCAGAAAACATTA
 TTAACCTATCTAAAGAAAAGCGATCAACCGCTAGTATCAGTTAATGATTT
 AAAATCTTTACCAATTGCTTATCTTTGAAATCACCATTGGGAACAGAAG
 TTAGTCAAGATGCTAAAAACGCTATTATGGACACAGTCACATTTCTAAGA
 AAACAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGC
 ATTAATGCGTGATTATTCAACCTTGGCTATTGGCATGGGAGGAGCTTTT
 CAACAATTGAAAAGACTTAAAAAACATGGTTTTTACTAAAGAAGAGCTT
 GATCCTATTACTTGGGCGATTCTATGTTATTTATCAAAATTCAGATAAGGC
 TGAACCTTAAGAAATCTATTATGGAAGCCAAAAACATATGGATGATTATC
 GTAAGGCAATGGAGAAGCTTACAAGCAATTTCTATTCTTCTATCGCCA
 ACGACCGCAAGTTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGA
 AGATLAAAAGAGCGATTATAATATGGAACCTTGAGCCAAGAAGAAAGAA
 TTGCTCTCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTT
 ACACAAATTTGCTAATATGACAGGACTCCAGCTATCAGTATCCCGACTTA
 CTATCTGAGTCTGGTTTACCCATAGGGACGATGTTAATGGCAGGTGCAA
 ACTATGATATGGTATTAAATTAATTTGCAACTTTCTTTGAAAACATCAT
 GGTTTTAATGTTAAATGGCAAAGAATAATAGATAAAGAAGTGAAACCATC
 TACTGGCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCAT
 TAGTAAATTTAGAAGAAAATTCACAAGTTACTCAAGTATCTATCTTAA
 AATGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCA
 AAAAGCA

SEQ ID NO: 4807

STRAIN M781

TGCTTCAGTAGCTCTACTACAAATACTATCGTTCAAACCTAATGACAGTA
 ATCTTACCGCAAAATTTGCATCAGAATCAGGACAACTCTGTAATAGGTCAA
 GTAAACAGCTAATCTGCGGCGCTTACAACAGTTGACACGCTCATAT

Table 48: Comparative Sequences relating to SAG1474

TTCAGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCGTTGAGA
 GTCCTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAGATGGTCAA
 GATTAGCCAAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACTCGT
 CAATATGGCATAACGATATTATCGCTAAAGAAAACCCATCTTTAAATGCAG
 TCATTACTACTAGACGCCAAGAAGCCATTGAAGAGGCTAGAAAACCTTAA
 GATACTAATCAGCCGTTTCTAGGTGTTCCCTTGTAGTCAAGGGGTTAGG
 GCACAGTATLAAAGGTGGTGAAACCAATAATGGCTTGATCTATGCAGATG
 GAAAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAAGATTTA
 GGATTTATTATTTTAGGACAAAAGaATTTCCAGAGTATGGGTGGCGTAA
 TATAACAGACTCTAAATTATACGGTCCAACGCATAATCCTTGGAaTCTTG
 CTCATAACGCTGGTGGCTCTTCTGGTGGAAAGTGCAGCAGCTATGTCTAGC
 GGAATGACGCCCAATTGCTAGCGGCAGTGTATGCTGGTGGTTCTATCCGTAT
 TCCATCTTCTTGGACGGGCTTAGTAGGTTTAAACCAACAGAGGATTGG
 TGAGTAATGAAAAGCCAGATTCTGTATAGTACAGCAGTTCAITTTCCATTGA
 ACTAAGTCATCTAGAGACGCAGAAAACATTGTTAACTTACCTAAAGAAAAG
 CGATCAACGCTAGTATCAGTTAATGATTTAAAACTTTTACCAATTGCTT
 ATACTTTGAAATCACCAATGGGAACAGAaTTAGTCAAGATGCTAAAAAT
 GCTATTATGGACAACGTCACATTCTTAAGAGAACAAGGATTCAAAGTGAC
 AGAGATAGATTACCAATTGATGGTAGAGCATTAATGCGTGATTTATCAA
 CCTTGGCTATTGGCATGGGAGGAGCTTTTCAACAATTGAAAAGAGCTTA
 AAAAAACATGGTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGT
 TCACTGTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTG
 TGGAAGCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTT
 CACAAGCAATTTCTATTCTTCTATCGCCAACGACCGCAAGTTTAGCCCC
 TCTAAATACAGATCCATATGTAAACAGaGAAAGATAAAGAGCGATTATA
 ATATGGAAAACCTTGAGCCAGAAGAAAGAAATGCTCTCTTAATCGCCAG
 TGGGAGCCTATGTTGGGTAGAACACCTTTTACACCAATTGCTAATAAGAC
 AGGACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTAC
 CCATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAAT
 AAATTTGCAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCA
 AAGAATATAGATAAAGAAGTGAACCATCTGCTGACCTAATACAGCCTA
 CTAACCTCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAT
 TCACAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGT
 TAAAAATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4810

STRAIN CJB110

TAGTTCTTACTACAAATACTATCGTTCAAACCTAATGACAGTAATCCTACC
 GCAAAATTTGTATCAGAAATCAGGACAATCTGTAATAGGTCAAGTAAACCC
 AGATAATTTCTGCGGCGCTTACAACAGTTGACACGCCTCATCATATTTAG
 CTCCAGATGCTTTAAAAACAACCTCAATCAAGTCCTGTCTGTGAGAGTACT
 TCTACTAAGTTAACTGAAGAGACTTACAAAACAAAAGATGGTAAAGATTT
 AGCCAACATGGTGAGAAGTGGTCAAGTTACTAGTGAGGAACCTCGTTAATA
 TGGCATACGATATTATGCTAAAGAAAACCCATCTTTAAATGCAGTCATT
 ACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACCTTAAAGATAC
 CAATCAGCCGTTTCTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGCACA
 GTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGATGGAAAA
 ATTAGCACATTGACAGTAGCTATGTCAAAAAATATAAGATTTAGGATT
 TATTATTTTAGGACAAAACGAATTTCCAGAGTATGGGTGGCGTAAATATA
 CAGATTCTAAATTTATACGGTCTAACGCATAATCCTTGGGATCTTGCTCAT
 AATGCTGGTGGCTCTTCTGGTGAAGTGCAGCAGCCATTGCTAGCGGAAT
 GAGCCCAATTGCTAGCGGTAGTGTGCTGGTGGTTCTATCCGTATTCCAT
 CTTCTTGGACGGGCTTGGTAGGTTTAAACCAACCAAGAGGATTGGTGAGT
 CATGAAAGCCAGATTCGTATAGTACAGCAGTTCAATTTCCATTAACTAA
 GTCATCTAGAGACGCAGAAAACATTATTAACCTTATCTAAAGAAAAGCGATC
 AAACGCTAGTATCAGTTAATGATTTAAATCTTTACCAATTGCTTATACT
 TTGAAATCACCATGGGAACAGAAGTTAGTCAAGATGCTAAAAACGCTAT
 TAGGACAAACGTCACATTCTTAAGAAAACAAGGATTCAAAGTAAACAGAGA
 TAGACTTACCAATTGATGGTAGAGCATTAATGCGGTGATTATTCAACCTTG
 GCTATTGGCATGGGAAGAGCTTTTCAACaATTGAAAAAGAcTTaaAAAA
 AcATGGTTTTACTAAAGAAGACGTTGATCCCTATTACTTGGGCAGTTCATG
 TTATTTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGGAA
 GCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCACAA
 GCAATTTCTATTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCTAA
 ATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATAATATG
 GAAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTTAATCGCCAGTGGGA
 GCCTATGTTGCGTAGAACACCTTTTACACAAATTGCTAATATGACAGGAC
 TCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCCATA
 gGGACgATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATTAAT
 TTGCAACTTTCTTTGAAAAACATCATGGTTTAAATGTTAAATGGCAAGAA
 TAATAGATAAAGAAGTGAACCATCTACTGGCCTAATACAGCCTACTAAC
 TCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAAATTCACA
 AGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTTAAAA
 ATAAACCATCCGTAATGGCATATCAAAAAGCA

SEQ ID NO: 4811

STRAIN 1169NT

AATAGTACTGAGACAAGTGCTTCAGTAGCTCCTACTACAAATACTATCGT
 TCAAACTAATGACAGTAATCCTACCGCAAAATTTGCATCAGAAATCAGGAC
 AATCTGTAATATGTCAAGTAAACAGATAAATCTGCGGCGCTTACACACA
 GTTGACACGCCTCATATTTAGCTCCAGATGATTAAAAACAACCTCAATC
 AAGTCTGTGCTGAGAGTACTTCTACTAAGTTAACTGAAGAGACATACA
 AACAAAAAGATGGTCAAGATTAGCCACATGGTGAGAAGTGGTCAAGTT

Table 48: Comparative Sequences relating to SAG1474

ACTAGTGAGGAACTCGTCAATATGGCATACGATATTATTGCTAAAGAAAA
 CCCCTCTTTAAATGCAGTCATTACTACTAGACGCCAAGAAGCCATTGAAG
 AGGCTAGAAAACCTTAAAGATACTAATCAGCCATTTTGGTGTTCCTTG
 TTAGTCAAGGGGTAGGGCAAGTATTAAAGGTGGTGAACCAATAATGG
 CTTGATCTATGCAGATGGAAAAATAGCACATTGACAGTAGCTATGTCA
 AAAATATAAAGATTAGGATTTATTTTATAGGACAAACGAACCTTCCA
 GAGTATGGGTGGCGTAATATAACAGATTCTAATTATACGGTCCAACGCA
 TAACCTCGGAATCTTGCTCATAATGCTGGTGGCTCTTCTGGTGAAGTG
 CAGCAGCCATTGCTAGCGGATGACGCCAATTGCTAGCGTAGTGATGCT
 GGTGGTCTATCCGATTTCCATCTTCTGGACGGGCTTGGTAGGTTTAAA
 ACCAACAGAGGATTGGTGAATTAAGAACCCAGATTTCGTATAGTACAG
 CAGTTTCATTTTCCATTAACTAAGTCACTAGAGACGCAGAAACATTATTA
 ACTTATCTAAAGAAAGCGATCAAAACGCTAGTATCAGTTAATGATTTAAA
 ATCTTTACCAATTGCTTATACTTTGAAATCACCAATGGGAACAGAAGTTA
 GTCAGATGCTAAAAACGCTATTATGGACACGTCACATTCTTAAGAAAA
 CAAGGATTCAAAGTAACAGAGATAGACTTACCAATTGATGGTAGAGCATT
 AATGCGTGAATTATCAACCTTGGCTATTGGCATGGGAGGAGCTTTTCAA
 CAATTGAAAAAGACTTAAAAAACATGGTTTACTAAAGAAGACGTTGAT
 CCTATTACTTGGGCAGTTTCATGTTATTTATCAAAATTGAGTAAGGCTGA
 CCTAAGAGTCTAAAAACGCTATTATGGAGGCCAAAAACATATGGATGATTATCGTA
 AGGCAATGGAGAGCTTCAACAGCAATTTCCTATTTCTTATCGCCAAACG
 ACCGCAAGTTTAGCCCTCTAAATACAGATCCATATGTAACAGAGGAAGA
 TAAAGAGCGATTATATATATGGAAAACTTGAGCCAAAGAAAGAAAGATTG
 CTCCTTTAATCGCCAGTGGGAGCCTATGTTGCGTAGAACACCTTTTACA
 CAAATTGCTAATATGACAGGACTCCAGCTATCAGTATCCGACTTACTT
 ATCTGAGTCTGGTTTACCCTAGGGACGATGTTAATGGCAGGTGCAAACT
 ATGATATGGTATTAATTAATTTGCAACTTTCTTTGAAAAACATCATGGT
 TTTAATGTTAAATGGCAAGAAATATAGATAAAGAAGTGAACCATCTAC
 TGGCCTAATACAGCCTACTAACTCCCTCTTTAAAGCTCATTCATCATTAG
 TAAATTTAGAAGAAAAATTCACAGTTACTCAAGTATCTATCTCTAAAAAA
 TGGATGAAATCGTCTGTTAAAAATAAACCATCCGTAATGGCATATCAAAA
 AGCA

SEQ ID NO: 4812

STRAIN JM9130013

TTTCAAGTACTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAATC
 CTACCGCAAAATTTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGTA
 AAACCAGCTAATCTGTGGCGCTTACAACAGTTGACACGCCCTCATATTTT
 AGCTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGTC
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGAG
 TTAGCCAAACATGGTGAAGTGGTCAAGTTACTAGTGAGGAACCTCGTCAA
 TATGGCATACGATATTATTGCTAAAGAAACCCATCTTTAAATGCAGTCA
 TTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGAT
 ACCAATCAGCCGTTTTAGGTGTTCCCTTGTAGTCAAGGGGTAGGGCA
 CAGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGAA
 AAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGGA
 TTTATTATTTTAGGACAAACGAACTTTCCAGAGTATGGATGGCGCAATAT
 AACAGATTCTAAATTATACGGTCCAACGCATAACCCCTTGGAACTCTGCTC
 ATAATGCTGGTGGCTCTTCTGGTGAAGTGCAGCAGTTATGCTAGCGGG
 ATGACGCCAATTTGCTAGCGGTAGTGATGCTGGTGGTTCTATCGTATTCC
 ATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAGAGGATTGGTGA
 GTAATGAAAGCCAGATTCTGTATAGTACAGCAGTTCAATTTCCATTAACT
 AAGTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAGCGA
 TCAAAACGCTAGTATCAGTTAATGATTTAAATCTTTTACCAATTTGCTTATA
 CTTTGAATACCAATGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGCT
 ATTAGGACAAACGTCATATTCTTAAGAAACCAAGGATTCAAAGTGACAGA
 GATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTAACCT
 TGGCTATTGGTATGGGAGGAGCTTTTCAACAATTGAAAAAGACTTAAAA
 AAACATGGTTTACTAAAGAAAGCAGTTGATCCCATTACTTGGGGAGTTCA
 TGTATTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATGG
 AAGCCCAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCAC
 AAGCAATTTCTATTTTCTTATCGCCAACGACCGCAAGTTTAGCCCTCT
 AAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATATAATA
 TGGAAAACTTGAGCCAAAGAAAGAAATTTGCTCTTTAATCGCCAGTGG
 GAGCCTATGTTGCGTAGAACACCTTTTACACAAATGCTAATATGACAGG
 ACTCCAGCTATCAGTATCCGACTTACTTATCTGAGTCTGGTTTACCCA
 TAGGACAGATGTTAATGGCAGGTGCAAACTATGATATGGTATTAAATAAA
 TTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAG
 AATAATAGATAAAGAGTGAACCATCTACTGGCCTAATACAGCCTACTA
 ACTCCCTCTTTAAAGCTCATTCATCATTAGTAAATTTAGAAGAAATTC
 CAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTTAA
 AAATAAACCATCCGTAATGGCATAT

SEQ ID NO: 4813

STRAIN H36B

CTTCAAGTACTCTACTACAAATACTATCGTTCAAACCTAATGACAGTAAT
 CCTACCGCAAAATTTTCATCAGAAATCAGGACAATCTGTAATAGGTCAAGT
 AAAACAGCTAATCTGTGGCGCTTACAACAGTTGACACGCCCTCATATTT
 CAGTCCAGATGCTTTAAAAACAACCTCAATCAAGTCTGTGCTGAGAGT
 CTTCTACTAAGTTAACTGAAGAGACATACAAACAAAAAGATGGTCAAGA
 TTTAGCCAAACATGGTGAAGAGTGGTCAAGTTACTAGTGAGGAACCTGCTCA
 ATATGGCATACGATATATTGCTAAAGAAACCCATCTTTAATGCAAGT
 ATTACTACTAGACGCCAAGAAGCTATTGAAGAGGCTAGAAAACTTAAAGA

Table 48: Comparative Sequences relating to SAG1474

TACCAATCAGCCGTTTTTAGGTGTTCCCTTGTAGTCAAGGGGTTAGGGC
ACAGTATTAAAGGTGGTGAACCAATAATGGCTTGATCTATGCAGGTGGA
AAAATTAGCACATTTGACAGTAGCTATGTCAAAAAATATAAGATTTAGG
ATTTATTATTTTAGGACAAACGAACCTTCCAGAGTATGGATGGCGCAATA
TAACAGATTCTAAATTATACGGTCCAACGCATAACCTTGGAACTTTGCT
CATAATGCTGGTGGCTCTTCTGGTGAAGTGACAGCAGTTATGCTAGCGG
GATGACGCCAATTGCTAGCGGTAGTGATGCTGGTGGTTCTATCCGTATTC
CATCTTCTTGGACGGGCTTGGTAGGTTTAAACCAACAAGAGGATTGGTG
AGTAATGAAAAGCCAGATTTCGTATAGTACAGCAGTTCAITTTCCATTAAAC
TAAGTCATCTAGAGACGCAGAAACATTATTAACCTTATCTAAAGAAAAGCG
ATCAAACGCTAGTATCAGTTAATGATTAAATCTTTACCAATTCGTATAT
ACTTTGAATCACCATTGGGAACAGAAAGTTAGTCAAGATGCTAAAAATGC
TATTATGGACAACGTCATATTCTTAAGAAAACAAGGATTCAAAGTGACAG
AGATAGACTTACCAATTGATGGTAGAGCATTAAATGCGTGATTATTCACCC
TTGGCTATTGGTATGGGAGGAGCTTTTCAACAATGAAAAAGACTTAA
AAAACTGGTTTTACTAAAGAAGACGTTGATCCCATTACTTGGGCAGTTTC
ATGTTATTATCAAAATTCAGATAAGGCTGAACCTTAAGAAATCTATTATG
GAAGCCCCAAAAACATATGGATGATTATCGTAAGGCAATGGAGAAGCTTCA
CAAGCAATTTCCATTCTTCTATCGCCAACGACCGCAAGTTTAGCCCCCTC
TAAATACAGATCCATATGTAACAGAGGAAGATAAAAGAGCGATTATTAAT
ATGGAAACCTTGAGCCAAGAAGAAAGAAATGCTCTCTTAAATCGCCAGTG
GGAGCCTATGTTGCGTAGAACACCTTTTACACAAATGCTAATATGACAG
GACTCCCAGCTATCAGTATCCCGACTTACTTATCTGAGTCTGGTTTACCC
ATAGGGACGATGTTAATGGCAGGTGCAAACTATGATATGTTAATTAATA
ATTTGCAACTTTCTTTGAAAAATATCATGGTTTAAATGTTAAATGGCAAA
GAATAATAGATAAAGAGTGAACCATCTATGGCCCTAATACAGCCCTACT
AACTCCCTCTTTAAAGCTCAITTCATCATAGTAAATTTAGAAGAAAATTC
ACAAGTTACTCAAGTATCTATCTCTAAAAATGGATGAAATCGTCTGTTA
AAAAATAA

PRETTY of: /biotmp/msa71927.2{*} January 22, 2003 07:23 ..

	1		50
msa71927.2{173_18RS21}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_2603}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_A909}	-----	-----	---TACTACAA ATACTATCGT
msa71927.2{173_090}	aatagtactg agacaagtgc ttcagtagtt ccTACTACAA ATACTATCGT		
msa71927.2{173_CJB110}	-----	-----tagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_COH1}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
msa71927.2{173_M781}	-----tgc	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_M732}	-----	-tcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_H36B}	-----c	ttcagtagtt	ccTACTACAA ATACTATCGT
msa71927.2{173_JM9130013}	-----	ttcagtagct	ccTACTACAA ATACTATCGT
msa71927.2{173_1169NT}	aatagtactg agacaagtgc ttcagtagct ccTACTACAA ATACTATCGT		
Consensus	-----	-----	--***** *****

	51		100
msa71927.2{173_18RS21}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_2603}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_A909}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_090}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_CJB110}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgtATCA GAATCAGGAC		
msa71927.2{173_COH1}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M781}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_M732}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
msa71927.2{173_H36B}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_JM9130013}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTtcATCA GAATCAGGAC		
msa71927.2{173_1169NT}	TCAAACCTAAT GACAGTAATC CTACCGCAAA ATTTgcATCA GAATCAGGAC		
Consensus	*****	*****	*****_****

	101		150
msa71927.2{173_18RS21}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_2603}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_A909}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_090}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_CJB110}	AATCTGTAAT AgGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_COH1}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M781}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_M732}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGcGGC GCTTACAACA		
msa71927.2{173_H36B}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA		
msa71927.2{173_JM9130013}	AATCTGTAAT AgGTCAAGTA AAACCAGcTA ATTCTGtGGC GCTTACAACA		
msa71927.2{173_1169NT}	AATCTGTAAT AtGTCAAGTA AAACCAGaTA ATTCTGcGGC GCTTACAACA		
Consensus	*****	*_*****	*****_****

	151		200
msa71927.2{173_18RS21}	GTTGACACGC CteaTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_2603}	GTTGACACGC CteaTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_A909}	GTTGACACGC CteaTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_090}	GTTGACACGC CteaTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_CJB110}	GTTGACACGC CteaTCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_COH1}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M781}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		
msa71927.2{173_M732}	GTTGACACGC C...TCATAT TTCAGTCCA GATGcTTTAA AAACAACCTCA		

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_H36B}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_JM9130013}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGcTTTAA	AAACAACCTCA
msa71927.2{173_1169NT}	GTTCACACGC	C...TCATAT	TTCAGCTCCA	GATGaTTTAA	AAACAACCTCA
Consensus	*****	*-*****	*****	****-*****	*****
201					
msa71927.2{173_18RS21}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_2603}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_A909}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_090}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_CJB110}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACtT
msa71927.2{173_COH1}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M781}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_M732}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_H36B}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_JM9130013}	ATCAAGTCCT	GTCGTTGAGA	GtcCTTCTAC	TAAGTTAACT	GAAGAGACaT
msa71927.2{173_1169NT}	ATCAAGTCCT	GTCGTTGAGA	GtaCTTCTAC	TAAGTTAACT	GAAGAGACaT
Consensus	*****	*****	*-*****	*****	*****
251					
msa71927.2{173_18RS21}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_2603}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_A909}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_090}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_CJB110}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_COH1}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M781}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_M732}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_H36B}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_JM9130013}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
msa71927.2{173_1169NT}	ACAAACAAAA	AGATGGTcAA	GatTTAGCCA	ACATGGTGAG	AAGTGGTCAA
Consensus	*****	*****-*	*-*****	*****	*****
301					
msa71927.2{173_18RS21}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_2603}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_A909}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_090}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_CJB110}	GTTACTAGTG	AGGAACTCGT	tAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_COH1}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M781}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_M732}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_H36B}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TcGCTAAAGA
msa71927.2{173_JM9130013}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
msa71927.2{173_1169NT}	GTTACTAGTG	AGGAACTCGT	cAATATGGCA	TACGATATTA	TtGCTAAAGA
Consensus	*****	*****	-*****	*****	*-*****
351					
msa71927.2{173_18RS21}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_2603}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_A909}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_090}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_CJB110}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_COH1}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M781}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_M732}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_H36B}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
msa71927.2{173_JM9130013}	AAACCCaTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCtATTG
msa71927.2{173_1169NT}	AAACCCtTCT	TAAATGCAG	TCATTACTAC	TAGACGCCAA	GAAGCcATTG
Consensus	*****-*	*****	*****	*****	*****-*
401					
msa71927.2{173_18RS21}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_2603}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_A909}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_090}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_CJB110}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_COH1}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M781}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_M732}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_H36B}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_JM9130013}	AAGAGGCTAG	AAAACCTAAA	GATACcAATC	AGCCgTTTTT	AGGTGTTCCC
msa71927.2{173_1169NT}	AAGAGGCTAG	AAAACCTAAA	GATACtAATC	AGCCaTTTTT	AGGTGTTCCC
Consensus	*****	*****	*****-*	*****-*	*****
451					
msa71927.2{173_18RS21}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_2603}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_A909}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_090}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_CJB110}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_COH1}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_M781}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M732}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_H36B}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_JM9130013}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
msa71927.2{173_1169NT}	TTGTTAGTCA	AGGGGTTAGG	GCACAGTATT	AAAGGTGGTG	AAACCAATAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_2603}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_A909}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_090}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_CJB110}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_COH1}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M781}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_M732}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_H36B}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_JM9130013}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
msa71927.2{173_1169NT}	TGGCTTGATC	TATGCAGaTG	GAAAAATTAG	CACATTTGAC	AGTAGCTATG
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_2603}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_A909}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_090}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_CJB110}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_COH1}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_M781}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_M732}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_H36B}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_JM9130013}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
msa71927.2{173_1169NT}	TCAAAAAATA	TAAAGATTTA	GGATTATTAT	TTTtaggaca	AACGAaCTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_2603}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_A909}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_090}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_CJB110}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_COH1}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_M781}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_M732}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_H36B}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_JM9130013}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
msa71927.2{173_1169NT}	CCAGAGTATG	GgTGGCGtAA	TATAACAGat	TCTAAATTAT	ACGGTCTaAC
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_2603}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_A909}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_090}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_CJB110}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_COH1}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M781}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_M732}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_H36B}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_JM9130013}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
msa71927.2{173_1169NT}	GCATAAatCCT	tGGgATCtTG	CTCATAatGC	TGGTGGCTCT	TCTGGTGGAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_2603}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_A909}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_090}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_CJB110}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_COH1}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M781}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_M732}	GTGCAGCAGc	cATTGCTAGC	GGaATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_H36B}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_JM9130013}	GTGCAGCAGt	tATTGCTAGC	GGgATGACGC	CAATTGCTAG	CGGtAGTGAT
msa71927.2{173_1169NT}	GTGCAGCAGc	cATTGCTAGC	GGrATGACGC	CAATTGCTAG	CGGtAGTGAT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_2603}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_A909}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_090}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_CJB110}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_COH1}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_M781}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_M732}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TaGTAGGTTT
msa71927.2{173_H36B}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_JM9130013}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
msa71927.2{173_1169NT}	GCTGGTGGTT	CTATCCGTAT	TCCATCTTCT	TGGACGGGCT	TgGTAGGTTT
Consensus	*****	*****	*****	*****	*_*****
801	850				
msa71927.2{173_18RS21}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_2603}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_A909}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_090}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_CJB110}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_COH1}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M781}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_M732}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_H36B}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_JM9130013}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
msa71927.2{173_1169NT}	AAAACCAACA	AGAGGATTGG	TGAGTaATGA	AAAGCCAGAT	TCGTATAGTA
Consensus	*****	*****	*****	*****	*****
851	900				
msa71927.2{173_18RS21}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_2603}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_A909}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_090}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_CJB110}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_COH1}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M781}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_M732}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTg
msa71927.2{173_H36B}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_JM9130013}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
msa71927.2{173_1169NT}	CAGCAGTTCA	TTTTCCATTA	ACTAAGTCAT	CTAGAGACGC	AGAAACATTa
Consensus	*****	*****	*****	*****	*****
901	950				
msa71927.2{173_18RS21}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_2603}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_A909}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_090}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_CJB110}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_COH1}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M781}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_M732}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_H36B}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_JM9130013}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
msa71927.2{173_1169NT}	TTAACTTatC	TAAAGAAAAG	CGATCAAACG	CTAGTATCAG	TTAATGATTT
Consensus	*****	*****	*****	*****	*****
951	1000				
msa71927.2{173_18RS21}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_2603}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_A909}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_090}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_CJB110}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_COH1}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_M781}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_M732}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_H36B}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_JM9130013}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
msa71927.2{173_1169NT}	AAAATCTTTA	CCAAATTGCTT	ATACITTTGAA	ATCACCAGATG	GGAACAGAAG
Consensus	*****	*****	*****	*****	*****
1001	1050				
msa71927.2{173_18RS21}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_2603}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_A909}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_090}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_CJB110}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_COH1}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M781}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_M732}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_H36B}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_JM9130013}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
msa71927.2{173_1169NT}	TTAGTCAAGA	TGCTAAAAAa	GCTATTATGG	ACAACGTCac	ATTCTTAAGA
Consensus	*****	*****	*****	*****	*****
1051	1100				
msa71927.2{173_18RS21}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_2603}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_A909}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_090}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC
msa71927.2{173_CJB110}	aaACAAGGAT	TCAAAGTaAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_COH1}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M781}	gAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_M732}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAT	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_H36B}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_JM9130013}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC		
msa71927.2{173_1169NT}	aAACAAGGAT	TCAAAGTgAC	AGAGATAGAc	TTACCAATTG	ATGGTAGAGC		
Consensus	*****	*****	*****	*****	*****		
msa71927.2{173_18RS21}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_2603}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_A909}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_090}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_CJB110}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_COH1}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M781}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_M732}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_H36B}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_JM9130013}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
msa71927.2{173_1169NT}	1101	ATTAATGCGT	GATTATTCAA	CCTTGGCTAT	1150	TGGcATGGGA	GGAGCTTTTT
Consensus	1101	*****	*****	*****	1150	*****	*****
msa71927.2{173_18RS21}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_2603}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_A909}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_090}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_CJB110}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_COH1}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M781}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_M732}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_H36B}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_JM9130013}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
msa71927.2{173_1169NT}	1151	CAACAATTGA	AAAAGACITa	AAAAAACATG	1200	GTTTTACTAA	AGAAGACGTT
Consensus	1151	*****	*****	*****	1200	*****	*****
msa71927.2{173_18RS21}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_2603}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_A909}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_090}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_CJB110}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_COH1}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M781}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_M732}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_H36B}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_JM9130013}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
msa71927.2{173_1169NT}	1201	GATCCTATTA	CTTGGGcAGT	TCATGTTATT	1250	TATCAAAATT	CAGATAAGGC
Consensus	1201	*****	*****	*****	1250	*****	*****
msa71927.2{173_18RS21}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_2603}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_A909}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_090}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_CJB110}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_COH1}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M781}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_M732}	1251	TGAACCTTAAG	AAATCTATTg	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_H36B}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_JM9130013}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
msa71927.2{173_1169NT}	1251	TGAACCTTAAG	AAATCTATTa	TGGAAGCCCA	1300	AAAACATATG	GATGATTATC
Consensus	1251	*****	*****	*****	1300	*****	*****
msa71927.2{173_18RS21}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_2603}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_A909}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_090}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_CJB110}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_COH1}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M781}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_M732}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_H36B}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_JM9130013}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
msa71927.2{173_1169NT}	1301	GTAAGGCCAAT	GGAGAAGCIT	CACAAGCAAT	1350	TTCCCTATTTT	CTTATCGCCA
Consensus	1301	*****	*****	*****	1350	*****	*****
msa71927.2{173_18RS21}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_2603}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_A909}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA
msa71927.2{173_090}	1351	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	1400	GATCCATATG	TaACAGAGgA

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_CJB110}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_COH1}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M781}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGaA
msa71927.2{173_M732}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TtACAGAGaA
msa71927.2{173_H36B}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_JM9130013}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
msa71927.2{173_1169NT}	ACGACCGCAA	GTTTAGCCCC	TCTAAATACA	GATCCCATATG	TaACAGAGgA
Consensus	*****	*****	*****	*****	*-*****
msa71927.2{173_18RS21}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_2603}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_A909}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_090}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_CJB110}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_COH1}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M781}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_M732}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_H36B}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_JM9130013}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
msa71927.2{173_1169NT}	AGATAAAAGA	GCGATTATATA	ATATGGAAAA	CTTGAGCCAA	GAAGAAAGAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_2603}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_A909}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_090}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_CJB110}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_COH1}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M781}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_M732}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_H36B}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_JM9130013}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
msa71927.2{173_1169NT}	TTGCTCTCTT	TAATCGCCAG	TGGGAGCCTA	TGTTGCGTAG	AACACCTTTT
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_2603}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_A909}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_090}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_CJB110}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_COH1}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M781}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_M732}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_H36B}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_JM9130013}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
msa71927.2{173_1169NT}	ACACaAATTG	CTAATATGAC	AGGACTCCCA	GCTATCAGTA	TCCCGACTTA
Consensus	****-*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_2603}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_A909}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_090}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_CJB110}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_COH1}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M781}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_M732}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_H36B}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_JM9130013}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
msa71927.2{173_1169NT}	CTTATCTGAG	TCTGGTTTAC	CCATAGGGAC	GATGTTAATG	GCAGGTGCAA
Consensus	*****	*****	*****	*****	*****
msa71927.2{173_18RS21}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_2603}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_A909}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_090}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_CJB110}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_COH1}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M781}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_M732}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_H36B}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_JM9130013}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
msa71927.2{173_1169NT}	ACTATGATAT	GGTATTAAAT	AAATTGCAA	CTTTCCTTGA	AAAACATCAT
Consensus	*****	*****	*****	*****	****-*****
msa71927.2{173_18RS21}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_2603}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC
msa71927.2{173_A909}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAACCATC

Table 48: Comparative Sequences relating to SAG1474

msa71927.2{173_090}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_CJB110}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_COH1}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M781}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_M732}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_H36B}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_JM9130013}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
msa71927.2{173_1169NT}	GGTTTTAATG	TTAAATGGCA	AAGAATAATA	GATAAAGAAG	TGAAACCATC
Consensus	*****	*****	*****	*****	*****

1701

msa71927.2{173_18RS21}

msa71927.2{173_2603}

msa71927.2{173_A909}

msa71927.2{173_090}

msa71927.2{173_CJB110}

msa71927.2{173_COH1}

msa71927.2{173_M781}

msa71927.2{173_M732}

msa71927.2{173_H36B}

msa71927.2{173_JM9130013}

msa71927.2{173_1169NT}

Consensus

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

TgCTGaCCTA

TgCTGaCCTA

TgCTGaCCTA

TaCTGgCCTA

TaCTGgCCTA

TaCTGgCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

ATACAGCCTA

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTAACTCCCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CTTTAAAGCT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

CATTTCATCAT

1750

msa71927.2{173_18RS21}

msa71927.2{173_2603}

msa71927.2{173_A909}

msa71927.2{173_090}

msa71927.2{173_CJB110}

msa71927.2{173_COH1}

msa71927.2{173_M781}

msa71927.2{173_M732}

msa71927.2{173_H36B}

msa71927.2{173_JM9130013}

msa71927.2{173_1169NT}

Consensus

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

1800

msa71927.2{173_18RS21}

msa71927.2{173_2603}

msa71927.2{173_A909}

msa71927.2{173_090}

msa71927.2{173_CJB110}

msa71927.2{173_COH1}

msa71927.2{173_M781}

msa71927.2{173_M732}

msa71927.2{173_H36B}

msa71927.2{173_JM9130013}

msa71927.2{173_1169NT}

Consensus

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

TAGTAAATTT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

AGAAGAAAAT

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

TCACAAGTTA

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

CTCAAGTATC

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

TATCTCTAAA

1801

msa71927.2{173_18RS21}

msa71927.2{173_2603}

msa71927.2{173_A909}

msa71927.2{173_090}

msa71927.2{173_CJB110}

msa71927.2{173_COH1}

msa71927.2{173_M781}

msa71927.2{173_M732}

msa71927.2{173_H36B}

msa71927.2{173_JM9130013}

msa71927.2{173_1169NT}

Consensus

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AAATGGATGA

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

AATCGTCTGT

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

TAAAAATAAA

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

ccatccgtaa

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

tggcatatca

1850

msa71927.2{173_18RS21}

msa71927.2{173_2603}

msa71927.2{173_A909}

msa71927.2{173_090}

msa71927.2{173_CJB110}

msa71927.2{173_COH1}

msa71927.2{173_M781}

msa71927.2{173_M732}

msa71927.2{173_H36B}

msa71927.2{173_JM9130013}

msa71927.2{173_1169NT}

Consensus

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

aaaagca

SEQ ID NO: 4814

STRAIN 2603 frame: 1

NSTETASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDPHHISAP

DALKTTQSSPVVESTSTKLTEETIKQKQDLANMVRSGQVTEBELVNMAYDI IAKENPS

LNAVITTRRQEAIEBEARKLKDNTQPPFLGVPLLVKGLGHSI KGETNNGLIYADGKI STFD

SSYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGGSSGCSAAAIAS

GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPKDSYSTAVHPLTKSSRDAETL

LTYLKKSDQTLVSVNDLSKSLPIATYTKSPMGTEVSQDAKNAIMDNVTFLRKQGFVKTEID

LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGFTKEDVDPIWAVHVIYQNSDKAELK

KSIMEAQKHMDYRKAMEKLHKQFPFLSPTASLAPLNTDPYVTEEDKRAIYMNENLSQ

EERIALFNRRQWEPMLRRTPFTQIANMTGLPAISIPTYLSSEGLPIGTMAGANYDMVLI

KFATFFEKHHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLBENSQVTQVSISK

KWKSSVKNKPSVMAYQKA

SEQ ID NO: 4815

STRAIN_090 frame: 1

NSTETASVVPITNTIVQINDSNPTAKFVSESGQSVIGQVKPDNSAALTIVDPHHISAP

Table 48: Comparative Sequences relating to SAG1474

DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPS
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFD
 SSVYKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIAS
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEID
 LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 ERIALFNRQWEPMLRRTPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
 KFATFFEKHHGFFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK
 KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4816

STRAIN A909 frame: 2

TTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAPDALKTTQSSPV
 VESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPSLNAVITTRRQ
 AIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSVYKKYKDLG
 FIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIASGMTPIASGSDA
 GGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSDQTL
 VSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEIDLPIDGRALMRD
 YSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIMEAQKHMD
 DYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALFNRQW
 EPMRLRTPPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFFEKHHG
 FNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSVKNK
 SVMAYQKA

SEQ ID NO: 4817

STRAIN COH1 frame: 1

NSTETSASVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPD
 ALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPSL
 NAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSVYKKYK
 SYVKKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASG
 MTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLL
 TYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEIDLP
 PIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK
 SIVEAQKHMDYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 ERIALFNRQWEPMLRRTPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
 FATFFEKHHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK
 WMKSSVKNKPSVMAYQKA

SEQ ID NO: 4818

STRAIN M732 frame: 1

SVAPTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQS
 SPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPSLNAVITTR
 RQEAIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSVYKKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEIDLPIDGRAL
 MRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
 KHMDYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALFN
 RQWEPMLRRTPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFEK
 HHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSV
 NKPSVMAYQKA

SEQ ID NO: 4819

STRAIN 18RS21 frame: 1

NSTETSASVVPNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPDNSAALTVDTPHISAP
 DALKTTQSSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPS
 LNAVITTRRQEAIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFD
 SSVYKKYKDLGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGGSAAAIAS
 GMTPIASGSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETL
 LTYLKKSDQTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEID
 LPIDGRALMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELK
 KSIMEAQKHMDYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQ
 ERIALFNRQWEPMLRRTPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLI
 KFATFFEKHHGFFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVSISSK
 KMKSSVKNKPSVMAYQKA

SEQ ID NO: 4820

STRAIN M781 frame: 2

ASVAPTNTNTIVQTNDSNPTAKFVSESGQSVIGQVKPANSAAALTVDTPHISAPDALKTTQ
 SSPVVESTSTKLTEETYKQKDGQDLANMVRSGQVTSEELVNMAIDI IAKENPSLNAVITTR
 RQEAIEEARKLKDTNQPFLLVGLGHSIKGGETNNGLIYADGKISTFDSSVYKKYK
 KDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGGSAAAIASGMTPIAS
 GSDAGGSIRIPSSWTGLVGLKPTRGLVSNKPDYSYTAHVHPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSLPIAYTLKSPMGTEVSQDAKNAIMDNVTLFRKQGFVTEIDLPIDGRA
 LMRDYSTLAIGMGGAFFSTIEKDLKKGHFTKEDVDPITWAVHVIYQNSDKAELKKSIVEAQ
 KHMDYRKAMEKLHKQFPFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQERIALF
 NRQWEPMLRRTPTPIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATFEK
 HHGFFNVKQRIIDKEVKPSADLIQPTNSLFKAHSSLVNLEENSQVTQVSISSKMKSSV
 KNKPSVMAYQKA

SEQ ID NO: 4821

STRAIN CJB110 frame: 3

Table 48: Comparative Sequences relating to SAG1474

VPTTNTIVQTNDSNPTAKFVSESQSVIGQVKPDNSAALTVDTPHHISAPDALKTTQSS
 PVVESTSTKLTEETKYKQKDGQDLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTRR
 QEAEIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDSYVVKYK
 LGFIILGQTNFPEYGWRNITDSKLYGLTHNPWDLAHNAGSSGSSAAAIASGMTPIASG
 DAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSDQ
 TLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL
 RDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELKKSIMAQKH
 MDDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFNR
 QWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATPFEEKH
 HGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK
 KPVSVMAYQKA

SEQ ID NO: 4822

STRAIN 1169NT frame: 1

NSTETSASVAPTNTNTIVQTNDSNPTAKFSESQSVIGQVKPDNSAALTVDTPHHISAPD
 DLKTTQSSPVVESTSTKLTEETKYKQKDGQDLANMVRSGQVTSEELVNMAVDIIAKENPSL
 NAVITTRRQEAEIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYADGKIISTFDS
 SYVVKYKDLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGSSAAAIASG
 MTPIASGDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLL
 TYLKKSDQTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL
 MRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELKKSIMAQKH
 SIMEAQKHMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEB
 ERIALFNRQWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIK
 FATPFEEKHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKK
 WMKSSVKNPVSVMAYQKA

SEQ ID NO: 4823

STRAIN JM9130013 frame: 2

SVAPTNTNTIVQTNDSNPTAKFSESQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
 SPVESPSTKLTEETKYKQKDGQDLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR
 RQEAEIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVVKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGSSAAAIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL
 MRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELKKSIMAQKH
 HMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATPFEEK
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK
 NKPSVMAY

SEQ ID NO: 4824

STRAIN H36B frame: 3

SVVPTTNTIVQTNDSNPTAKFSESQSVIGQVKPANSVALTTVDTPHHISAPDALKTTQSS
 SPVESPSTKLTEETKYKQKDGQDLANMVRSGQVTSEELVNMAVDIIAKENPSLNAVITTR
 RQEAEIEARKLKDTNQPFGLVPLLVKGLGHSIKGGETNNGLIYAGGKIISTFDSYVVKYK
 DLGFIILGQTNFPEYGWRNITDSKLYGPTHNPWDLAHNAGSSGSSAAAIASGMTPIASG
 SDAGGSIRIPSSWTGLVGLKPTRGLVSHKPDYSYSTAVHFPPLTKSSRDAETLLTYLKKSD
 QTLVSVNDLKSPLIAYTLKSPMGTEVSQDAKNAIMDNVTFRLKQGFVTEIDLPIDGRAL
 MRDYSTLAIGMGGAFTIEKDLKKGFTKEDVDPITWAVHVIYQNSDKAELKKSIMAQKH
 HMDYRKAMEKLHKQFPIFLSPTTASLAPLNTDPYVTEEDKRAIYNMENLSQEBERIALFN
 RQWEPMLRRTPTFTQIANMTGLPAISIPTYLSESGLPIGTMLMAGANYDMVLIKFATPFEEK
 YHGFNVKQRIIDKEVKPSTGLIQPTNSLFKAHSSLVNLEENSQVTQVVSISKKWMKSSVK
 NK

PRETTY of: /biotmp/msa72034.2{*} January 22, 2003 07:25 ..

	1		50
msa72034.2{173_090}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_18RS21}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_2603}	nstetsasvv	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_A909}	-----	-TTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_CJB110}	-----	pTTNTIVQTN DSNPTAKFvS	ESGQSVigQV KpDnSaALTT
msa72034.2{173_COH1}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M732}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_M781}	-----	-asva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSaALTT
msa72034.2{173_1169NT}	nstetsasva	pTTNTIVQTN DSNPTAKFaS	ESGQSVicQV KpDnSaALTT
msa72034.2{173_H36B}	-----	-svv pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
msa72034.2{173_JM9130013}	-----	-sva pTTNTIVQTN DSNPTAKFaS	ESGQSVigQV KPaNSvALTT
Consensus	-----	-*****	*****

	51		100
msa72034.2{173_090}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_18RS21}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_2603}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_A909}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_CJB110}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGk dLANMVRSGQ
msa72034.2{173_COH1}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M732}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_M781}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_1169NT}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_H36B}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ
msa72034.2{173_JM9130013}	VDTPHHISAP	DaLKTQSSP VVEStSTKLt	EETyKQKDGq dLANMVRSGQ

Table 48: Comparative Sequences relating to SAG1474

Consensus	***--*****	*-*****	****-*****	*****--	-*****
msa72034.2{173_090}	101				150
msa72034.2{173_18RS21}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_2603}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_A909}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_CJB110}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_COH1}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_M732}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_M781}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_1169NT}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_H36B}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
msa72034.2{173_JM9130013}	VTSEELVNMA	YDIIAKENPS	LNAVITTRRQ	EAIEEARKLK	DTNQPFLLGVP
Consensus	*****	*****	*****	*****	*****
msa72034.2{173_090}	151				200
msa72034.2{173_18RS21}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_2603}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_A909}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_CJB110}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_COH1}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_M732}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_M781}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_1169NT}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_H36B}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
msa72034.2{173_JM9130013}	LLVKGLGHSI	KGGETNNGLI	YADGKISTFD	SSYVKKYKDL	GFIILGQTNF
Consensus	*****	*****	*****	*****	*****
msa72034.2{173_090}	201				250
msa72034.2{173_18RS21}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_2603}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_A909}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_CJB110}	PEYGWRNITD	SKLYGLTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_COH1}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_M732}	PEYGWRNITD	SKLYGxTHNP	wdLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_M781}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_1169NT}	PEYGWRNITD	SKLYGpTHNP	rnLAHNAGGS	SGGSAAaIAS	GMPPIASGSD
msa72034.2{173_H36B}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAvIAS	GMPPIASGSD
msa72034.2{173_JM9130013}	PEYGWRNITD	SKLYGpTHNP	wnLAHNAGGS	SGGSAAvIAS	GMPPIASGSD
Consensus	*****	*****	*****	*****	*****
msa72034.2{173_090}	251				300
msa72034.2{173_18RS21}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_2603}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_A909}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_CJB110}	AGGSIRIPSS	WTGLVGLKPT	RGLVShEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_COH1}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_M732}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_M781}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_1169NT}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_H36B}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
msa72034.2{173_JM9130013}	AGGSIRIPSS	WTGLVGLKPT	RGLVSnEKPd	SYSTAVHFPL	TKSSRDAETL
Consensus	*****	*****	*****	*****	*****
msa72034.2{173_090}	301				350
msa72034.2{173_18RS21}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_2603}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_A909}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_CJB110}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_COH1}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_M732}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_M781}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_1169NT}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_H36B}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
msa72034.2{173_JM9130013}	LTYLKKSDQT	LVSVDLKS	PIAYTLKSPM	GTEVSQDAKN	AIMDNVtFLR
Consensus	*****	*****	*****	*****	*****
msa72034.2{173_090}	351				400
msa72034.2{173_18RS21}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_2603}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_A909}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_CJB110}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_COH1}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_M732}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_M781}	eQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_1169NT}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
msa72034.2{173_H36B}	kQGFkvTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV

Table 48: Comparative Sequences relating to SAG1474

msa72034.2{173_JM9130013}	kQGFVKTEID	LPIDGRALMR	DYSTLAIGMG	GAFSTIEKDL	KKHGFTKEDV
Consensus	*****	*****	*****	*****	*****
	401				450
msa72034.2{173_090}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_18RS21}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_2603}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_A909}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_CJB110}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_COH1}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M732}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_M781}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_1169NT}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_H36B}	DPITWavHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
msa72034.2{173_JM9130013}	DPITWgVHVI	YQNSDKAELK	KSImEAQKHM	DDYRKAMEKL	HKQFPiFLSP
Consensus	*****	*****	*****	*****	*****
	451				500
msa72034.2{173_090}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_18RS21}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_2603}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_A909}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_CJB110}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_COH1}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_M732}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_M781}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_1169NT}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_H36B}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
msa72034.2{173_JM9130013}	TTASLAPLNT	DPYVTEeDKR	AIYNMENLSQ	EEERIALFNRO	WEPMLRRTPF
Consensus	*****	*****	*****	*****	*****
	501				550
msa72034.2{173_090}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_18RS21}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_2603}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_A909}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_CJB110}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_COH1}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M732}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_M781}	TpIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_1169NT}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKhh
msa72034.2{173_H36B}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
msa72034.2{173_JM9130013}	TqIANMTGLP	AISIPTYLSE	SGLPIGTMLM	AGANYDMVLI	KFATFFFEKyh
Consensus	*..*****	*****	*****	*****	*****_*
	551				600
msa72034.2{173_090}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_18RS21}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_2603}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_A909}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_CJB110}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_COH1}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M732}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_M781}	GFNVKQRII	DKEVKPSadL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_1169NT}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_H36B}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
msa72034.2{173_JM9130013}	GFNVKQRII	DKEVKPstgL	IQPTNSLFKA	HSSLVNLEEN	SQVTQVSISK
Consensus	*****	*****	*****	*****	*****
	601				619
msa72034.2{173_090}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_18RS21}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_2603}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_A909}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_CJB110}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_COH1}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M732}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_M781}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_1169NT}	KWMKSSVKNK	psvmayqka			
msa72034.2{173_H36B}	KWMKSSVKNK	~~~~~			
msa72034.2{173_JM9130013}	KWMKSSVKNK	psvmay---			
Consensus	*****	~~~~~			

Table 49: Comparative Sequences related to SAG1502

SEQ ID NO: 4901

STRAIN 2603

aaacatccgatacttaaatgatcaaaaatccttagcaattgttgaacagat
 agaataatgatttttgataaattcgataattcagaagcttctttttatgcaa
 cattagctagawttcgcggttatggatagagaaatcaaaaaattattaga
 gaaaatccaaatagtc aaatcctttcaattgggtgtggacttgatacaag
 gtttgaaagagtcgataatggacaaaattaggtggatataaccttgatttgc
 cagaggttatggagataagaaaattatttttgaagagcatgaaagagtt
 actaatatagcaaaaatcagccctagatgaaacttggacacgggaggtaaa
 tccccaaaatgcccccttttctaactcgtgtcagaaggtgttttaattgtttc
 taaaagaagatgacgttagagacttttctcatatcctgacaaattcattt
 agccaatttatggcacaatttgatttgggtcataaggaaatgatttaataa
 aggaaagcaacatgatacagtaagatatggatcacagaatttcagtttg
 gtatcacagatgggtcatgagatttgggttagaccctaaattaaagcaa
 ataaatctgatttaactttacagatgagatgagcaaatgtgattaggcac
 acttcgctcttacttccaacaattcgtaaatataaattgttttaggtg
 tgtacgaataataaagcatc

SEQ ID NO: 4902

STRAIN 090

TAATGATCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTG
 ATAAATTTCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATT
 CGCGTTATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAG
 TCAAAATCCTTTCAATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCCG
 ATAAATGGACAAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAG
 ATAGAGAAAATTTATTTTGAAGAGCATGAAGAGTTACTAATATAGCAAA
 ATCAGCCATAGATGAAACTTGGACACGGGAGGTAAATCCCCAAAATGCC
 CTTTTCTAATCGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGAC
 GTAGAGACTTTTCTCATATCCTGACAAAATTCATTAGCCAATTTATGGC
 ACAATTTGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATG
 ATACAGTAAAGTATATGGATACAGAATTTGAGTTTGGTATCAGATGGT
 CATGAGATTGTGGATTAGACCCCTAAATTAAGCAAAATAAATCTGATTAA
 CTTTACAGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTAC
 TTCCAACAATTCGTAATTTAATAATTGTTTAGGTGTGTACGAATATAAA
 GCATC

SEQ ID NO: 4903

STRAIN A909

AAACATCCGATACTTAATGA

TCAAAAATCCTTAGCAATTGTTGAACAGATAGAATATGATTTTGATAAA
 TCGATAAATTGAGAAGCTTCTTTTATGCAACATTAGCTAGAATTGCGGTT
 ATGGATAGAGAAATCAAAAATTTATTAGAGAAAATCCAATAGTCAAT
 CcTTTCaATTGGTTGTGGACTTGATACAAGGTTTGAAAGAGTCGATAATG
 GACAAATTAGGTGGTATAACCTTGATTGGCAGAGGTTATGGAGATAAGA
 AAATTaTTTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAAATCAGC
 CCTAGATGAaACTTGGACACGGGAGGTAAATCCCCAAAATGCCCTTTTC
 TAATCGGTGTGAGAAGGTGTTTAAATGTTTCTAAAAGAAGATGACGTAGAG
 ACTTTTCTTCATATCCTGACAAAATTCATTAGCCAATTTATGGCACAATT
 TGATTGTGTGATAAGGAAATGATTAAATAAGGAAAGCAACATGATACAG
 TAAAGTATATGGATACAGAATTTGAGTTTGGTATCAGATGGTTCATGAG
 ATTGTGGATTAGACCCCTAAATTAAGCAAAATAAATCTGATTAACTTTAC
 AGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCA
 CAATTCGTAAATTTAATAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4904

STRAIN H36B

AAACATCCGATACTTAATGATCAAAAATCCTTAGCA

ATTGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAATTGAGAAGC
 TTCTTTTATGCAaCATTAGCTAGAATTGCGGTTATGGATAGAGAAATCA
 AAAAAATTATTAGAGAAAATCCAATAGTCATATCCTTTCAATTGGCTGT
 GgACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTA
 TAACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTGAAG
 AGCATGAAAGAGTTACTAATATAGCAAAAATCAGCCcTAGATGAAACTTGG
 ACACGGGAGGTAAATCCCCAAAATGCCCTTTTCTAATCGTGTGAGAAG
 TGTTTAAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCC
 TGACAAATTCATTTAGCCAATTTATGGCACAATTGATTGTGTGcAGAG
 GAAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATAC
 AGAATTTCAAGTTGGGTATCAGATGGTTCATGAAATTGTGGATTAGACC
 CTAAATTAAGCAAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAA
 TTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAA
 TAATTGTTTAGGTGTGTACGAATATAAGCATC

SEQ ID NO: 4905

STRAIN 18RS21

AACATCCGATACTTAATGATCAAAAATCCTTAGCAAT

TGTTGAACAGATAGAATATGATTTTGATAAAATTCGATAAATTGAGAAGCTT
 CTTTTATGCAACATTAGCTAGAATTGCGGTTATGGATAGAGAAAATCAAA
 AAATTTATTAGAGAAAATCCAATAGTCAaATCCTTTCAATTGGTTGTGG
 ACTTGATACAAGGTTTGAAAGAGTCGATAATGGACAAATTAGGTGGTATA
 ACCTTGATTGGCAGAGGTTATGGAGATAAGAAAATTATTTTGAAGAG
 CATGAAAGAGTTACTAATATAGCAAAAATCAGCCCTAGATGAAACTTGGAC
 ACCGGAGGTAAATCCCCAAAATGCCCTTTTCTAATCGTGTGcAGAGGTG
 TTTTAAATGTTTCTAAAAGAAGATGACGTAGAGACTTTCTTCATATCCTG

Table 49: Comparative Sequences related to SAG1502

ACAAATTCATTTAGCCAAATTTATGGCACaATTTGATTGTGTGCATaAGGA
AATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG
AATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCT
AAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATA
ATTGTTTAGGTGTACGAATATAaGCATC

SEQ ID NO: 4906

STRAIN M732

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAATTGTTGAACA
GATAGAAATATGATTGGATAAATTCGATAATTCAGAAGCTTCTTTTATG
CAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAAAAATTTATT
AGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTGGACTTGATC
AAGGTTTGAAGAGTCGATAATGGACAAATTAGGTGGTATAACCTTGATT
TGCCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGAGCATGAAAGA
GTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGACACGGGAGGT
AAATCCCCAAATGCCCTTTTCTAATCGTGTGAGAAGGTGTTTAAATGT
TTCTAAAAGAAAGATGACGTAGAGACTTTTCTTCAATCTCTGACAAATTC
TTTAGCCAAATTTATGGGCAAAATTTGATTGTGTGCATAGGAAATGATTAA
TAAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAGAAATTTCAAT
TTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCCTAAATTAAG
CAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAATTTGAGTTAG
CACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATAATTTGTTAG
GtGTGTACGAATATAAAGCATC

SEQ ID NO: 4907

STRAIN COH1

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT
TCCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG
GACTTGATACAAGGTTTGAAGAGTCGATAATGGACAAATTAGGTGGTAT
AACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGA
GCATGAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGGA
CACGGGAGGTAAATCCCCAAATGCCCTTTTCTAATCGTGTGAGAAGGT
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCAATCTCT
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAAT
AATTGTTTAGGTGTACGAATATAAAGCATC

SEQ ID NO: 4908

STRAIN M781

AAACATCCGATACCTTAATGATCA
AAAATCCTTAGCAATTTGTTGAACAGATAGAATATGATTGGATAAATTCG
ATAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGAATTCGCGTTATG
GATAGAGAAATCAAAAATTTATTAGAGAAAATCCAAATAGTCAAATCCT
TTCAATTGGTTGTGGACTTGATACAAGGTTTGAAGAGTCGATAATGGAC
AAATTAGGTGGTATAACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAA
TTATTTTGAAGAGCATGAAAGAGTTACTAATATAGCAAAATCAGCCCT
AGATGAAACTTGGACACGGGAGGTAAATCCCCAAATGCCCTTTTCTAA
TCGTGTGAGAAGGTGTTTTAATGTTTCTAAAAGAAAGATGACGTAGAGACT
TTTCTTCAATCTCTGACAAATTCATTAGCCAAATTTATGGCACAATTTGA
TTGTGTGCATAGGAAATGATTAAATAAGGAAAGCAACATGATACAGTAA
AGTATATGGATACAGAAATTCAGTTGGTATCACAGATGGTCATGAGATT
GTGGATTAGACCCCTAAATTAAGCAAATAAATCTGATTAACTTTACAGA
TGAGATGAGCAAATTTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAA
TTGTAATTTAATAATGTTTAGGTGTACGAATATAAAGCATC

SEQ ID NO: 4909

STRAIN CJB110

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAA
TTGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCT
TCCTTTTATGCAACATTAGCTAGAATTCGCGTTATGGATAGAGAAATCAA
AAAATTTATTAGAGAAAATCCAAATAGTCAAAATCCTTTCAATTGGTTGTG
GACTTGATACAAGGTTTGAAGAGTCGATAATGGACAAATTAGGTGGTAT
AACCTTGATTGCGCAGAGGTTATGGAGATAAGAAAATTTATTTTGAAGA
GCATGAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAAACTTGGGA
CACGGGAGGTAAATCCCCAAATGCCCTTTTCTAATCGTGTGAGAAGGT
GTTTTAATGTTTCTAAAAGAAGATGACGTAGAGACTTTTCTTCAATCTCT
GACAAATTCATTTAGCCAAATTTATGGCACAATTTGATTGTGTGCATAAGG
AAATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACA
GAATTTCAAGTTGGTATCACAGATGGTCATGAGATTGTGGATTAGACCC
TAAATTAAGCAAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAT
TTGAGTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAAT
AATTGTTTAGGTGTACGAATATAAAGCATC

SEQ ID NO: 4910

STRAIN 1169NT

AAACATCCGATACCTTAATGATCAAAAATCCTTAGCAAT
TGTTGAACAGATAGAATATGATTGGATAAATTCGATAATTCAGAAGCTT

Table 49: Comparative Sequences related to SAG1502

CTTTTATGCAACATTAGCTAGAAATTCGCGTTATGGATAGAGAAATCAAA AAATTTATTAGAGAAAATCCAAATAGTCATATCCTTTCTATTGGTTGTGG ACCTTGATACAAGGTTTGAAGAGTCGATAATGGACAAATAGGTGGTATA ACCTTGATTGTCAGAGGTTATGGAGATAAGAAAATTATTTTTGAAGAG CATGAAAGAGTTACTAATATAGCAAAATCAGCCCTAGATGAACTTGGAC ACAGGAGGTAAATCCCCAAATGCCCTTTTCTGATCGTGTGAGAGGTG TTTTAATGTTTCTAAAGAAAGATGACGTAGAGACTTTTCTCATATCCTG ACAAATTCATTTAGCCCAATTTATGGCCACAATTTGATTGTGTGCAGAAGGA AATGATTAAATAAGGAAAGCAACATGATACAGTAAAGTATATGGATACAG AATTTTCAGTTTGGTATCACAGATGGTCATGAAATTGTGGATTAGACCCCT AAATTAAGCAATAAATCTGATTAACTTTACAGATGAGATGAGCAAAATT TGAGTTTAGGCACACTTCGCTCTTTACTTCCAACAATTCGTAATTTAATA ATTGTTTAGGTGTGTACGAATATAAAGCATC					
SEQ ID NO: 4911 STRAIN JM9130013 AGCAATTTGTTGAACAGATAGAATATGATT TTGATAAAATTCGATAAATTCAGAAGCTTCTTTTATGCAACATTAGCTAGA ATTTCGCGTTATGGATAGAGAAATCAAAAAATTTATTAGAGAAAATCCAA TAGTCATATCCTTTCAATTGGCTGTGGACTTGATACAAGGTTTGAAGAG TCGATAATGGACAAAATTAGGTGGTATAACCTTGATTGGCCAGAGGTTATG GAGATAAGAAAATTATTTTTGAAGAGCATGAAAGAGTTACTAATATAGC AAAATCAGCCCTAGATGAAACTTGGACACGGGAGGTAAATCCCCAAATG CCCCCTTTCTAATCTGTGTCAGAAAGGTGTTTAAATGTTTCTAAAGAAAGAT GACGTAGAGACTTTTCTCATATCCTGACAAATTCATTTAGCCAAITTTAT GGCACAATTTGATTTGTGTGAGAAAGAAATGATTAAATAAGGAAAGCAAC ATGATACAGTAAAGTATATGGATACAGAATTTTCAGTTTGGTATCACAGAT GGTCATGAAAATTGTGGATTAGACCCTTAAATTAAGCAAAATAAATCTGAT TAACTTTACAGATGAGATGAGCAAAATTTGAGTTAGGCACACTTCGCTCTT TACTTCCAACAATTCGTAATTTAATAATTTGTTTAGGTGTGTACGAATAT AAAGCATC					
PRETTY of: /biotmp/msa42193.2{*} January 21, 2003 05:04 ..					
msa42193.2{176_090}	1	-----	-----	-----	50
msa42193.2{176_CJB110}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_18RS21}	-AACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_2603}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_A909}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_COH1}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_M732}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_M781}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_H36B}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
msa42193.2{176_JM9130013}	-----	-----	-----	--AGCAATTG	TTGAACAGAT
msa42193.2{176_1169NT}	AAACATCCGA	TACTtaatga	tcaaaaatcc	ttAGCAATTG	TTGAACAGAT
Consensus	*****	*****	-----	*****	*****
msa42193.2{176_090}	51	AGAATATGAT	TTtGATAAAT	TCGATAATTC	100
msa42193.2{176_CJB110}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_18RS21}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_2603}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_A909}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_COH1}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_M732}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_M781}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_H36B}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_JM9130013}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
msa42193.2{176_1169NT}	AGAATATGAT	TTtGATAAAT	TCGATAATTC	AGAAGCTTCT	TTTTATGCAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	101	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	150
msa42193.2{176_CJB110}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_18RS21}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_2603}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_A909}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_COH1}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_M732}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_M781}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_H36B}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_JM9130013}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
msa42193.2{176_1169NT}	CATTAGCTAG	AaTTCGCGTT	ATGGATAGAG	AAATCAAAAA	ATTTATTAGA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	151	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	200
msa42193.2{176_CJB110}	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_18RS21}	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_2603}	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_A909}	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_COH1}	GAAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_M732}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_M781}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_H36B}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_JM9130013}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
msa42193.2{176_1169NT}	GAAAATCCAA	ATAGTCAaAT	CCTTTCaATT	GGtTGTGGAC	TTGATACAAG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	201	250			
msa42193.2{176_CJB110}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_18RS21}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_2603}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_A909}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_COH1}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M732}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_M781}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_H36B}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_JM9130013}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
msa42193.2{176_1169NT}	GTTTGAAAGA	GTCGATAATG	GACAAATTAG	GTGGTATAAC	CTTGATTTCG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	251	300			
msa42193.2{176_CJB110}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_18RS21}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_2603}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_A909}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_COH1}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M732}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_M781}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_H36B}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_JM9130013}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
msa42193.2{176_1169NT}	CAGAGGTTAT	GGAGATAAGA	AAATTATTTT	TTGAAGAGCA	TGAAAGAGTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	301	350			
msa42193.2{176_CJB110}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_18RS21}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_2603}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_A909}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_COH1}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M732}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_M781}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_H36B}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_JM9130013}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
msa42193.2{176_1169NT}	ACTAATATAG	CAAAATCAGC	CaTAGATGAA	ACTTGGACAC	gGGAGGTAAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	351	400			
msa42193.2{176_CJB110}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_18RS21}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_2603}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_A909}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_COH1}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M732}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_M781}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_H36B}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_JM9130013}	TCCCCAAAAT	GCCCCCTTTTC	TaATCGTGTC	AGAAGGTGTT	TTAATGTTTC
msa42193.2{176_1169NT}	TCCCCAAAAT	GCCCCCTTTTC	TgATCGTGTC	AGAAGGTGTT	TTAATGTTTC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	401	450			
msa42193.2{176_CJB110}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_18RS21}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_2603}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_A909}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_COH1}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M732}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_M781}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_H36B}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_JM9130013}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
msa42193.2{176_1169NT}	TAAAAGAAGA	TGACGTAGAG	ACTTTTCTTC	ATATCCTGAC	AAATTCATTT
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	451	500			
msa42193.2{176_CJB110}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_18RS21}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_2603}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CaTAAGGAAA	TGATTAATAA
msa42193.2{176_A909}	AGCCAATTTA	TGGCACAATT	TGATTGTGT	CaTAAGGAAA	TGATTAATAA

Table 49: Comparative Sequences related to SAG1502

msa42193.2{176_COH1}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_M732}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_M781}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CATaAGGAAA	TGATTAATAA
msa42193.2{176_H36B}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_JM9130013}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
msa42193.2{176_1169NT}	AGCCAATTTA	TGGCACAATT	TGATTTGTGT	CAGaAGGAAA	TGATTAATAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_CJB110}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_18RS21}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_2603}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_A909}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_COH1}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M732}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_M781}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_H36B}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_JM9130013}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
msa42193.2{176_1169NT}	AGGAAAGCAA	CATGATACAG	TAAAGTATAT	GGATACAGAA	TTTCAGTTtG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_CJB110}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_18RS21}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_2603}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_A909}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_COH1}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M732}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_M781}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_H36B}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_JM9130013}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
msa42193.2{176_1169NT}	GTATCACAGA	TGGTCATGag	ATTGTGGATT	TAGACCCTAA	ATTAAAGCAA
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_CJB110}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_18RS21}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_2603}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_A909}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_COH1}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M732}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_M781}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_H36B}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_JM9130013}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
msa42193.2{176_1169NT}	ATAAATCTGA	TTAACTTTAC	AGATGAGATG	AGCAAATTTG	AGTTAGGCAC
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_CJB110}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_18RS21}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_2603}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_A909}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_COH1}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_M732}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_M781}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_H36B}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_JM9130013}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
msa42193.2{176_1169NT}	ACTTCGCTCT	TTACTTCCAA	CAATTTCGTAA	ATTAAATAAT	TGTTTAGGTG
Consensus	*****	*****	*****	*****	*****
msa42193.2{176_090}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_CJB110}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_18RS21}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_2603}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_A909}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_COH1}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M732}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_M781}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_H36B}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_JM9130013}	TGTACGAATA	TAAAGCATC			
msa42193.2{176_1169NT}	TGTACGAATA	TAAAGCATC			
Consensus	*****	*****			

SEQ ID NO: 4912

STRAIN 2603 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARKXRVMDREIKKFIRENPNSQILSI
 CGGLDTRFRVDNGQIRWYNLDLFEVMEIRKLFFEEHERVTNIAKSALDETWTRVNPQN
 APFLIVSEGLVLMFLKEDDVETFLHILNFSFSQFMAQFDLCHKEMINKGKHDTVKYMDTE

Table 49: Comparative Sequences related to SAG1502

FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4913

STRAIN 090 frame: 2

NDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIGCGLD
TRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSAIDETWTREVNPNQAPFLI
VSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTEFQFGI
TDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4914

STRAIN A909 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4915

STRAIN H36B frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4916

STRAIN 18RS21 frame: 3

HPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSIG
CGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
PFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4917

STRAIN M732 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4918

STRAIN COH1 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4919

STRAIN M781 frame: 1

KHPILNDQKSLAIVEQIEYDLDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4920

STRAIN CJB110 frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSQILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSAIDETWTREVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4921

STRAIN 1169NT frame: 1

KHPILNDQKSLAIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSI
GCGLDTRFERVDNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTQEVNPNQ
APFLIVSEGVLMLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTE
FQFGITDGHEIVDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

SEQ ID NO: 4922

STRAIN JM9130013 frame: 2

AIVEQIEYDFDKFDNSEASFYATLARIRVMDREIKKFIRENPNSHILSIGCGLDTRFERV
DNGQIRWYNLDLPEVMEIRKLFFEEHERVTNIAKSALDETWTREVNPNQAPFLIVSEGVL
MLFKEDDVETFLHILTNFSQFMAQFDLCHKEMINKGKQHDVTKYMDTEFQFGITDGHEI
VDLDPKLGKQINLINFTDEMSKFELGTLRSLPTIRKFNCLGVYEYKA

PRETTY of: /biotmp/msa42204.2{*} January 21, 2003 05:05 ..

	1		50
msa42204.2{176_H36B}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_JM9130013}	-----	-AIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_090}	-----ndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_18RS21}	-hpiilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_2603}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARxRV MDREIKKFIR	
msa42204.2{176_A909}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	
msa42204.2{176_CJB110}	khpilndqks	LAIVEQIEYD fDKFDNSEAS FYATLARiRV MDREIKKFIR	

Table 49: Comparative Sequences related to SAG1502

msa42204.2{176_COH1}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_M732}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_M781}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
msa42204.2{176_1169NT}	khpilndqks	LAIVEQIEYD	LDKFDNSEAS	FYATLARIRV	MDREIKKFIR
Consensus	-----	*****	*****	*****	*****
51					
msa42204.2{176_H36B}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_JM9130013}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_090}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_18RS21}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_2603}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_A909}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_CJB110}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_COH1}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M732}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_M781}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
msa42204.2{176_1169NT}	ENPNShILSI	GCGLDTRFER	VDNGQIRWYN	LDLPEVMEIR	KLFFEEHERV
Consensus	*****	*****	*****	*****	*****
101					
msa42204.2{176_H36B}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_JM9130013}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_090}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_18RS21}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_2603}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_A909}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_CJB110}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_COH1}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M732}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_M781}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
msa42204.2{176_1169NT}	TNIAKSALDE	TWTrEVNPNQ	APFLIVSEGV	LMFLKEDDVE	TFLHILTNSE
Consensus	*****	***-*****	*****	*****	*****
151					
msa42204.2{176_H36B}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_JM9130013}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_090}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_18RS21}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_2603}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_A909}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_CJB110}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_COH1}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_M732}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_M781}	SQFMAQFDLC	hKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
msa42204.2{176_1169NT}	SQFMAQFDLC	qKEMINKGKQ	HDTVKYMDTE	FQfGITDGHE	IVDLDPKLLKQ
Consensus	*****	-*****	*****	***-*****	*****
201					
msa42204.2{176_H36B}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_JM9130013}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_090}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_18RS21}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_2603}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_A909}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_CJB110}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_COH1}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M732}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_M781}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
msa42204.2{176_1169NT}	INLINFTDEM	SKFELGTLRS	LLPTIRKFNN	CLGVYHEYKA	
Consensus	*****	*****	*****	*****	
239					

Table 50: Comparative Sequences relating to SAG 1024

SEQ ID NO. 5001

STRAIN 2603

ATGAAAAACAAAACTATTACTGCTTATTGGAGGCTTATTAATAATGATAATGATGACA
 GCATGTAAGGATTCAAAAATCCCGAAAAACCGCACAAGGAAGAGTACCAAGCTGAACAA
 AATTTTAAACCGTTTTTTGAGTTTTTAGCACAAGAAAGATAAGATTGAGCAAAATACAA
 AAATACTTACTATTAGTATCGGATTGAGGTGATGCATTAGATTAGAAATATTTCTATAGT
 ATTCAAGATTTAAAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAAATA
 GAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCAITTTGAATATTTTAAA
 AATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACATTTGATGACTTTATTATCGGA
 GCAATGGATACTAAAGAATTAAAGAATTAAAAAATTAAAAAGTAAAAAGTTATTATTATA
 AAACATCCGGAACCTGAGTTGAAGATATAACATATGAATTGCCGACACAGTCAAGCTT
 ATTAATAAA

SEQ ID NO. 5002

STRAIN 090

TAAGGATTCAAAAATCCCGAAAAACCGCACAAG
 GAAGAGTACCAAGCTGAACAAAATTTTAACTGTTTTTGGAGTTTTTAGC
 ACAAAAATATAAGATTGGAACAAAATACAAAATACCTTACTATTAGTAT
 CGGATTGAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGAT
 TTAATAAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAAAT
 AGAAAAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTG
 AATATTTTAAAAATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACA
 TTTGATGACTTTATTATCGGAGCAATGGATACAAAGATTAAAAAATT
 AAAAGTAAAAAGTTATTATTAAACATCCGGAACCTGAGTTGAAAGATA
 TAACATATGAATTGCCGACACAGTCAAGCTTATTAAAAAA

SEQ ID NO. 5003

STRAIN 18RS21

TAAGGATTCAAAAATCCCGAAAAACCGCACAAGGAAG
 AGTACCAAGCTGAACAAAATTTTAAACCGTTTTTGGAGTTTTTAGCACA
 AAAGATAAGGATTTGAGCAAAATACAAAATACCTTACTATTAGTATCGGA
 TTCAGGTGATGCATTAGATTAGAAATATTTCTATAGTATTCAGATTAA
 AAAAAATAAGGATTTAGGGAAGTTTGAACAAGAAAAAGTCAAAATAGAA
 AAGCCGGTGGCTATAATGAGTTAGAAAATAAGAGGTCCCATTTGAATA
 TTTTAAAAATAATATAGTTTATCCAAAAGGAAAAACCGAATATTACATTTG
 ATGACTTTATTATCGGAGCAATGGATACAAAGAATTAAAGAATTAAAA
 GAATTAAAAAATTAAAGTAAAAAGTTATTATTAAAAACATCCGGAAC
 TGAGTTGAAAGATATAACATATGAATTGCCGACACAGTCAAGCTTATTATA
 AAAAA

PRETTY of: /biotmp/msa212269.2{*} February 10, 2003 05:07 ..

	1		50
msa212269.2{184_090}	-----	-----	-----
msa212269.2{184_2603}	atgaaaaaac	aaaaactatt	actgcttatt
msa212269.2{184_18RS21}	-----	-----	-----
Consensus	*****	*****	*****
	51		100
msa212269.2{184_090}	-----	-----TAAGG	ATTCAAAAAT
msa212269.2{184_2603}	aatgatgaca	gcatgTAAGG	ATTCAAAAAT
msa212269.2{184_18RS21}	-----	-----TAAGG	ATTCAAAAAT
Consensus	*****	*****	*****
	101		150
msa212269.2{184_090}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC
msa212269.2{184_2603}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC
msa212269.2{184_18RS21}	AAGAGTACCA	AGCTGAACAA	AATTTTAAAC
Consensus	*****	*****	*****
	151		200
msa212269.2{184_090}	CAAAAAtATA	AAGATTTGaa	CAAAATACAA
msa212269.2{184_2603}	CAAAAAGATA	AAGATTTGag	CAAAATACAA
msa212269.2{184_18RS21}	CAAAAAGATA	AAGATTTGag	CAAAATACAA
Consensus	*****-***	*****	*****
	201		250
msa212269.2{184_090}	GGATTGAGGT	GATGCATTAG	ATTTAGAAATA
msa212269.2{184_2603}	GGATTGAGGT	GATGCATTAG	ATTTAGAAATA
msa212269.2{184_18RS21}	GGATTGAGGT	GATGCATTAG	ATTTAGAAATA
Consensus	*****	*****	*****
	251		300
msa212269.2{184_090}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG
msa212269.2{184_2603}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG
msa212269.2{184_18RS21}	TAAAAAATAA	TAAGGATTTA	GGGAAGTTTG
Consensus	*****	*****	*****
	301		350
msa212269.2{184_090}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA
msa212269.2{184_2603}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA
msa212269.2{184_18RS21}	GAAAAGCCGG	GTGGCTATAA	TGAGTTAGAA
Consensus	*****	*****	*****

Table 50: Comparative Sequences relating to SAG 1024

msa212269.2{184_090}	351	400
msa212269.2{184_2603}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT	
msa212269.2{184_18RS21}	ATATTTTAAA AATAATATAG TTTATCCAAA AGGAAAACCG AATATTACAT	
Consensus	*****	*****
msa212269.2{184_090}	401	450
msa212269.2{184_2603}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....
msa212269.2{184_18RS21}	TTGATGACTT TATTATCGGA GCAATGGATA CT.....	..aaagaatta
Consensus	*****	*****
msa212269.2{184_090}	451	500
msa212269.2{184_2603}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTATA AACATCCGGA	
msa212269.2{184_18RS21}	AAAGAATTAA AAAAATTAAA AGTAAAAAGT TATTATTATA AACATCCGGA	
Consensus	*****	*****
msa212269.2{184_090}	501	550
msa212269.2{184_2603}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA	
msa212269.2{184_18RS21}	AACTGAGTTG AAAGATATAA CATATGAATT GCCGACACAG TCGAAGCTTA	
Consensus	*****	*****
msa212269.2{184_090}	551	
msa212269.2{184_2603}	TTAAAAAA	
msa212269.2{184_18RS21}	TTAAAAAA	
Consensus	*****	
SEQ ID NO. 5004		
STRAIN 2603 frame: 1		
MKKQKLLLLIGLLIMIMMTACKDSKIPENRTKEEYQAEQNFKPFFFFLAQKDKDLSKIQ		
KYLVLVSDSGDALDLEYFYFYSIQDLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFK		
NNIVYPKGKPNITFDDFIIGAMDTKELKELKLVKSYLLKHPETELKDITYELPTQSKL		
IKK		
SEQ ID NO. 5005		
STRAIN 090 frame: 2		
KDSKIPENRTKEEYQAEQNFKPFFFFLAQKYKDLNKKIQKYLVLVSDSGDALDLEYFYFYSIQ		
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFKNNIVYPKGKPNITFDDFIIGAM		
DTKELKELKLVKSYLLKHPETELKDITYELPTQSKLIKK		
SEQ ID NO. 5006		
STRAIN 18RS21 frame: 2		
KDSKIPENRTKEEYQAEQNFKPFFFFLAQKDKDLSKIQKYLVLVSDSGDALDLEYFYFYSIQ		
DLKKNKDLGKFETRKSQIEKPGGYNELENKEVPFPEYFKNNIVYPKGKPNITFDDFIIGAM		
DTKELKELKLVKSYLLKHPETELKDITYELPAQSKLIKK		
PRETTY of: /biotmp/msa212547.2{*} February 10, 2003 05:11 ..		
msa212547.2{184_18RS21}	1	50
msa212547.2{184_2603}	-----	-----
msa212547.2{184_090}	-----	-----
Consensus	*****	*****
msa212547.2{184_18RS21}	51	100
msa212547.2{184_2603}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYFYS IQDLKKNKDL GKFETRKSQI	
msa212547.2{184_090}	QKdKDLsKIQ KYLLLVSDSG DALDLEYFYFYS IQDLKKNKDL GKFETRKSQI	
Consensus	*****	*****
msa212547.2{184_18RS21}	101	150
msa212547.2{184_2603}	EKPGGYNELE NKEVPFPEYFK NNIVYPKGKP NITFDDFIIG AMDTkelkel	
msa212547.2{184_090}	EKPGGYNELE NKEVPFPEYFK NNIVYPKGKP NITFDDFIIG AMDT.....	
Consensus	*****	*****
msa212547.2{184_18RS21}	151	186
msa212547.2{184_2603}	KELKLVKVS YLLKHPETEL KDITYELPaQ SKLIKK	
msa212547.2{184_090}	KELKLVKVS YLLKHPETEL KDITYELPtQ SKLIKK	
Consensus	*****	*****

Table 51: Comparative Sequences relating to SAG0677

SEQ ID NO. 5101

STRAIN 2603

ttgaataataaagggtgtcggtggcgatgggtgtccaaatattatcaatacta
 tatcaaaatggacaacaataaaccttacttaagtcccaagataagacta
 ctgtagagaagttagaagatcgctggaaaaaatctcttcaaagttcag
 gatactggcattgggtttgaaagacgtttatcttcaatctgttaagtatgt
 tgggtgggtggcaataataatttagacctatcacacctccaggatttaaaa
 aagaagataaaaaagttgaaaaaccaaatttagacctccaccaggaaatt
 gatttaccagcaccaacttcaatgagaagttttgattattcaacccacc
 gggaactaagccaagcaaacccaaagatagtttatcaactcctccagggt
 tcccagatttaaacacgcccggatgaagcaccacaaaggatagtaaaaa
 gacgctattgaagataaatcaggagcaattaaatagctaaagtctctca
 acttagctttgtgatggccctatttttagctagcaaaagtaaatggcaaaa
 tattcaagtcgaatctgatggcaaattagtcatctcctagaatgctttg
 tcagctaataatcaatttgatgacactagctcttaaaatattcgtaataata
 tcgcaataaagaaattactatcacacagattattttgcagatacaaaat
 atgtcaatatcacagcggttgactatttgagcaataactacttttgagcaa
 tttagctactgggtgaaacagtagattaccatgccattgtattttcaagct
 tgctgctatttaagacacaggggtggaagatttatgttaacgataaattgc
 aagaaacttctcgtagcgcttaagataaatctgttaagatttggtatt
 gaattaccaaattgatgtcagacatatgtagtttatctgttctgctgtt
 gaatgaggttaaaactgttgataaatcttgaaaaatgatgaacaagaca
 ttaactcagcaaaaacttaccatttaaaatacaacccgacaaatcgctgt
 cttagagttactatttaataacattaaactcaagttcagaaatcatgaccac
 tttcaagatggaaagatgccagaattgggtgaaacaaaagatgtttctt
 tggatataaacgatattggacatgagtaagtttaaaactattcgacttgg
 cgaaaggattctgaatttaaggggacaacttattgcaaaaactggaaacgt
 tgaattagatatgtttttcaaacatctcagacccagcttcaattatta
 aaaaaatataccttatccaaatgggtgttccaaatgaattgaaaaaattt
 gactctgattttgggttaactgaaagtcagatagatggatactatattta
 taagatgcaattaaccttaaatttaaatcaaccagtggtgcaagcttta
 aagttgtttataaagggtcaagaagatccatatagtcacagaagaagat
 atgactaaaaaagggtgaacagctcagtcattcaactcaagccaatgaaaa
 tacagcaaaagtaacctttgctaatatgactgggtcactattatagtaagg
 ttactgtgaatggaaaagaagttgttaagggtagtgagttacctttaact
 aaaggatggacaacatttgtattacataaaacagaaaaattcattaaatgt
 taaaagtttgattatggagacgggttagtgtaagtaagaaagtcaacaac
 ttctcttaagtcctagatttatctaaaaatagcatatgagggatatgcta
 ctactatgcaaaaagattcagcgcttatcgaaacaaagtgacagctagct
 ccttcgaattaatctcactgcagatactaaacttaatttttaagtgttta
 aaggagcgagtgctcttactgaaaatgatgatgagacagtttgagtt
 gctggaccacaagatgatcctgttagtgaaacataaatacccatcagttat
 tctcttaactcctgccttatggaaactgctagtgaggcaactctaaatg
 gtaaggaaatcacagcatctggtattatcggtcactcaaggatgggtgat
 aaaaagcaagcatgttgaagtcaaaatgggtgaatgaaaatggagacatgct
 aggaacccctgttatttcaaggtaagacttgactaatcgacacaaac
 cattaatgagtggaacgtagagtaactttatgcccgttaacaatatgagttc
 cgggttaaataccacttagtcgttttaacacttggattagggttgaagt
 ggttaacagaagcaggagagaaagcaagttatgttctgctgcagttctttg
 accaatcagttccagagcttaacacagcagttgctaaacgtgatttgact
 tctgatactgctcttatccacatcggtgccaaagatgactctctaaact
 aaaaattatatcaagatgattcattacttgaattctgttgataaaacgggtc
 tttatagtttttagaaatgggttagaaatcactaaagatatgacagtacca
 ctagaatttggagataaatatttaagttatctgctgttgacttatcaaaa
 ttatcgctgtaataagagacccttatatctatagaaacgggttttgatgta
 aagcaagcccaatgacagctgacaaaggagctaaagtaactgtggatattg
 ttgatgaagcacttagttgttccagaatggcaggagcttatacattaac
 aatcgacgaagctccaaacacaaatgaatcaggaatgttaacaaacgcta
 aagtatcgattcattatgtaaatgggtggtgttgataaagttgatgttccg
 attaaagtagttgacttagaagctattcgtaagctgaagaagcagtaaa
 agctgaagaagcagctaaagctgaagaagcagctaaagctgaagaggac
 ataaaacccaagaagcacctatagttgaagaaggctacaaggttaataac
 gttcatcaaaactgatactacagttaaagcgtctgatttaccaaagactaa
 gacagtttccgagttcatatggctagaacagacaataaacagataaactt
 cacatcagacacatgttgaaaaacaaatataaaatcacattgccatccact
 ggtgacagcaaacgtgggttattatctactggaaatggctatcggttatgct
 gagtgattatttttagtttagctaaaaagtttaaaagcaaatat

SEQ ID NO. 5102

STRAIN A909

TTGAATAATAAAGGTGTCGGTGGCGAT

GGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTA
 CTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGA
 AAAAAATTACTTTCAAAGTTTCAAGATATCGGCATTGGTTTGAAGACGTT
 TATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCT
 TATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAA
 AATTAGACCGTCCACCAGGAATTGATTACCAACCAACTTCAATGAGA
 AGTTTGTATTATCAACCCACCGGGAAGTAAGCCAAGCAAAACCAAGA
 TAGTTTATCAACTCTCCAGGTTTCCAGATTTAACACGCGCCGGATG
 AAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCA
 ATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCTATTTT
 AGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAT
 TAGTCATTCCTAGAAATGCTTTGTGACGTAATCAATTTGATGACACTAGT

Table 51: Comparative Sequences relating to SAG0677

CTTAAATTTTATCGTAATAATAATCGCAATAAGAAATTACTATCACAAC
 AGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTATT
 TGAGCAATACACTTTTGAGCAATTAGTACTGGTGAACAGTAGATTAC
 CATGCCATTGTATTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAA
 GATTTATGTTTAAACGATAAATGCAAGAACTTCTCGTATAGCGCTTAAAG
 ATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGAGACATATT
 GATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATAT
 CTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTAA
 AATACAAACCCGACAAATCGTCTAGAGTTTACTATTAAATAACATTAACT
 TCAAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCAGAATT
 GGTGTAaCAAAAAGATGTTCTTTGGATATAaCGATATGGACATGAGTA
 AGTTTAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGACAA
 CTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAATC
 TCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGTG
 TTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGT
 CAGATAGATGGATATATATTTATAAAGATGCAATTAACTTAAATTTAA
 ATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGCAAGAAGATC
 CATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGT
 CATTTCACTCAAGCCAATGAAATACAGCAAAAGTAACTTTGCTAATAT
 TGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAGAAGTTGGTA
 AAGGTAGTGAGTTACTTTAACTAAAGGATGGACAACATTTGATTACAT
 AAAAAAGAAATTTCAATAATGTTAAAGTTGATTATGGAGACGGTAG
 TGTAAGTAAGAAAGTTCAACAACCTTCTTTAAGTCTTAGATTATCTAAAA
 ATAAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGGTAT
 TACGAaaCAAGTGAAGTCTAGTCTCGAATTAATCTCACTGACGATAC
 TAACTTAAATTTAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAAAATA
 TGATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTAGT
 GAACATAAATACCCATCAGTATTTCTTTAACTCCTGCTTATTGGAAAC
 TGCTAGTGAGGCACTCTAAATGGTAAGGAATCACAGCATCTGGTATTA
 TCCGTCACATCAAGGATGGTGAATAAAGCAAGCATGTTGAAGTCAAAATG
 GTGAATGAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAA
 AGACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTT
 ATGCCGGTAAACAATATGAGTTCCGGGCTAAATTACCCTTAGTCTGTTTT
 AACACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAG
 TATTGTTCTGTCGATGTTCTTTGACCAATCAGTCCAGAGCTTAAACACAG
 CAGTTGCTAAACGATTTGACTTCTGATATCTGCTTATCCACATCGTT
 GCCAAGATGACTCTCTAAACTAAATTTATCAAGATGATTCATTACT
 TGAATCTGTTGATAAAACCGGTCTTTATAGTTTTAGAAATGGTGTAGAAA
 TCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTATTAAG
 TTATCTGCTGTTGACTTATCAAAATATCGTCTGTAATGAGACCTTCAAT
 CTATAGAAACCGTTTTGATGTTAAAGCAAGCAATGACAGCTGACAAAG
 GAGCTAAAGTAACTGTGATATGTTGATGAAGCACTTAGTTGTTCCAGAA
 ATGGCAGGAGCTTATACATTAACAATCGACGAAGATCCAACACAATGTA
 ATCAGGAATGTTAAACAAACGCTAAAGTATCGATTCAATTATGTAATGGTG
 GTGTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTGAAGGCTATT
 CGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCACGTAAAGCTGAAGA
 AGCAGCTAAAGCTGAAGAAGCACGTAAAGCTGAAGAAGCACGTAAAGCTG
 AAGAGGGACATaAAAACCAAGAACCTTATAGTTGAAGAAGGCTACAAG
 GTTAATAACGTTTCATCAAACTGATACAGTTAAAGCGTCTGATTTACC
 AAAGACTAAGACAGTTTCCGAGTTTCAATGGCTAGAACAGACAATAAAC
 AGATAACTTCATCAGACACATGTTGAAAAACAATTTAAAAATA

SEQ ID NO. 5103

STRAIN H36B

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTT
 ACTTAAGTCCCAAGATAAGACTACTGTAGAGAAGTTAGaaGATCGCTGG
 AAAAAAATTACTTTCAAAGTTCCAGGATACTGGCATTGGTTTGAAGACGT
 TTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACC
 TTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCA
 AAATTAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAG
 AAGTTTGTATTATTCAACCCACCGGGAACCTAAGCCAAGCAACCCAAAG
 ATAGTTTATCAACTCTCCAGGTTTCCAGATTTAAACACGCCGCCGGAT
 GAAGCACTAAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGC
 AATTAAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCATTAT
 TAGCTAGCAAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAA
 TTAGTCATTCTTGAAGATGCTTTGTGAGCTAATCAATTTGATGACACTAG
 TCTTAAAAATTTATCGTAATAATAATCGCAATAAAGAAATTAATATCACAA
 CAGATTATTTTGCAGATACAAAATATGTCAATATCACAGCGGTGACTAT
 TTGAGCAATACTACTTTTGAAGCAATTAGCTACTGGTGAaaCAGTAGATTA
 CCATGCCATTGTAaTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTA
 AGATTTATGTCAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAG
 GATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTGACAGATAT
 TGATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATAATA
 TCTTGAAAAATGATGAACAAGACATTAACTCTCAGCAAACTTACCAATTA
 AAATACAACCCGACAATCTGCTAGAGTTTACTATTAAATAACATTAA
 CTCAGTTTCAGAAATCATGACCACTTCAAAGATGGAAAGATGCCGAAT
 TGGTTGAACAAAAGATGTTCTTTGGATATAAACGATATGGACATGAGT
 AAGTTTAAACTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGGACA
 ACTTATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACAAT
 CTCAAGACCCAGCTTCAATTATTTAAAAAATATACCTTATCCAAAATGGT
 GTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAG
 TCAGATAGATGGATATATTTATAAAGATGCAATTAACTTAAATTTA
 AATTAACAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGAT

Table 51: Comparative Sequences relating to SAG0677

CCATATAGTCATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAG
TCATTCAACTCAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATA
TTGACTGGTCACATTATAGTAAGGTACTGTGAATGGAAAAGAGTTGGT
AAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACA
TAAAACAGAAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGGGTA
GTGTAAGTAAGAAAGTTCAACAACCTCCTTTAAGTCCTAGATTATCTAAA
AATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTA
TTACGAAACAAGTGACAGTCTAGTCTTTCGAATTAATCTCACTGCAGATA
CTAAACTTAATTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAT
ATGATGATGAGACAGTTTGCAAGTTGCTGGACCACAAGATGATCCTGTTAG
TGAACATAAATACCCATCAGTATTTCTCTAACTCCTGCCTTATTGGAAA
CTGCTAGTGAGGCACTCTAAATGGTAAGGAAATCACAGCATCTGGTATT
ATCGGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAAT
GGTGAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTA
AAGACTTGACTAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTT
TATGCCGGTAAACAATATGAGTTCGGGGCTAAATTACCACCTAGTCGTTT
TAACACTTGGATTAGGGTTGAAGTGGTAACAGAGCAGGAGAGAAAGCAA
GTATTGTTTCGTGCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAACACA
GCAGTTGCTAAACGTTGATTGACTTCTGATAGTCTCTTATCCACATCGT
TGCCAAAGATGACTCTCTAAACTAAAAATTATATCAAGATGATTCAATTAC
TTGAATCTGTGATAAAACCGGCTTTTATAGTTTGAAGATGGGTAGAA
ATCACTAAAGATATGACAGTACCACTAGAATTTGGAGATAATATTACTAA
GTTATCTGCTGTTGACTTATCAAATTTATCGTCGTAATGAGACCCCTCATA
TCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAA
GGAGCTAAAGTAAGTGTGAGATATGTTGATGAAGCACTAGTTGTTCCAGA
AATGGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAAATG
AATCAGGAATGTTAACAACGCTAAAGTATCGATTCAATTATGTAATGGT
GGTGTGATAAAGTtGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTAT
TCGTAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAG
AAGCAGTAAAGCTGACGAAGCACATAAAGCTGAAGAAGTACGTAAGCT
GAAGAAGCACATAAAGCTGAAGAAGCAGTAAAGCTGAAGAAGGACATAA
AACCCAAGAAGCACCTATAGTTGAAGAAGCTACAAGTTAATAACGTTT
ATCAAACTGATACATACAGTTAAAGCGTCTGATTACCAAGACTAAGACA
GTTTCCGAGTTTATATGGCTAGAACAGACAATAAACAGATAACTTCACA
TCAGACACATG

SEQ ID NO. 5104

STRAIN 18RS21

TTGAATAATAAGGTGTGCGTGGCGATGGTGTCCAA
ATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTTAAGTCC
CAAAGATAAGACTACTGTAGAGAAGTTAGAGATCGCTGGAAAAAATTA
CTTTCAAAGTTGAGGATCTGGCATTGGTTTGAAGACGTTTATCTTCAA
TCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACACC
TCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAACCAAATTAGACC
GTCCACCAGGAATTGATTACCAGCACCACTCAATGAGAAGTTTGTAT
TATTCACCCCAACCGGAACTAAGCCAAAGCAAAACCAAAGATAGTTTATC
AACTCCTCCAGGTTTCCAGATTAAACACGCCGCCGCGGATGAAGCACCAA
AGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAATAT
GCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTAGCTAGCAA
AGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCATTC
CTAGAAATGCTTTGTCAGCTAATCAATTTGATGACACTAGTCTTAAATTT
TATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTATTT
TGAGATACAAAATATGTCAATATCACAGCGTTGACTATTTGAGCAATA
CTACTTTTGAAGCAATTAGCTACTGGTGAAACAGTAGATTACCATGCCATT
GTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTATGT
TAACGATAAATTGCAAGAACTTCTCGTATAGCGCTTAAAGATAAATCTG
TTAAGATTGGTATTGAATTAACCAATGATGTCAGACATATTGATAGTTTA
TCTGTTCTGTCGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAAAAA
TGATGAACAAGCATTAAATCTCAGCAAACTTACCAATTAATAACAAACC
CGACAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTCAAGTTCA
GAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATTGGTTGAACA
AAAAGATGTTTCTTTGGATATTAACGATATGGACATGAGTAAGTTTAAAA
CTATTGCACTTGACGAAAGGATTCTGAATTTAAGGGACAACCTTATTGCA
AAAACCTGGACAGTTGAATTAGATATGTTTTCAACAATCTCAAGACCC
AGCTTCAATTTATAAAAAAATATACCTTATCCAAATGGTGTTCCAAATG
AATTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATAGAT
GGATACTATATTATAAAGATGCAATTAACCTTAATTTAAATTAACAGG
TGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATAGTC
ATCAGAAAGAAGATATGACTAAAAAAGGTGAACAGCTCAGTCATTCAACT
CAAGCCAATGAAATACAGCAAAAGTAACCTTTGCTAATATTGACTGGTC
ACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGTTAAAGGTAGTG
AGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAAAACAGAA
AATTCAATAAATGTTAAAGTTTGTATTATGGAGACGGGTAGTGAAGTAA
GAAAGTTCAACAACCTCCTTTAAGTCTTAGATTATCTAAAAATTAAGCATA
TGAGGGATATGCTACTTACTATGCAAAAAGATTGACGCTATTACGAAACA
AGTGACAGTCTAGTCTTTCGAATTAATCTCACTGCAGATACTAACTTAA
TTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATGATGATGA
GACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGAACATAAA
TACCCATCAGTATTTCTTAACTCCTGCCTTATTGGAACCTGCTAGTGA
GGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTCA
TCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGTGAATGAA
AATGGAGACATGCTAGGAACCCCTGTTATTATCAAGGTAAGACTTGAC
TAATCGAACAAAACCATTAATGAGTGGACGTAGAGTACTTTATGCCGGTA

Table 51: Comparative Sequences relating to SAG0677

AACAAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAACTTGG
 ATTAGGGTTGAAGTGGTAAACAGAAGCAGGAGAGAAAGCAAGTATTGTTCC
 TCGCATGTTCTTTGACCAATCAGTTCAGAGCTTAACACAGCAGTTGCTA
 AACGTGATTTGACTTCGATAGTCTCTTATCCACATCGTTGCCAAAGAT
 GACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATACCTGAATCTGT
 TGATAAAACCGGTCCTTATAGTTTGAAGTGGTGTAGAAATCACTAAAG
 ATATGACAGTACCCTAGAAATTGGAGATAATATATTAAGTTATCTGCT
 GTTGACTTATCAAAATTATCGTCGTAATGAGACCCCTTCATATCTATAGAAA
 CCGTTTGTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTAAAG
 TAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCAGGA
 GCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGGAAT
 GTTAACAAACCGCTAAAGTATCGATTCAATTATGTAATGGTGGTGTGATA
 AAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCTGTAAGCT
 GAAGAAGCACGTAAGCTGAAGAAGCACGTAAGCTGAAGAGGGACATAA
 AACCCAAAGACCTATAGTTGAAGAAGGCTACAAGGTAAATAACGTTT
 ATCAAACCTGATACAGTTAAAGCGTCTGATTACCAAAGACTAAGACA
 GTTTCGCGAGTTTATATGGCTAGAACAGACAATAACAGATAACTTCACA
 TCAGACACATGTTGAA

SEQ ID NO. 5105

STRAIN M732

TTGAATAATAAAGGTGTCGGTGGCGATGGTGTCC

AAATTTATCAATACTATATCAAAATGGACAAACATAAACCTTACTTAAGT
 CCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAAAAT
 TACCTTCAAGTTCCAGGATACTGGCATTGGTTTGAAGACGTTTATCTTC
 AATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTATCACA
 CATTCCAGGATTTAAAAAGAAAGATAAAAAAGTTGAAAAACCAAAATTAGA
 CCGTCCaCAGGAATTGATTTACCAGCACCACTTCAATGAGAAGTTTGT
 ATTATTCAACCCACCGGGAACCTAAGCCAAAGCAACCCAAAGATAGTTTA
 TCAACTCCTCCAGGTTTCCAGATTAAACACGCGCCGAGTGAAGCCAC
 CAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAATTAAA
 TATGCTAAGTCTCTCAACTTAGCTTTGTTGATGACCCATTTTATGCTAG
 CAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTAGTCA
 TTCTTAGAAATGCTTTGTGAGCTAATCAATTTGATGACACTAGTCTTAAA
 ATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACACAGATTA
 TTTTGCAGATACAAAATATGTCAATATCACAGCGGTTGACTATTTGAGCA
 ATACTACTTTTGGAGCAATAGCTACTGGTGAACAGTAGATTACCATGCC
 ATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGATTTA
 TGTTAACGATAAAATGCAAGAACTTCTCGTATAGCGCTTAAAGATAAAT
 CTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGATAGT
 TTATCTGTTCTGCTGTTTGAATGAGGTTAAACTGTTGATAATATCTTGAA
 AAATGATGAACAAGACATTAATCTCAGCAAACTTACCAATTAAATACA
 ACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTCAAGT
 TCAGAAATCATGACCACTTTCAAAGATGGAAGATGCCAGAAATGGTTGA
 ACAAAAAGATGTTTCTTTGGATATAAACGATATGGACATGAGTAAGTTTA
 AAACCTATTGCACTTGGACGAAAGGATTCTGAATTTAAGGACAACTTATT
 GCAAAAACCTGGAAACAGTTGAATTAGATATGTTTTCAAACAACTCAAGA
 CCCAGCTTCAATTTAATAAAAAATATACCTTATCCAAATGGTGTTCCTAA
 ATGAATGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCAGATA
 GATGATACTATATTTATAAAGATGCAATTAACTTAAATTTAAATTAAC
 CAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCATATA
 GTCATCAGAAAGAAATATGACTAAAAAAGGTGAACAGCTCAGTCATTCA
 ACTCAAGCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTGACTG
 GTCACATTATAGTAAGGTTACTGTGAATGGAAGAAAGTTGGTAAAGGTA
 GTGAGTTACCTTTAACTAAAGGATGGACAACTTTGTATTACATAAAACA
 GAAAATTCAATTAATGTTAAAGTTTGAATTATGGAGACCGGTAGTGTAG
 TAAGAAAGTTCAACAACTTCTTTAAGTCTTAGATTATCTAAAAATAAGC
 ATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTACGAA
 ACAAGTGACAGTCTAGTCTTCGAATTAATCTCACTGCAGATACTAACT
 TAATTTAATGCTGTTAAAGGAGCGAGTCTCTTACTGAAAATATGATGA
 TGAGACAGTTTGCAGTTGCTGGACCAACAGATGATCCTGTTaGTGAACAT
 AAATACCCATCAGTaTTCTCTTAACTCCTGCCCTATTGGAAaCTGCTAG
 TGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATCGGTC
 ACATCAAGGATGGTGATAAAGCAAGCATGTGAAGTCAAAATGGTGAAT
 GAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAGACTT
 GACTAATCGAACAAAACCTAATGAGTGGACGTAGAGTACTTTATGCCG
 GTAAACAAATATGAGTTCCGGGCTAAATTACCACCTAGTCTGTTTAACT
 TGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTATTGT
 TCGTGCATGTTCTTTGACCAATCAGTTCAGAGCTTAACACAGCAGTTG
 CTAAACGTGATTTGACTTCTGATACTGCTCTTATCCACATCGTTGCCAAA
 GATGACTCTCTAAAACCTAAAATTATATCAAGATGATTCAATCTTGAATC
 TGTGTGATAAAACCGGTCCTTATAGTTTGAAGTGGTGTAGAAATCACTA
 AAGATATGACAGTACCCTAGAAATTGGAGATAATATTTAAGTTATCT
 GCTGTTGACTTATCAAAATTATCGTCGTAATGAGACCCCTTCATATCTATAG
 AAACCGTTTGTGATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGAGCTA
 AAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAATGGCA
 GGAGCTTATACATTAACAATCGACGAAGCTCCAAACACAAATGAATCAGG
 AATGTTAACAAACGCTAAAGTATCGATTCAATTATGTAATGGTGGTGGT
 ATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCTGTAA
 GCTGAAGAGACATAAAGCTGACGAAGCACGTAAGCTGAAGAAGCACG
 TAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAGCTGAAGAAG
 CACATAAAGTCGAAGAAGCACGTAAGCTGAAGAAGGACATAAACCACAA
 GAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTATCAAC

Table 51: Comparative Sequences relating to SAG0677

TGATACTACAGTTAAAGCGTCTGATTACCAAAGACTAAGACAGTTTCCG
CAGTTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCAGACA
CATGTTGAAAA

SEQ ID NO. 5106

STRAIN COH1

TTGAATAATAAAGGTGTCCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTAAAAAGAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG
TTTATCAACTCTCCAGGTTCCAGATTAAACACGCCGCCGGATGAAG
CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
TAAATATGCTAAGTCTTCAACTTAGCTTGTGTGATGACCTATTATTAG
CTAGCAAGATAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTA
GTCAATCTAGAAATGCTTGTGAGCTAATCAATTTGATGACACTAGTCT
TAAATTTATCGTAATAATAATCGCAATAAAGAAATTACTATCACAACAG
ATTATTTTGCAGATACAAATATGTCAATATCACAGCGTTGACTATTG
AGCAATACTACTTTTGGAGCAATAGCTACTGGTGAACAGTAGATTACCA
TGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA
TTTATGTTAAGCATAAATGCAAGAACTTCTCGTATAGCGCTTAAAGAT
AAATCTGTTAAGATTGTTATGAATTACCAATGATGTCAGACATATTGA
TAGTTTATCTGTTTCGTCGTTTGAATGAGGTTAAACTGTTGATAATATCT
TGAAAAATGATGAACAAGACATTAACTCTAGCAAACTTACCAATTAATA
TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAATAACATTAACTC
AAGTTTCAAGAAATCATGACCACTTCAAGATGGAAGATGCCAGAAATGG
TTGAACAAAAAGATGTTCTTTGGATATAACGATATGGACATGAGTAAG
TTTAAACTATTTCGACTTGGACGAAAGGATTCTGAATTTAAGGGACAAC
TATTTGCAAAACTGGAACAGTTGAATTAGATATGTTTTCAAACAACTCTC
AAGACCCAGCTTCAATTATTAATAAATAATATACCTTATCCAAATGGTGT
CCAAATGAATGAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA
GATAGATGGATACTATATTATAAAGATGCAATTAACCTTAAATTTAAAT
TAACCAAGTGGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
TATAGTCATCAGAAAGAGATATGACTAAAAAGGTGAACAGCTCAGTCA
TTCAACTCAAGCCAATGAAAAATACAGCAAAAGTAACCTTTGCTAATATTG
ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGGTAAA
GGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTTGTATTACATAA
AACAGAAAAATTCATTAAATGTTAAAGTTTGAATATGGAGACGGGTAGTG
TAAGTAAGAAAGTTCAACAACCTCCTTTAAGTCTTAGATTATCTAAAAAT
AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATTA
CGAAACAAAGTGACAGTCTAGTCCTTCGAATTAATCTCACTGCAGATACTA
AACTTAATTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAAATATG
ATGATGAGACAGTTTGCAGTTGCTGGACCACAAGATGATCCTGTTAGTGA
ACATAAAATACCCATCAGTATTTCTCTTAACCTCTGCCCTTATTGGAAACTG
CTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGTATTATC
GGTCACATCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGT
GAATGAAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
ACTTGACTAATCGAACAAAACCAATTAATGAGTGGACGTAGAGTACTTTAT
GCCGGTAAACAATATGAGTTCCGGGCTAAATTAACCACTTAGTCGTTTAA
CACTTGGATTAGGGTTGAAGTGGTAACAGAAGCAGGAGAGAAAGCAAGTA
TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCCAGAGCTTAAACAGCA
GTTGCTAAACGTGATTGACTTCTGATATGCTCTTATCCACATCGTTGTC
CAAGATGACTCTCTAAACCTAAATTTATATCAAGATGATTCAATTACTTG
AATCTGTTGATAAAACCGGCTCTTTATAGTTTGAAGATGGTGTAGAAATC
ACTAAAGATATGACAGTACCAGTGAATTTGGAGATAAATATTATTAAAGTT
ATCTGCTGTTGACTTATCAAATTTATCGTCTGAATGAGACCTTCATATCT
ATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGACAAAGGA
GCTAAAGTAACGTGGATATGTTGATGAAGCACTAGTTGTTCCAGAAAT
GGCAGGAGCTTATACATTAAACATCGACGAAGCTCCAAACACAAATGAAT
CAGGAATGTTAAACAAACGCTAAAGTATCGATTCTTATGTAATGGTGGT
GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCTG
TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG
CAGCTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
GAAGCACATAAAGCTGAAGAAGCAGCTAAAGCTGAAGAAGGACATAAAAC
CCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTCATC
AACTGATACACTACAGTTAAAGCGTCTGATTACCAAGACTAAGACAGTT
TCCGCGATTTCATATGGCTAGAACAGACAATAAACAGATAACTTCACATCA
GACACATGT

SEQ ID NO. 5107

STRAIN M781

TTGAATAATAAAGGTGTCCGGTGGCGATGGT
GTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAACCTTACTT
AAGTCCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGCTGGAAAA
AAATTACTTTCAAAGTTCAGGATACTGGCATTGGTTTGAAAGACGTTTAT
CTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTTAGACCTTAT
CACACCTCCAGGATTAAAAAGAGATAAAAAAGTTGAAAAACCAAAAT
TAGACCGTCCACCAGGAATTGATTTACCAGCACCAACTTCAATGAGAAGT
TTTGATTATTCAACCCACCGGGAAGTAAGCCAAGCAACCCAAAGATAG
TTTATCAACTCTCCAGGTTTCCAGATTAAACACGCCGCCGGATGAAG

Table 51: Comparative Sequences relating to SAG0677

CCaCCAAAGGATAGTAAAAAGACGCTATTGAAGATAAATCAGGAGCAAT
 TAAATATGCTAAGTCTCTTCAACTAGCTTTGTTGATGACCCATTTTAG
 CTAGCAAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGCAAAATTA
 GTCAATTCCTAGAAATGCTTTGTGACGTAATCAATTTGATGACACTAGTCT
 TAAaATTATCGTAATAATAATCGCAATAAAGAAATTaCTATCACAACAG
 ATTATTTTGAGATACAAAATATGTCAATATCACAGCGGTTGACTATTG
 AGCAATTAAGTCTTTGAGCAATTAGCTACTGGTGAAACAGTAGATTACCA
 TGCCATTTGATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGGTAAGA
 TTTATGTTAAGGATAAATTCGAAGAACTTCTCGTATAGCGCTTAAAGAT
 AAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACATATTGA
 TAGTTTATCTGTTCTGTTGAAATGAGGTTAAACTGTTGATAATATCT
 TGAAAAATGATGAACAAGACATTAACTCTAGCAAAAACCTTACCAATTAAAA
 TACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACATTAACTC
 AAGTTCAGAAATCATGACCACCTTCAAGATGGAAGATGCCAGAAATGG
 TTGAACAAAAAGATGTTTCTTTGGATATAACGATATGACATGAGTAAG
 TTTAAAACTATTGCACTTGGACGAAAGGATTCTGAATTAAGGGGCAAACT
 TATTGCAAAAACCTGGAACAGTTGAATTAGATATGTTTTCAAACCAATCTC
 AAGACCCAGCTTCAATTATTAAAAAATATACCTTATCCAAATGGTGT
 CCAAATGAATTAAGAAATTTGACTCTAGTTTGGTTTAACTGAAAGTCA
 GATAGATGGATACATATAATTATAAAGATGCAATTAACTTAAATTTAAAT
 TAACCAAGTGGTGCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAAGATCCA
 TATAGTCATCAGAAAGAAGATATGACTAAAAAGGTGAACAGCTCAGTCA
 TTAACCTCAAGCCCAATGAAAATACAGCAAAAGTAACCTTTGCTAATATTG
 ACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAGAAGTTGGTAAA
 GGATGAGTTTACCTTAACTAAAGGATGGACAACATTGTTATTACATAA
 AACAGAAAATTCATTAAATGTTAAAGTTTGAATTATGAGAGCGGGTAGTG
 TAAGTAAGAAAGTTCAACCACTTCTTAAAGTCTAGATTATCTAAAAAT
 AAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAGCGTATT
 CGAAACAGTGACAGTCTAGTCTTGAATTAATCTCACTGACAGATACTA
 AACCTTAATTTTAATGCTGTTAAAGGAGCGAGTGTCTTACTGAAAATATG
 ATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGTTAGTGA
 ACATAAATACCCATCAGTATTCTCTTAACTCTGCTTATTGGAACCTG
 CTAGTGAGGCAACTCTAATGTTAAGGAAATCACAGCATCTGGTATTATC
 GGTCACTCAAGGATGGTGATAAAGCAAGCATGTTGAAGTCAAAATGGT
 GAATGAAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAGGTAAAG
 ACTTGACTAATCGAACAAAACCAATTATAGTGGACGTAGAGTACTTTAT
 GCCGGTAAACAATATGAGTTCCGGGCTAAATTACCACTTAGTCGTTTAA
 CACTTGGATTAGGGTTGAAGTGGTAAACAGAGCAGGAGAGAAAGCAAGTA
 TTGTTCTGTCGATGTTCTTTGACCAATCAGTTCAGAGCTTAAACAGCA
 GTTGCTAAACGTTGATTGACTCTGATAGTCTTATCCACATCGTTGC
 CAAAGATGACTCTTAAACTAAAATTTATATCAAGATGATTCACTACTTG
 AATCTGTTGATAAAACCGGCTTTTATAGTTTGAAGTGGTGTAGAAATC
 ACTAAAGATATGACAGTACCCTAGAAATTTGGAGATAATATTATTAGTT
 ATCTGCTGTTGACTTATCAAAATATCGTCTGAATGAGACCCCTCATATCT
 ATAGAAAACCGTTTGTATGTTAAAGCAAGCAAAATGACAGCTGACAAAGGA
 GCTTAAAGTAACTGTGGATATGTTGATGAAGCACTTAGTTGTTCCAGAAAT
 GGCAGGAGCTTATACATTAAACCAATCGACGAAGCTTCAACACAAATGAAT
 CAGGAATGTTTAAACAAAGCTAAGTATCGATTCAATTATGTAATGGTGGT
 GTTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGCTATTCG
 TAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTGAAGAAG
 CACGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAAAGCTGAA
 GAAGCACATAAAGCTGAAGAAGCACCGTAAAGCTGAAGAAGGACATAAAA
 CCCAAGAAGCACCTATAGTTGAAGAAGGCTACAAAGTTAATAACGTTTAT
 CAACTGATACATACAGTTAAAGCGTCTGATTACCAAGACTAAGACAGT
 TTCCGAGTTTATATGGCTAGAACAGACAATAAACAGATAAATTCACATC
 AGACACATGTTG

SEQ ID NO. 5109

STRAIN JM9130013

TGGTGTCCAAATTTATCAATACTATATCAAAATGGACAACAATAAAC
 CTTACTTAAAGTCCAAAGATAAGACTACTGTAGAGAAGTTAGAAGATCGC
 TGGAAAAAATTTACTTTCAAAGTTTCAAGGATGCTGGCATTGGTTTGAAGA
 CGTTTATCTTCAATCTGTTAAGTATGTTGGTGGTGGCAATAATAATTAG
 ACCCTTATCACACCTCCAGGATTTAAAAAAGAAGATAAAAAAGTTGAAAAA
 CCAAAATTAGACCGTCCACCAGGAATTGATTACCAGCACCAACTTCAAT
 GAGAAGTTTGTATTATCAACCCACCGGGAACCTAAGCCAAGCAACCCA
 AAGATAGTTTATCAACTCTTCCAGGTTTCCAGATTAAACACGCGCGCG
 GATGAAGCACCAAGGATAGTAAAAAAGACGCTATTGAAGATAAATCAGG
 AGCAATTAATATGCTAAGTCTCTTCAACTTAGCTTTGTTGATGACCCCTA
 TTTTAGCTAGCAAGTAAATGGCAAAATATTACAAGTCGAATCTGATGGC
 AAATTAGTCATTCTTAGAAATGCTTTGTGAGCTAATCAATTTGATGACAC
 TAGTCTTAAATTTATCGTAATAATAATCGCAATAAAGAAATTAATATCA
 CAACAGATTATTGTCAGATACAAAATATGTAATATCACAGCGGTTGAC
 TATTGAGCAaTACTACTTTTGAAGCAATTAGCTACTGGTGAAACAGTAGA
 TTACCATGCCATTGTATTTTCAAGCTTTGCTGCTATTAAAGACAAGGGTG
 GTAAGATTATGTTAAGGATAAATTGCAAGAACTTCTCGTATAGCGCTT
 AAAGATAAATCTGTTAAGATTGGTATTGAATTACCAATGATGTCAGACA
 TATTGATAGTTTATCTGTTCTGTTGAATGAGGTTAAACTGTTGATA
 ATATCTGAAAAATGATGAACAAGACATTAACTCTAGCAAAAACCTTACCA
 TTAAATACAACCCGACAAATCGTCTGCTAGAGTTTACTATTAAATACAT
 TAATCTAAGTTTCAAGAAATCATGACCACCTTCAAAGATGGAAGATGCCAG
 AATTGGTTGAACAAAAAGATGTTTCTTTGGATATAAAGATATGGACATG
 AGTAAGTTTAAACTATTGCACTTGGACGAAGGATTCTGAATTTAAGGG

Table 51: Comparative Sequences relating to SAG0677

ACAACCTTATTGCAAAACTGGAACAGTTGAATTAGATATGTTTTTCAAAC
 AATCTCAAGACCCAGCTTCAATTATTAATAAATATACCTTATCCAAAAT
 GGTGTTCCAAATGAATTGAAAAAATTTGACTCTAGTTTGGTTAACTGA
 AAGTCAGATAGATGGATACATATTTATAAAGATGCAATTAACTTAAAT
 TTAAATTAAACAGTGGTGCAGTCTTAAAGTTGTTTATAAGGGCAAGAA
 GATCCATATAGTCATCAGAAAGAGATATGACTAAAAAGGTGAACAGCT
 CAGTCATTCAACTCAAGCCATGAAAAATACAGCAAAAGTAACCTTTGCTA
 ATATTGACTGGTCACATTATAGTAAGGTTACTGTGAATGGAAAAGAGTT
 GGTAAAGGTAGTGAGTTACCTTTAACTAAAGGATGGACAACATTGTATT
 ACATAAAACAGAAAATTCATTAAATGTTAAAGTTTGATTATGGAGACGG
 GTAGTGAAGTAAGAAAGTTCAACAACTTCCCTTAAAGTCCAGATTATCT
 AAAAAATAAGCATATGAGGGATATGCTACTTACTATGCAAAAAGATTGAG
 GTATTACGAACAAGTGACAGTCTAGTCCTTCGAATTAACTCTCACTGCAG
 ATACTAACTTAATTTTAAATGCTGTTAAAGGAGCGAGTGCTCTTACTGAA
 AATATGATGATGAGACAGTTTGCAGTTGCTGGACCAAGATGATCCTGT
 TAGTGAACATAAAATCCCATCAGTATTTCTCTTAACTCCTGCCCTATTGG
 AAACCTGCTAGTGAGGCAACTCTAAATGGTAAGGAAATCACAGCATCTGGT
 ATTATCGGTCACATCAAGGATGGTGATAAAAGCAAGCATGTTGAAGTCAA
 AATGGTGAATGAAATGGAGACATGCTAGGAACCCCTGTTATTATTCAAG
 GTAAAGACTTGACTAATCGAACAACCAATTAATGAGTGGACGTAGAGTA
 CTTTATGCCGGTAAACAATATGAGTTCCGGGCTAAATTAACCACTTAGTCG
 TTTTAACTTTGATTAGGGTTGAAGTGGTAACGAAGCAGGAGaGaaag
 cAagTATTGTTTCGTCGATGTTCTTTGACCAATCAGTCCAGAGCTTAAC
 ACAGCAGTTGCTAAACGTGATTGACTTCTGATAGTCTCTTATCCACAT
 CGTTGCCAAGATGACTCTTAAACTAAAATATATCAAGATGATTCTAT
 TACTTGAATCTGTGATAAAACCGGCTTTTATAGTTTGAAGATGGTGA
 GAAATCACTAAAGATATGACAGTACCACTAGAAATTTGGAGATAATATTAT
 TAAAGTTATCTGCTGTTGACTTATCAAATTTATCGTAAATGAGACCCCTC
 ATATCTATAGAAACCGTTTGTATGTTAAAGCAAGCCAAATGACAGCTGAC
 AAAGGAGCTAAAGTAAGTAACTGTGATATGTTGATGAAGCACTTAGTTGTTCC
 AGAAATGGCAGGAGCTTATACATTAACTCGACGAAGCTCCAAACACAA
 ATGAATCAGGAATGTTAAACAACGCTAAAGTATCGATTCAATTATGTAAT
 GGTGGTGTGATAAAGTTGATGTTCCGATTAAAGTAGTTGACTTAGAAGC
 TATTTCGTAAAGCTGAAGAAGCACATAAAGCTGACGAAGCAGTAAAGCTG
 AAGAAGCAGTAAAGCTGAAGAAGCACATAAAGCTGAAGAAGTACGTAA
 GCTGAAGAAGCACATAAAGTGAAGAAGCACCGTAAAGCTGAAGAGGGAC
 ATAAACCCGAAGACCTATAGTTGAAGAAGCTACAAGTTAATAAC
 GTTCATCAAACTGATACACTACAGTTAAAGCGTCTGATTACCAAGACTAA
 GACAGTTTCGCGAGTTCATATGGCTAGAACAGACAATAAACAGATAACTT
 CACATCAGACACATGTTG

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa235280.2{*} December 10, 2002 05:12 ..

	1		50
msa235280.2{195_COH1}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_M732}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_M781}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_H36B}	-----TGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_JM9130013}	-----TGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_18RS21}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_2603}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
msa235280.2{195_A909}	ttgaataata aaggtgtcgg tggcgaTGGT GTCCAAATTT ATCAATACTA		
Consensus	-----*****		
	51		100
msa235280.2{195_COH1}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_M732}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_M781}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_H36B}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_JM9130013}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_18RS21}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_2603}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
msa235280.2{195_A909}	TATCAAAATG GACAACAATA AACCTTACTT AAGTCCCAA GATAAGACTA		
Consensus	*****		
	101		150
msa235280.2{195_COH1}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_M732}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_M781}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_H36B}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_JM9130013}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_18RS21}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_2603}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
msa235280.2{195_A909}	CTGTAGAGAA GTTAGAAGAT CGCTGGAAAA AAATTACTTT CAAAGTTCAG		
Consensus	*****		
	151		200
msa235280.2{195_COH1}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_M732}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_M781}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		
msa235280.2{195_H36B}	GATACTGGCA TTGGTTTGAA AGACGTTTAT CTTCAATCTG TTAAGTATGT		

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_JM9130013}	GATACTGGCA	TGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_18RS21}	GATACTGGCA	TGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_2603}	GATACTGGCA	TGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
msa235280.2{195_A909}	GATACTGGCA	TGGTTTGAA	AGACGTTTAT	CTTCAATCTG	TTAAGTATGT
Consensus	*****	*****	*****	*****	*****
201					
msa235280.2{195_COH1}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M732}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_M781}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_H36B}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_JM9130013}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_18RS21}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_2603}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
msa235280.2{195_A909}	TGGTGGTGGC	AATAATAATT	TAGACCTTAT	CACACCTCCA	GGATTTAAAA
Consensus	*****	*****	*****	*****	*****
250					
251					
msa235280.2{195_COH1}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M732}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_M781}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_H36B}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_JM9130013}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_18RS21}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_2603}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
msa235280.2{195_A909}	AAGAAGATAA	AAAAGTTGAA	AAACCAAAT	TAGACCGTCC	ACCAGGAATT
Consensus	*****	*****	*****	*****	*****
300					
301					
msa235280.2{195_COH1}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_M732}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_M781}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_H36B}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_JM9130013}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_18RS21}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_2603}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
msa235280.2{195_A909}	GATTTACCAG	CACCAACTTC	AATGAGAAGT	TTTGATTATT	CAACCCACCC
Consensus	*****	*****	*****	*****	*****
350					
351					
msa235280.2{195_COH1}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M732}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_M781}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_H36B}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_JM9130013}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_18RS21}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_2603}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
msa235280.2{195_A909}	GGGAACTAAG	CCAAGCAAAC	CCAAAGATAG	TTTATCAACT	CCTCCAGGTT
Consensus	*****	*****	*****	*****	*****
400					
401					
msa235280.2{195_COH1}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M732}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_M781}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	cCACcAAAGG	ATAGTAAAAA
msa235280.2{195_H36B}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
msa235280.2{195_JM9130013}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_18RS21}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_2603}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACcAAAGG	ATAGTAAAAA
msa235280.2{195_A909}	TCCCAGATT	AAACACGCCG	CCGGATGAAG	.CACTAAAGG	ATAGTAAAAA
Consensus	*****	*****	*****	*****	*****
450					
451					
msa235280.2{195_COH1}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M732}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_M781}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_H36B}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_JM9130013}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_18RS21}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_2603}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
msa235280.2{195_A909}	AGACGCTATT	GAAGATAAAT	CAGGAGCAAT	TAAATATGCT	AAGTCTCTTC
Consensus	*****	*****	*****	*****	*****
500					
501					
msa235280.2{195_COH1}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M732}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_M781}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_H36B}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_JM9130013}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_18RS21}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_2603}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
msa235280.2{195_A909}	AACCTAGCCT	TGTTGATGAC	CCTATTTTAG	CTAGCAAAGT	AAATGGCAAA
Consensus	*****	*****	*****	*****	*****
550					

Table 51: Comparative Sequences relating to SAG0677

		551			600
msa235280.2{195_COH1}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M732}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_M781}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_H36B}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_JM9130013}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_18RS21}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_2603}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
msa235280.2{195_A909}	ATATTACAAG	TCGAATCTGA	TGGCAAATTA	GTCATTCCTA	GAAATGCTTT
Consensus	*****	*****	*****	*****	*****
		601			650
msa235280.2{195_COH1}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M732}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_M781}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_H36B}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_JM9130013}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_18RS21}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_2603}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
msa235280.2{195_A909}	GTCAGCTAAT	CAATTGTATG	ACACTAGTCT	TAAAATTTAT	CGTAATAATA
Consensus	*****	*****	*****	*****	*****
		651			700
msa235280.2{195_COH1}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M732}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_M781}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_H36B}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_JM9130013}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_18RS21}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_2603}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
msa235280.2{195_A909}	ATCGCAATAA	AGAAATTACT	ATCACAACAG	ATTATTTTGC	AGATACAAAA
Consensus	*****	*****	*****	*****	*****
		701			750
msa235280.2{195_COH1}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M732}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_M781}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_H36B}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_JM9130013}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_18RS21}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_2603}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
msa235280.2{195_A909}	TATGTCAATA	TCACAGCGGT	TGACTATTTG	AGCAATACTA	CTTTTGAGCA
Consensus	*****	*****	*****	*****	*****
		751			800
msa235280.2{195_COH1}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M732}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_M781}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_H36B}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_JM9130013}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_18RS21}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_2603}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
msa235280.2{195_A909}	ATTAGCTACT	GGTGAAACAG	TAGATTACCA	TGCCATTGTA	TTTTCAGGCT
Consensus	*****	*****	*****	*****	*****
		801			850
msa235280.2{195_COH1}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M732}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_M781}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_H36B}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_JM9130013}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_18RS21}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_2603}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
msa235280.2{195_A909}	TTGCTGCTAT	TAAAGACAAG	GGTGGTAAGA	TTTATGTTAA	CGATAAATTG
Consensus	*****	*****	*****	*****	*****
		851			900
msa235280.2{195_COH1}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M732}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_M781}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_H36B}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_JM9130013}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_18RS21}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_2603}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
msa235280.2{195_A909}	CAAGAAACTT	CTCGTATAGC	GCTTAAAGAT	AAATCTGTTA	AGATTGGTAT
Consensus	*****	*****	*****	*****	*****
		901			950
msa235280.2{195_COH1}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M732}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_M781}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_H36B}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_JM9130013}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_18RS21}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_2603}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
msa235280.2{195_A909}	TGAATTACCA	AATGATGTCA	GACATATTGA	TAGTTTATCT	GTTTCGTCGTT
Consensus	*****	*****	*****	*****	*****
951					1000
msa235280.2{195_COH1}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M732}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_M781}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_H36B}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_JM9130013}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_18RS21}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_2603}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
msa235280.2{195_A909}	TGAATGAGGT	TAAAACTGTT	GATAATATCT	TGAAAAATGA	TGAACAAGAC
Consensus	*****	*****	*****	*****	*****
1001					1050
msa235280.2{195_COH1}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M732}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_M781}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_H36B}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_JM9130013}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_18RS21}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_2603}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
msa235280.2{195_A909}	ATTAATCTCA	GCAAACTTA	CCAATTAAAA	TACAACCCGA	CAAATCGTCG
Consensus	*****	*****	*****	*****	*****
1051					1100
msa235280.2{195_COH1}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M732}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_M781}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_H36B}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_JM9130013}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_18RS21}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_2603}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
msa235280.2{195_A909}	TCTAGAGTTT	ACTATTAATA	ACATTAACTC	AAGTTCAGAA	ATCATGACCA
Consensus	*****	*****	*****	*****	*****
1101					1150
msa235280.2{195_COH1}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M732}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_M781}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_H36B}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_JM9130013}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_18RS21}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_2603}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
msa235280.2{195_A909}	CTTTCAAAGA	TGGAAAGATG	CCAGAATTGG	TTGAACAAAA	AGATGTTTCT
Consensus	*****	*****	*****	*****	*****
1151					1200
msa235280.2{195_COH1}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_M732}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_M781}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_H36B}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_JM9130013}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_18RS21}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_2603}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
msa235280.2{195_A909}	TTGGATATAA	ACGATATGGA	CATGAGTAAG	TTTAAACTA	TTGCACTTGG
Consensus	*****	*****	*****	*****	*****
1201					1250
msa235280.2{195_COH1}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M732}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_M781}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_H36B}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_JM9130013}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_18RS21}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_2603}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
msa235280.2{195_A909}	ACGAAAGGAT	TCTGAATTTA	AGGGACAAC	TATTGCAAAA	ACTGGAACAG
Consensus	*****	*****	*****	*****	*****
1251					1300
msa235280.2{195_COH1}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M732}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_M781}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_H36B}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_JM9130013}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_18RS21}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_2603}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
msa235280.2{195_A909}	TTGAATTAGA	TATGTTTTTC	AAACAATCTC	AAGACCCAGC	TTCAATTATT
Consensus	*****	*****	*****	*****	*****
1301					1350

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_COH1}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M732}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_M781}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_H36B}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_JM9130013}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_18RS21}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_2603}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
msa235280.2{195_A909}	AAAAAAATAT	ACCTTATCCA	AAATGGTGTT	CCAAATGAAT	TGAAAAAATT	
Consensus	*****	*****	*****	*****	*****	
1351						1400
msa235280.2{195_COH1}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M732}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_M781}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_H36B}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_JM9130013}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_18RS21}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_2603}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
msa235280.2{195_A909}	TGACTCTAGT	TTTGGTTTAA	CTGAAAGTCA	GATAGATGGA	TACTATATTT	
Consensus	*****	*****	*****	*****	*****	
1401						1450
msa235280.2{195_COH1}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M732}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_M781}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_H36B}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_JM9130013}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_18RS21}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_2603}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
msa235280.2{195_A909}	ATAAAGATGC	AATTAACCTT	AAATTTAAAT	TAACCAAGTGG	TGCAAGTCTT	
Consensus	*****	*****	*****	*****	*****	
1451						1500
msa235280.2{195_COH1}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M732}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_M781}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_H36B}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_JM9130013}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_18RS21}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_2603}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
msa235280.2{195_A909}	AAAGTTGTTT	ATAAAGGGCA	AGAAGATCCA	TATAGTCATC	AGAAAGAAGA	
Consensus	*****	*****	*****	*****	*****	
1501						1550
msa235280.2{195_COH1}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M732}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_M781}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_H36B}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_JM9130013}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_18RS21}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_2603}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
msa235280.2{195_A909}	TATGACTAAA	AaAGGTGAAC	AGCTCAGTCA	TTCAACTCAA	GCCAAATGAAA	
Consensus	*****	*-*****	*****	*****	*****	
1551						1600
msa235280.2{195_COH1}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M732}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_M781}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_H36B}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_JM9130013}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_18RS21}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_2603}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
msa235280.2{195_A909}	ATACAGCAAA	AGTAACCTTT	GCTAATATTG	ACTGGTCACA	TTATAGTAAG	
Consensus	*****	*****	*****	*****	*****	
1601						1650
msa235280.2{195_COH1}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M732}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_M781}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_H36B}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_JM9130013}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_18RS21}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_2603}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
msa235280.2{195_A909}	GTTACTGTGA	ATGGAAAAGA	AGTTGgTAAA	GGTAGTGAGT	TACCTTTAAC	
Consensus	*****	*****	*****-****	*****	*****	
1651						1700
msa235280.2{195_COH1}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M732}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_M781}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_H36B}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_JM9130013}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	
msa235280.2{195_18RS21}	TAAAGGATGG	ACAACATTTG	TATTACATAA	AACAGAAAAT	TCATTAAATG	

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_2603}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
msa235280.2{195_A909}	TAAAGGATGG	ACAACATTGG	TATTACATAA	AACAGAAAAT	TCATTAAATG
Consensus	*****	*****	*****	*****	*****
1701					
msa235280.2{195_COH1}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M732}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_M781}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_H36B}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_JM9130013}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_18RS21}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_2603}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
msa235280.2{195_A909}	TTAAAAGTTT	GATTATGGAG	ACGGGTAGTG	TAAGTAAGAA	AGTTCACAA
Consensus	*****	*****	*****	*****	*****
1750					
1751					
msa235280.2{195_COH1}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M732}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_M781}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_H36B}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_JM9130013}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_18RS21}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_2603}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
msa235280.2{195_A909}	CTTCCTTTAA	GTCCTAGATT	ATCTAAAAAT	AAGCATATGA	GGGATATGCT
Consensus	*****	*****	*****	*****	*****
1800					
1801					
msa235280.2{195_COH1}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M732}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_M781}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_H36B}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_JM9130013}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_18RS21}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_2603}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
msa235280.2{195_A909}	ACTTACTATG	CAAAAAGATT	CAGCGTATTA	CGAAACAAGT	GACAGTCTAG
Consensus	*****	*****	*****	*****	*****
1850					
1851					
msa235280.2{195_COH1}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M732}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_M781}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_H36B}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_JM9130013}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_18RS21}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_2603}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
msa235280.2{195_A909}	TCCTTCGAAT	TAATCTCACT	GCAGATACTA	AACTTAATTT	TAATGCTGTT
Consensus	*****	*****	*****	*****	*****
1900					
1901					
msa235280.2{195_COH1}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M732}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_M781}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_H36B}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_JM9130013}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_18RS21}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_2603}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
msa235280.2{195_A909}	AAAGGAGCGA	GTGCTCTTAC	TGAAAATATG	ATGATGAGAC	AGTTTGCACT
Consensus	*****	*****	*****	*****	*****
1950					
1951					
msa235280.2{195_COH1}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M732}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_M781}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_H36B}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_JM9130013}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_18RS21}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_2603}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
msa235280.2{195_A909}	TGCTGGACCA	CAAGATGATC	CTGTTAGTGA	ACATAAATAC	CCATCAGTAT
Consensus	*****	*****	*****	*****	*****
2000					
2001					
msa235280.2{195_COH1}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M732}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_M781}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_H36B}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_JM9130013}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_18RS21}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_2603}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
msa235280.2{195_A909}	TTCTCTTAAC	TCCTGCCTTA	TTGGAAACTG	CTAGTGAGGC	AACTCTAAAT
Consensus	*****	*****	*****	*****	*****
2050					
2051					
msa235280.2{195_COH1}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
2100					

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M732}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_M781}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_H36B}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_JM9130013}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_18RS21}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_2603}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
msa235280.2{195_A909}	GGTAAGGAAA	TCACAGCATC	TGGTATTATC	GGTCACATCA	AGGATGGTGA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M732}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_M781}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_H36B}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_JM9130013}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_18RS21}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_2603}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
msa235280.2{195_A909}	TAAAAGCAAG	CATGTTGAAG	TCAAAATGGT	GAATGAAAAT	GGAGACATGC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M732}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_M781}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_H36B}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_JM9130013}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_18RS21}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_2603}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
msa235280.2{195_A909}	TAGGAACCCC	TGTTATTATT	CAAGGTAAAG	ACTTGACTAA	TGGAACAAAA
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M732}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_M781}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_H36B}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_JM9130013}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_18RS21}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_2603}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
msa235280.2{195_A909}	CCATTAAATGA	GTGGACGTAG	AGTACTTTAT	GCCGGTAAAC	AATATGAGTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M732}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_M781}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_H36B}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_JM9130013}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_18RS21}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_2603}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
msa235280.2{195_A909}	CCGGGCTAAA	TTACCACTTA	GTCGTTTTAA	CACCTGGATT	AGGGTTGAAG
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M732}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_M781}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_H36B}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_JM9130013}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_18RS21}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_2603}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
msa235280.2{195_A909}	TGGTAACAGA	AGCAGGAGAG	AAAGCAAGTA	TTGTTTCGTCG	CATGTTCTTT
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M732}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_M781}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_H36B}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_JM9130013}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_18RS21}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_2603}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
msa235280.2{195_A909}	GACCAATCAG	TTCCAGAGCT	TAACACAGCA	GTTGCTAAAC	GTGATTTGAC
Consensus	*****	*****	*****	*****	*****
msa235280.2{195_COH1}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M732}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_M781}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_H36B}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_JM9130013}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_18RS21}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
msa235280.2{195_2603}	TTCTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAAC
Consensus	*****	*****	*****	*****	*****

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_A909}	TTCTGTGATACT	GCTCTTATCC	ACATCGTTGC	CAAAGATGAC	TCTCTAAAC		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2451	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT	2500
msa235280.2{195_M732}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_M781}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_H36B}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_JM9130013}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_18RS21}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_2603}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
msa235280.2{195_A909}	TAAAATTATA	TCAAGATGAT	TCATTACTTG	AATCTGTTGA	TAAAACCGGT		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2501	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC	2550
msa235280.2{195_M732}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_M781}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_H36B}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_JM9130013}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_18RS21}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_2603}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
msa235280.2{195_A909}	CTTTATAGTT	TTAGAAATGG	TGTAGAAATC	ACTAAAGATA	TGACAGTACC		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2551	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA	2600
msa235280.2{195_M732}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_M781}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_H36B}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_JM9130013}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_18RS21}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_2603}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
msa235280.2{195_A909}	ACTAGAAATTT	GGAGATAATA	TTATTAAGTT	ATCTGCTGTT	GACTTATCAA		
Consensus	*****	*****	***_*****	*****	*****		
msa235280.2{195_COH1}	2601	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT	2650
msa235280.2{195_M732}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_M781}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_H36B}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_JM9130013}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_18RS21}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_2603}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
msa235280.2{195_A909}	ATTATCGTCG	TAATGAGACC	CTTCATATCT	ATAGAAACCG	TTTTGATGTT		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2651	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT	2700
msa235280.2{195_M732}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_M781}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_H36B}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_JM9130013}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_18RS21}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_2603}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
msa235280.2{195_A909}	AAAGCAAGCC	AAATGACAGC	TGACAAAGGA	GCTAAAGTAA	CTGTGGATAT		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2701	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA	2750
msa235280.2{195_M732}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_M781}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_H36B}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_JM9130013}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_18RS21}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_2603}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
msa235280.2{195_A909}	GTTGATGAAG	CACCTTAGTTG	TTCCAGAAAT	GGCAGGAGCT	TATACATTAA		
Consensus	*****	*****	*****	*****	*****		
msa235280.2{195_COH1}	2751	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT	2800
msa235280.2{195_M732}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_M781}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_H36B}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_JM9130013}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_18RS21}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_2603}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
msa235280.2{195_A909}	CAATCGACGA	AGcTCCAAAC	ACAAATGAAT	CAGGAATGTT	AACAAACGCT		
Consensus	*****	**_*****	*****	*****	*****		
msa235280.2{195_COH1}	2801	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC	2850
msa235280.2{195_M732}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC		

Table 51: Comparative Sequences relating to SAG0677

msa235280.2{195_M781}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_H36B}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_JM9130013}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_18RS21}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_2603}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
msa235280.2{195_A909}	AAAGTATCGA	TTCATTATGT	AAATGGTGGT	GTTGATAAAG	TTGATGTTCC
Consensus	*****	*****	*****	*****	*****
2851					
msa235280.2{195_COH1}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M732}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_M781}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_H36B}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_JM9130013}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
msa235280.2{195_18RS21}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_2603}	GATTAAAGTA	GTTGACTTAG	AAGCTATT..
msa235280.2{195_A909}	GATTAAAGTA	GTTGACTTAG	AAGCTATTcg	taaagctgaa	gaagcacata
Consensus	*****	*****	*****	*****	*****
2901					
msa235280.2{195_COH1}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M732}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_M781}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_H36B}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_JM9130013}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_18RS21}CGTAAAGC	TGAaGAAGCA
msa235280.2{195_2603}cgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
msa235280.2{195_A909}	aagctgacga	agcacgtaaa	gctgaagaag	caCGTAAAGC	TGAaGAAGCA
Consensus	-----	-----	-----	-----	-----
2951					
msa235280.2{195_COH1}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M732}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_M781}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_H36B}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_JM9130013}	CaTAAAGCTG	AAGAAGtAcg	taaagctgaa	gaagcacata	aagtcgaaga
msa235280.2{195_18RS21}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_2603}	CgTAAAGCTG	AAGAAGcA..
msa235280.2{195_A909}	CgTAAAGCTG	AAGAAGcA..
Consensus	*-*****	*****-*	-----	-----	-----
3001					
msa235280.2{195_COH1}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M732}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_M781}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_H36B}	agca.CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_JM9130013}	agcacCGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_18RS21}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_2603}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
msa235280.2{195_A909}CGTAA	AGCTGAAGAG	GGACATAAAA	CCCAAGAAGC	ACCTATAGTT
Consensus	-----	*****	*****	*****	*****
3051					
msa235280.2{195_COH1}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M732}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_M781}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_H36B}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_JM9130013}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_18RS21}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_2603}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
msa235280.2{195_A909}	GAAGAAGGCT	ACAAaGTTAA	TAACGTTTCAT	CAAAC TGATA	CTACAGTTAA
Consensus	*****	*****	*****	*****	*****
3101					
msa235280.2{195_COH1}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M732}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_M781}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_H36B}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_JM9130013}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_18RS21}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_2603}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
msa235280.2{195_A909}	AGCGTCTGAT	TTACCAAAGA	CTAAGACAGT	TTCCGCAGTT	CATATGGCTA
Consensus	*****	*****	*****	*****	*****
3151					
msa235280.2{195_COH1}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	-----
msa235280.2{195_M732}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAA----
msa235280.2{195_M781}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_H36B}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATG~	-----
msa235280.2{195_JM9130013}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TG-----
msa235280.2{195_18RS21}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAA-----
msa235280.2{195_2603}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA
msa235280.2{195_A909}	GAACAGACAA	TAAACAGATA	ACTTCACATC	AGACACATGt	TGAAAAACAA

Table 51: Comparative Sequences relating to SAG0677

Consensus	*****	*****	*****	*****	*****
	3201				3250
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	ATTAAAAATA	cattgccatc	cactgggtgac	agcaaactgt	gttattatat
msa235280.2{195_A909}	ATTAAAAATA	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3251				3300
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	cactggaatg	gctatcgta	tgctgagtgt	attatttagt	ttagctaaaa
msa235280.2{195_A909}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	3301		3317		
msa235280.2{195_COH1}	-----	-----	-----	-----	-----
msa235280.2{195_M732}	-----	-----	-----	-----	-----
msa235280.2{195_M781}	-----	-----	-----	-----	-----
msa235280.2{195_H36B}	-----	-----	-----	-----	-----
msa235280.2{195_JM9130013}	-----	-----	-----	-----	-----
msa235280.2{195_18RS21}	-----	-----	-----	-----	-----
msa235280.2{195_2603}	agtttaaaag	caaatat	-----	-----	-----
msa235280.2{195_A909}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----

SEQ ID NO. 5110

STRAIN 2603 frame: 1

LNKGVGGDGVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY
 LQSVKYVGGGNNL DLTTPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TK
 PSKPKDLSLTPPGFPDLNTPPDEAPKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNITAV
 DYLNTTTFEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI
 ELPNDVRHIDSLSVRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS
 SSEIMTTFKDGMPPELVEQKDVSLDINDMMSKFKTIRLGRKDSEFKGQLIAKTGTVELD
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
 VVGKSELPLTKGWTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
 HKYPSVFLTLTALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMNVNENGDM LGTP
 VI IQGKDLTNRTPKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASI VRR
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR
 KAEEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVN NVHQDTDTTVKASDLPKTKTVS
 AVHMARTDNKQITSHQTHVEKQIKNTLPSTGDSKRGYITGMAIVMLSVLFLSLAKKFKSK
 Y

SEQ ID NO. 5111

STRAIN A909 frame: 1

LNKGVGGDGVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY
 LQSVKYVGGGNNL DLTTPPGFKKEDKKVEKPKLDRPPGIDLPPTSMRSFDYSTPPG TK
 PSKPKDLSLTPPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKV
 NGKILQVESDGLVI PRNALSANQFDDTSLKIYRNNRNKEITITTDYFADTKYVNITAV
 DYLNTTTFEQLATGETVDYHAI VFSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGI
 ELPNDVRHIDSLSVRLNEVKTVDNILKNDEQDINLSKTYQLKYNPTNRRLEFTINNINS
 SSEIMTTFKDGMPPELVEQKDVSLDINDMMSKFKTIRLGRKDSEFKGQLIAKTGTVELD
 MFFKQSQDPASI IKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTS G
 ASLKVYVYKGQEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFANIDWSHYSKVTVNGKE
 VVGKSELPLTKGWTFVLHKTENSLNVKSLIMETGSVSKKVQQLPLSPRLSKNKHMRDML
 LTMQKDSAYYETSDSLVLRINLTADTKLNFNAVKGASALTENMMMRQFAVAGPQDDPVSE
 HKYPSVFLTLTALLETASEATLNGKEITASGIIGHIKDGDKSKHVEVKMNVNENGDM LGTP
 VI IQGKDLTNRTPKPLMSGRRVL YAGKQYEFRAKLPLSRFNTWIRVEVVTEAGEKASI VRR
 MFFDQSVPELNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKTGLYSFRNG
 VEITKDMTVPLEFGDNI IKLSAVDLSNYRRNETLHIYRNRFDVKASQMTADKGAKVTVD M
 LMKHLVVP EMAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVDKVDVPIKVVDLEAIR
 KAEEAHKADEARKAEEARKAEEARKAEEGHKTQEAPIVEEGYKVN NVHQDTDTTVKASDLPKTKTVS
 AVHMARTDNKQITSHQTHVEKQIKN

SEQ ID NO. 5112

STRAIN H36B frame: 2

GVQIYQYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKD VY LQSVKYVGG
 GNNL DLTTPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPG TKPSKPKDLS
 TTPGFPDLNTPPDEALKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES

DGKLVIPRNALSAGQFDDTSLKILRNRRNNRKEITITDDYFADTKYVINATVDYLSNTFFB
DLATGETVDYHAIVSSFAAIIKDKGGKIIYVNDKLQGETSRIALKDKSVKIGIELNDVRHI
DLSLSEVRNLEVKTVDNLIKNDREQDINLSKTYQLKYNPTRNRLEFTINNINSSEIMTFFQ
DKGMPLEVBQKQVSLDINDMDSFKFTILRLRGDKSEFGKQLAKTQTEVLDMDFKQSQDP
ASIIKKIYLIQNGVPNELKFPDSSGFLTESQIDGYYIKDAILNFKPLTSGASLKVHYVKG
QEDPYSHQKEDMTKKGEQLSHSTQANENTAKVTFLANDWSHYSKTVNGVBKGVGKSELPL
TKGWTITVFLHKETNSLVKSLIMETGSSVKVKQQLPLSPKSNKHKMRMDLTMQKSDS
YETSDSLVLRINLTADTKLNFNAVKGASALTENMMRQFQAVAGQPDQPFVSEHKYPSVFL
TPALLETASEATINGBKII TASGIIGHIKDGGSKHVEVKMNVNENGDMLGTPVIIQGDGLT
NRTKPLMSGRRVLYAGQYEFRAKLPSEFRNTWIRVEVUTEAGEKASIVRMFPDQSVPE
LNTAVAKRDLTSDALIKIIVAKDSSKLKLQYDSSLLESVDKTLTYSFRNGVETITKMTV
PLEFGDNIITKLSAVDLSNRYRRNETLIIYRNRFDVKASQMTADKGAKVTVDMLMKHLVPE
MAGAYTLTIDEAPNTNBSGMLTNAKVISHYVNGGVDKVDVPIKVVDLEAIRKAEAAHKD
BARKEAERAKDAEAAKAEVRKAEAAHKAEAAHKGKAEAGHKTQEAPIVEEGYKVNNVHTD
TTVKASDLPKKTKTVSAVHMARTDNQIITSHQTH

LNSVKGVGDDGNVLQYQQYYIKMDNNKPYLSPKDKTITVEKLEDRWNKIYFKVQDTGIGLKDVQI
LQKKYKVGCGNNLIDLITPPGFKKEDBKVEKPKLDRPPGIDLAPMSTSMRFSFDYSTPPGTK
PSKPKDLSLSTPPGFPDLNTPDEAPKDSKDLAIBDKSKAIKYAKSLQLSFQDTPALASKV
NGKILQVESDQGLVIRPRNALSANQFDDTSKKIYRNNNRNKAITITTDYFADTKVNIITAV
DYLNSNTFEQLATGETVDYIHAIVFSSFAAIKDKGGKIYVNDKLQETSRIALKOKSVKIG
ELPNDVRHIDLSLVRRLNEKVLNDLNKDEQDINLSKTYQLKYNPTNRRLFEITINNNS
SSEIMTTHFKDGMPELVQKVQDVLNDNMDMSFKPTIRLGRDKSEFGKQLLAKTGTVELD
MFFKQSQDEPASIKKIYLVIQNGVNPENKLFDFSFLQBTQSQIDGYYIKYKDALNFKFLTSG
ASLKVYVKGQEDPYSHQKEDMTKKEGLSHSTQANTAKVTANIDWSHYSKVNTVNGKE
VVMGSELPLTKGWTFLVHLKHTENS LNVLKSIMETGVSKKVQVQLPLSPRLSKNKHMRMDL
TLMQKDSAYEYTESDLSVLIRNLNTADTKLNFNAVGKASALTENNMMRQFVAVAGPQDVPSE
HKYPSVFLTLPALLETASEATLNGKIEITAGSIIGHIKDGDKSKHVEKVMYNENMDMLPTG
YIIOGKDLNTRTKPLMSGRVLYAGKQYEFRAKLPLSRFNTYIRVEVYTBAGBKASIYRR
MFFDQSQVPELNTAVAKRDLTSDTALIHIVAKDDSLKLYQDSSLQDSLEMTDKGLVYSFRNG
VEITKDMTVPLEFGDNIKLSAVALNPNYRNNETLHIYRNRVQVKSQMTADKGAKYTVDM
LMHKLVPVMEAGAYTLIDEAPNTNESGMLTNAKVSIHYVNGGVQDKVDVPIKVVDLEAIR
KAEERAKAEARKAEAGBKGTQEAPIVEEGYKVNNVHQDTTTVKASDLPKTKTVSAVHMAR
TQDQITSHQTHVE

LNNKVGVGDDGVGVIYQYVYIMDNKNPKYLPSPDKTITVEKLEDRWKTIFFKVQDGTIGLKDDVY
LQSVKYVQGGGNNMLDLITPPGFKEDBKXPKEDRPPGDLDPAPTSRMSFSDYSTPGPKT
PSKPDKDLSLTPPGFFDLNTPPEATKQ. KRRY. R. IRSN. IC. VNST. LC. PYFS. QS
KWQNTISRT. WQISHS. KCFVS. SI. . H. S. NLS. . SQ. RNYIYHNLRCFLCYKICQYHSG
.LFEQYVF. AISW. NSRLPCHCIFKLCCY. RQGW. DLC. R. IARNFSYSA. R. IC. DWY
. ITK. CQTY. F. CFCSSP. G. NC. YLEK. . TRH. SQONLPIQIOPDKSSSRVY. . H. L
KFRNHDHFQRWKDARI. G. TKRCFFGYKRYGHE. V. NYSTWTGKF. I. GTYCKWNNS. IR
YVFOTISRPSFN. Y. KNIPYPKWCSC. IEKI. I. L. FWFN. KSDRWILYL. RCN. P. I. INQW
CS. SCL. RARRSI. SEBERRY. KR. TAQSFNSQ. KYSKNLC. Y. LVTL. . GYCEKWR
SW. R. . VTFN. RMDNICIT. NKRKFIK. KFDYDGC. CK. ESSTSPKS. I. I. K. AYEYGA
TYYAKRFSVLNRK. QSSPNS. SHCRY. T. F. CC. RSECSY. KYDDTEVCSWTR. SC. .
T. IPIGISLNSCLIGNC. . GNSKW. GNHSIYYRSHQW. . QKAC. SQNGE. KWRHARNP
CYYSR. RLD. SNKTINEWT. SLTCL. TI. VFG. IIT. SF. HLD. G. SGNRSRRESCYCS
HVL. PISSRA. HSSC. T. FDF. YCSYPHRCQR. LSKTKIISR. FIT. IC. . NRSL. F. KW
CRNH. RYDSTR1RW. Y. VICC. LKILKS. . DPSYL. KPF. C. SKPENS. QRS. SNGCY
VDEALCSNRGRSLYINNRSSKIK. IRNVNR. SIDLCKKWC. . S. CSD. SS. LRSYS
. S. RST. S. RST. S. RST. S. RST. S. RST. S. RST. SRRT. S. RGT. NPRSTYS. RRL
QS. . RSSN. YYS. SV. FTKD. DFSRSSY. NRQ. TDNFTSDTC. K

LNNKGVGGGDQYIQQYIYIMDMNKNPKYLSPOKDTIWEKLEDRWKCTIFKVKQDITGLGKDQVY
LQSVKIVGGGNNLIDLITPPGPFKEKDEWPEKPLDRPGGIDLPAFTSMRFSFDYSTPPGTK
PSKPKDLSLSTPPGPFDLNTPPEADTEQ. .KRRY.R.IRSN.T.C.VSST.LC..PYFS.QS
KQONITRSI..WQISHS.KCFVS.SI..H.S.NLGS..SQ..RNYHYNRLFCRYKICQVHS
..LFEQYFYF.AISYV.NSRLPCHCIFKLCCY.RQGW.DLC.R.IARNFSYSAR..IC.DWY
..ITK.CQTY..FICSSPF.G.NC..YLEK..TRH.SQONLPIQIDPKSSSRVY..H.L
KFRNHDDHFQRWARDIGF.TKRCFFGYKRYGHE.V.NYSTWTGKF.I.GTTYCKWNNS.IR
YVFPQITSRPSFNY.KNIYPKWKSC.IEKT.I.L.FWFN.KSDRWILY.RCN.P.I.INQW
CKS.SCL.RARRSI.SBERRYR.KR.TAQFSNSQ.KYSKNLC.Y.LVTL..GYCEWKR
SW.R..VTFN.RMDNICIT.NRKFIK.KFDYGDG.CK.ESSTSFKS.II.K.AYEBYA
TYIAKRFSLVRNK.QSSPSN.SHCY.T.F.CC.RSECSY.KYDDTEVCSWCTR..SC..
T.IPISISLNSCLICNC..GNSKW.GNHSIYYRSHQW..QKAC.SONGE.KWRHARNP
CYYSR.RLD.SNKTINEWT.STLCR.TI.VPG.IIT.FV.HLD.G.SGNRSRRESCYSS
HVL.PISSRA.HSSC.T.DFV.YCSYPHRCQR.LSKTKIISR.FIT.IC..NRSL.F.KW
CRNH.RYDSTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPNDS.QRS.SNCGY
VDEALSCNRGRSLYNNNRSSKHK.IRNVNKR.SIDSLCKNWC..S.CSD.SS.LRYSY
..S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRST.S.RGT.NPRSTYS.RRL
QS..RSSN.YYS.SV.FTKD.DFSRSSYG.NRQ.TDNFSDTDC

LNKKGVGGDGVQVQIYQYYIKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVY
LOS VKYVGGGNNLDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSFDYSTPPGTK

Table 51: Comparative Sequences relating to SAG0677

PSKPKDSLSTPPGFPDLNTPPDEATKG..KRRY.R.IRSN.IC.VSST.LC..PYFS.QS
 KWQNTSRI.WQISHS.KCFVS.SI..H.S.NLS...SQ.RNYHNLFCRYKICQYHSG
 .LFEQYF.AISYW.NSRLEPCHCIFLCCY.RQGW.DLC.R.IARNFSYSA.R.IC.DWY
 .ITK.CQTY..FICSSFE.G.NC..YLEK..TRH.SQONLPIKIOPDKSSSRVY..H.L
 KFRNHDHFQRWQDARIG.TKRCFFGYKRYGHE.V.NYSTWTKGF.I.GITYCKNWS.IR
 YVQTISRPSFNY.KNIPYKPKCSK.IEKI.L.FWFN.KSDRWILYL.RCN.P.I.INQW
 CKS.SCL.RARRSI.SSERRYD.KR.TAQSFNSQ.KYSKSNLC.Y.LVTL..GYCEWKR
 SW.R..VTFN.RMDNICIT.NRKFIKC.KPDYGDG.CK.ESSTTSFKS.II.K.AYEGYA
 TTYAKRFSVLNKK.QSSPSN.SHCYR.T.F.CC.RSECSY.KYDDETVCSWTTT.RC..
 T.IPISISLNSCLIGNC..GNSKW.GNHSIWYRSHQGW..KQAC.SQNGE.KWRHARNP
 CYYSR.RLD.SNKTINWT.STLCR.TI.VPG.ITT.SF.HLD.G.SGNRSRRESKYCSS
 HVL.PISSRA.HSSC.T.PDF.YCSYPHRCOR.LSKTKLISR.FIT.IC..NRSL.F.KW
 CRNH.RYDSTTRIWR.YY.VICC.LIKLSS..DPSYL.KPF.C.SKPND.S.QRS.SNCGY
 VDEALSCSRNGRSLYINNRRSSKHK.IRNVNKR.SIDSLCKWWC..S.CSD.SS.LRSYS
 .S.RST.S.RST.S.RST.S.RST.S.RST.S.RST.SRRSTVKLRDIPKPKHL.LKKA
 TKLITFIKLILQLKRLIYQRLRQFPQFIWLEQTINR.LHIRHML

SEQ ID NO. 5117

STRAIN JM9130013 frame: 2

GVQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
 GNNLIDLITPPGFKKEDKKVEKPKLDRPPGIDLPAPTSMRSDYSTPPGTPSKPKDSL
 TTPGFPDLNTPPDEAPKDSKDAIEDKSGAIKYAKSLQLSFVDDPILASKVNGKILQVES
 DGKLVIPRNALSANQFDDTSLKIYRNNNRNKEITITTDYFADTKYVNITAVDYLNTTTFE
 QLATGETVDYHAIVPSSFAAIKDKGGKIYVNDKLQETSRIALKDKSVKIGIELPNDVRHI
 DSLSVRRLENEKTVNINLKNDEQDINLSKTYQLKYNPTNRRLEFTINNINSSEIMTTFK
 DGKMPLEVEQKDVSLDINDMDSKFKTIRLGRKDESEFGQLIAKTGTVELDMPFKQSQDP
 ASIKKIYLIQNGVPNELKKFDSSFGLTESQIDGYIYKDAINLKFKLTSGLASKVYVKG
 QEDPYSHQKEDMTKKGEQSLSHSTQANENTAKVTTFANIDWSHYSKVTVNGKEVKGSGELPL
 TKGWTTFLVHKTENSLNVKSLIMETGSGVSKVQQLPLSPRLSKNKHMRDMLLTQKDSAY
 YETSDSLVLRINLTADTKLNFNAVKASALTENMMMRQFAVAGQDDPVSSEHKYPSVFLN
 TPALLEATSEATLNGKEITASGIIIGHIKDGGKSHVEVKMVNENGDMLGTPVILQKDLT
 NRTKPLMSGRVLYAGKQYEFRAKLPLSRFNTWIRVEVVTGEAKASIVRRMFDQSVPE
 LNTAVAKRDLTSDTALIHIVAKDDSLKLKLYQDDSLLESVDKGLYSFRNGVEITKDMTV
 PLEFGDNI.IKLSAVDLSNYYRNNETLHIYRNRFVQASQMTADKGAQVTVDMMLKHLVPE
 MAGAYTLTIDEAPNTNESGMLTNAKVSIIHYVNGGVKDVDPKVVLEAIRKAEAAHKA
 EARKAEAEARKAEAAHKAEEVRKAEAAHKAEEAP.S.RGT.NPRSTYS.RRLQG..RSSN.
 YYS.SV.FTKD.DSFRSSYG.NRQ.TDNFTSDTC

PRETTY of: /biotmp/msa235427.2{*} December 10, 2002 05:18 ..

msa235427.2{195_H36B}	1	50
msa235427.2{195_JM9130013}	-----G	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_18RS21}	-----G	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_2603}	LNNKGVGGDG	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_A909}	LNNKGVGGDG	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_COH1}	LNNKGVGGDG	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_M732}	LNNKGVGGDG	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
msa235427.2{195_M781}	LNNKGVGGDG	VQIYQYIYKMDNNKPYLSPKDKTTVEKLEDRWKKITFKVQDTGIGLKDVLQSVKYVGG
Consensus	*****	*****
msa235427.2{195_H36B}	51	100
msa235427.2{195_JM9130013}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_18RS21}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_2603}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_A909}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_COH1}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_M732}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
msa235427.2{195_M781}	DTGIGLKDVLQSVKYVGGG	NNLIDLITPPGFKKEDKKVEKPKLDRPPGI
Consensus	*****	*****
msa235427.2{195_H36B}	101	150
msa235427.2{195_JM9130013}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_18RS21}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_2603}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_A909}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_COH1}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_M732}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
msa235427.2{195_M781}	DLPaPTSMRS	FDYSTPPGTPSKPKDSLSTPPGFPDLNTPPDEALKdskK
Consensus	***-*****	*****
msa235427.2{195_H36B}	151	200
msa235427.2{195_JM9130013}	daiedksgai	kyakslqlsfvddPilaaskvngkilqvsgdglviprnl
msa235427.2{195_18RS21}	daiedksgai	kyakslqlsfvddPilaaskvngkilqvsgdglviprnl
msa235427.2{195_2603}	daiedksgai	kyakslqlsfvddPilaaskvngkilqvsgdglviprnl
msa235427.2{195_A909}	daiedksgai	kyakslqlsfvddPilaaskvngkilqvsgdglviprnl
msa235427.2{195_COH1}	rry.r.irs	ic.vsst.lc..Pyfs.qskwqnitari.wqishs.kcf
msa235427.2{195_M732}	rry.r.irs	ic.vsst.lc..Pyfs.qskwqnitari.wqishs.kcf
msa235427.2{195_M781}	rry.r.irs	ic.vsst.lc..Pyfs.qskwqnitari.wqishs.kcf
Consensus	-----	-----

Table 51: Comparative Sequences relating to SAG0677

		201			250
msa235427.2{195_H36B}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_JM9130013}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_18RS21}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_2603}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_A909}	sanqfddtsl	kiyrnnnrnk	eitittddyFa	dtKyvntav	dylsnttFeq
msa235427.2{195_COH1}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M732}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
msa235427.2{195_M781}	vs.si..h.s	.nls...sq.	rnyyhnrlFc	ryKicqyhsq	.lfeqyyF.a
Consensus		-----	-----*	-----*	-----*
		251			300
msa235427.2{195_H36B}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_JM9130013}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_18RS21}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_2603}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_A909}	latgetvdyh	aivfssfaai	kdkGgkiyvn	dklqetsria	lkdksvkigi
msa235427.2{195_COH1}	isyw.nsrtp	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M732}	isyw.nsrtp	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
msa235427.2{195_M781}	isyw.nsrtp	chcifklccy	.rqGw.dlc.	r.iarnfsys	a.r.ic.dwy
Consensus		-----	-----*	-----*	-----*
		301			350
msa235427.2{195_H36B}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_JM9130013}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_18RS21}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_2603}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_A909}	elpndvrhid	slsvrrlnev	ktvndiLknd	eqdinlskty	qlKynPtnrr
msa235427.2{195_COH1}	.itk.cqty.	.ficssfe.g	.nc..ylek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M732}	.itk.cqty.	.ficssfe.g	.nc..ylek.	.trh.sqgnl	piKiqPdkas
msa235427.2{195_M781}	.itk.cqty.	.ficssfe.g	.nc..ylek.	.trh.sqgnl	piKiqPdkas
Consensus		-----	-----*	-----*	-----*
		351			400
msa235427.2{195_H36B}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_JM9130013}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_18RS21}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_2603}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_A909}	leftinnins	sseimttFkd	gKmpelveqK	dvldindmd	mskfktirlg
msa235427.2{195_COH1}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M732}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
msa235427.2{195_M781}	srvyv..h.l	kfrnhdhFqr	wKdarig.tK	rcffgykryg	he.v.nystw
Consensus		-----	-----*	-----*	-----*
		401			450
msa235427.2{195_H36B}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_JM9130013}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_18RS21}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_2603}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_A909}	rKdsefkGql	iaKtgtveld	mfFkqsqdpA	siikKiyliq	ngvpnelkKf
msa235427.2{195_COH1}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M732}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
msa235427.2{195_M781}	tKgf.i.Gtt	ycKnwns.ir	yvFqtisrPs	fny.Knipyp	kwcsk.ieKi
Consensus		-----	-----*	-----*	-----*
		451			500
msa235427.2{195_H36B}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_JM9130013}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_18RS21}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_2603}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_A909}	dssFgltesq	idgyyiykda	inlkfkltsg	aslkvvykgq	edpyshqked
msa235427.2{195_COH1}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M732}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
msa235427.2{195_M781}	.l.Fwfn.ks	drwilyl.rc	n.p.i.inqw	cks.scl.ra	rrsi.sserr
Consensus		-----	-----*	-----*	-----*
		501			550
msa235427.2{195_H36B}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_JM9130013}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_18RS21}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_2603}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_A909}	mtkkgeqlsh	stqanentaK	vtfanidwsh	yskvtvngKe	vgkgselplt
msa235427.2{195_COH1}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M732}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
msa235427.2{195_M781}	yd.kr.taqs	fnssq.kysK	snlc.y.lvt	l..gycewKr	sw.r..vtfn
Consensus		-----	-----*	-----*	-----*
		551			600
msa235427.2{195_H36B}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_JM9130013}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_18RS21}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl
msa235427.2{195_2603}	kgwttfvlhk	tenslnvksl	imetGsvskk	vqqlplsprl	sknkhmrdbl

Table 51: Comparative Sequences relating to SAG0677

msa235427.2{195_A909}	kgwtffvlhk	tenslnvksl	imetGavskk	vqqlplsprl	sknkhmrndl
msa235427.2{195_COH1}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M732}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
msa235427.2{195_M781}	.rmdnicit.	nrkfiko.kf	dygdG.ck.e	ssttsfks.i	i.k.ayegy.
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	601				650
msa235427.2{195_JM9130013}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_18RS21}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_2603}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_A909}	lTmqkdsayy	etsdsivlri	Nltadtklmf	navkgaSalt	enmmmrqfav
msa235427.2{195_COH1}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M732}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
msa235427.2{195_M781}	aTyyakrfsv	lrnk.qsps	N.shcry.t.	f.cc.rSecs	y.kyddetvc
Consensus	-*-----	-----	*-----	-----*	-----
msa235427.2{195_H36B}	651				700
msa235427.2{195_JM9130013}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_18RS21}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_2603}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_A909}	agpqddpvse	hkypsvflit	palLetasea	tlngkeitaS	giighikdGd
msa235427.2{195_COH1}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M732}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
msa235427.2{195_M781}	scwttr.sc.	.t.ipisisl	nscLignc..	gnskw.gnhS	iwyrrshqGw
Consensus	-----	-----	-----*	-----*	-----*
msa235427.2{195_H36B}	701				750
msa235427.2{195_JM9130013}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_18RS21}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_2603}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_A909}	ksKhvevkmv	nEngdmlgtp	viiggkdltN	rtkplmsgr	vlyagkqyef
msa235427.2{195_COH1}	..Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M732}	..Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
msa235427.2{195_M781}	..Kqac.sqn	gE.kwrharn	pcyyr.rld	.snktinewt	.stlcr.ti.
Consensus	--*-----	*-----	-----	-----	-----
msa235427.2{195_H36B}	751				800
msa235427.2{195_JM9130013}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_18RS21}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_2603}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_A909}	raklplsrfrn	twirvevte	agekaSivrr	mffdqsvpel	ntavakrdlt
msa235427.2{195_COH1}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M732}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
msa235427.2{195_M781}	vpg.itt.sf	.hld.g.sgn	rsrreSkycs	shvl.pissr	a.hssc.t.f
Consensus	-----	-----	-----*	-----	-----
msa235427.2{195_H36B}	801				850
msa235427.2{195_JM9130013}	sdtalihiva	kddsLklkly	qddallesvd	ktglysfng	veitkdmtp
msa235427.2{195_18RS21}	sdtalihiva	kddsLklkly	qddallesvd	ktglysfng	veitkdmtp
msa235427.2{195_2603}	sdtalihiva	kddsLklkly	qddallesvd	ktglysfng	veitkdmtp
msa235427.2{195_A909}	sdtalihiva	kddsLklkly	qddallesvd	ktglysfng	veitkdmtp
msa235427.2{195_COH1}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
msa235427.2{195_M732}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
msa235427.2{195_M781}	df.ycsyphr	cqr.Lsktki	isr.fit.ic	..nrsl.f.k	wcrnh.ryds
Consensus	-----	-----*	-----	-----	-----
msa235427.2{195_H36B}	851				900
msa235427.2{195_JM9130013}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_18RS21}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_2603}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_A909}	lefgdnitkl	savdlsnyrr	netlhiYrnr	fdvkaSqmta	dkgakvtvdm
msa235427.2{195_COH1}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncc
msa235427.2{195_M732}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncc
msa235427.2{195_M781}	ttriwr.yy.	vicc.likls	s..dpsYl.k	pf.c.Skpnd	s.qrs.sncc
Consensus	-----	-----	-----*	-----*	-----
msa235427.2{195_H36B}	901				950
msa235427.2{195_JM9130013}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_18RS21}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_2603}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_A909}	lmkhlvpem	aGaytl tide	apntnesgml	tNakvSIhyv	nggvdkvdvp
msa235427.2{195_COH1}	yvdealcsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M732}	yvdealcsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
msa235427.2{195_M781}	yvdealcsr	nGrsllyinnr	rsskhk.irn	vNkr.SIdsl	ckwwc..s.c
Consensus	-----	-----	-----*	-----*	-----

Table 51: Comparative Sequences relating to SAG0677

		951			1000
msa235427.2{195_H36B}	ikvvdleair	kaeeahkade	arkaeeearka	deahkaeevr	kaeeahkvee
msa235427.2{195_JM9130013}	ikvvdleair	kaeeahkade	arkaeeearka	eeahkaeevr	kaeeahkvee
msa235427.2{195_18RS21}	ikvvdlea..irkaee	arkaeeearka	eeghktqeap	iveegykvnn
msa235427.2{195_2603}	ikvvdleair	kaeearkaee	arkaeeearka	eeghktqeap	iveegykvnn
msa235427.2{195_A909}	ikvvdleair	kaeeahkade	arkaeeearka	eearkaeear	kaeehktqe
msa235427.2{195_COH1}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M732}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
msa235427.2{195_M781}	sd.ss.lrsy	s.s.rst.s.	rst.s.rst.	s.rst.s.rs	t.s.rst.sr
	Consensus	-----	-----	-----	-----
		1001			1050
msa235427.2{195_H36B}	arkaeeeghkt	geapiveegy	kvnnvhqtdt	tvkasdlpkt	ktvsavhmar
msa235427.2{195_JM9130013}	ap.s.rgt.n	prstys.rrl	gg..rssn.y	ys.sv.ftkd	.dsfrssyg.
msa235427.2{195_18RS21}	vhqtdttvka	sdlpktktvs	avhmardnk	qitshqthve	-----
msa235427.2{195_2603}	vhqtdttvka	sdlpktktvs	avhmardnk	qitshqthve	kqikntlpst
msa235427.2{195_A909}	apiveegykv	nnvhqtdttv	kasdlpktkt	vsavhmardt	nkqitshqth
msa235427.2{195_COH1}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M732}	rst.s.rgt.	nprstys.rr	lqs..rssn.	yps.sv.ftk	d.dsfrssyg
msa235427.2{195_M781}	rstvklkrdi	kpkkh1.lkk	atklitfikl	ilqlkrliyy	rlrqfpqfiw
	Consensus	-----	-----	-----	-----
		1051		1081	
msa235427.2{195_H36B}	tdnkqitshq	th-----	-----	-----	~
msa235427.2{195_JM9130013}	nrq.tdnfts	dte-----	-----	-----	~
msa235427.2{195_18RS21}	-----	-----	-----	-----	~
msa235427.2{195_2603}	gdskrgyyit	gmaivmlsvl	fslakkfksk	y	~
msa235427.2{195_A909}	vekqikn---	-----	-----	-----	~
msa235427.2{195_COH1}	.nrq.tdnft	sdTC-----	-----	-----	~
msa235427.2{195_M732}	.nrq.tdnft	sdTC.k----	-----	-----	~
msa235427.2{195_M781}	leqtinr.lh	irhml-----	-----	-----	~
	Consensus	-----	*****	*****	*

Table 52: Comparative Sequences relating to SAG 1823

SEQ ID NO. 5201

STRAIN 090

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA
 CAACAAGCCAAACTGGGCAAATGCGCTTTTGGAAAACTAACACCAGCA
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 CGGCGATCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA
 TGTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAA
 TGCTCATTGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATT
 GCTTCTATTGAATCGAGTCAAGCCGAGGCTGCTAATCGTGCAAGCCACTT
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA
 AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG
 GCATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAG
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
 TGTCAACGCTAATAATGACGATTCAGATGCTGGCTGAACTAGTAAAG
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTGGAATCTG
 CTGTTATTAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA
 AGTTGATGAGTCT

SEQ ID NO. 5202

STRAIN A909

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGA
 CAATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGA
 CAACAAGCCAAACTGGGCAAATGCGCTTTTGGAAAACTAACACCAGCA
 CAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 CGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCG
 TTAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATT
 CCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
 TATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA
 ACTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTT
 TATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAA
 TGTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAA
 TGCTCATTGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTAWT
 GCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTT
 ACAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA
 AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAG
 CAACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACC
 ACAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG
 GCATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAG
 TTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTAT
 TGTCAACGCTAATAATGACGATTCAGATGCTGGCTGAACTAGTAAAG
 AAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
 AAATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGGTAT
 TATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTG
 CTGTTATTAATCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGAT
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAA
 AGTTGATGAGTCT

SEQ ID NO. 5203

STRAIN H36B

AGCGaTACCTTTAATTTTGATATTGACCAAATTGCAGAC
 AATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC
 AACAAAGCCAAACTGGGCAAATGCGCTTTTGGAAAACTAACACCAGCAC
 AAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACTTTTGT
 GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGAGTAGAAGGCGT
 TAATACCACTGTAAATCATATCTTGTCTGAGCAGAAAAAATTCAAATTC
 CTCAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAATGGATT
 ATTGCCAAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAACCAA
 CTTGATTCAAAAATTATTCAAACAAAGCAAGACCTCGCTACAGGAATTTT
 ATTTTGACTCACAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
 GTTGTCAACAAGAGATACCTTTGGCAAGAAATATCGTCTCTGCTGAAAT
 GCTCATTGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTG
 CTCTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
 CAACAAGAAATCTAGCATTAGATAGCCAAACGTCCGAGTATCAAAATTA
 AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAGC
 AACATACTGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACACCA
 CAGATGCGAAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTG
 CATGTTACGTCGAAATACCATTCCAACAATGAACTCTCAATCGCTCAGT
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
 GTCAACGCTAATAATGACGATTCAGATGCTGGCTGAACTAGTAAAGA
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATT
 AATCTGTCACTGCATTATCTGAAAGCTTAGTGGCTCAAAATAATGGTATT
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGAAATCTGC

Table 52: Comparative Sequences relating to SAG 1823

TGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATa
 AAAAAATAGTTGAAGCCTTACTCaCGAAGGTaAATCTACCCAAGAAAAA
 GTTGATGAGTCT

SEQ ID NO. 5204

STRAIN 18RS21

TTTTGATATTGACCAAATTGCAGACAATGCTATCACTAAAAACAGATAAAA
 CAACAGAAATTATTTCCAACCAGACAACAAGCCAAACTGGGCAAAATGGCC
 TTTTTTGAAAAAATAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
 ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAAATGCGCTCCTTGATT
 TTGGACAATCCGCGTAGAAGGCGTTAATACCACCTGTTAATCATATCTTG
 TCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
 TGCTAATCGCGAACTAAATGGATTTATTGCCAAATATAAAGATGCTACTC
 CGCAGAAATTAGAGAAAAAACCAAACTTGATTCAAAAATTATTCAAACAA
 AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
 AAAAAATGGATATGATGGCAGCGAATGTTGTCAAACAAGAGATACCTTGG
 CAAGAAATATCGTCTCTGCTGAAATGCTCATGGAAGATAATCTAAATCT
 ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
 GGTCTGCTAATCGTGCAAGCCACTTACAACAGAAATTCTAGCATTAGATA
 GCCAAACGCTCCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT
 GAAGTTATCAATACCCTCGAACAGCAACATCCTGAATATGTCAGCCGTCT
 CTACGTTGCATGGGCAACAACCAACAGATGCGAAACTTGGTCAAAGTAT
 CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCAATCCA
 ACAATGAATCTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
 ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
 AGATGCTGGCTGAACTAGTAAAGAAGCGATTCCGATGTTAGAGAAGACC
 GCACAAGCCCACTGTTTCTATTAAATCTGTCACTGCATTAGCTGAAAG
 CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
 AGGAACGTGCCCaATTGGAATCTGCTGTTATTAAATCGGCTGAAACAATC
 AATGATTCTGTCAAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
 CGAAGGTaAATCTACCCAAGAAAAGTTGATGAGTCT

SEQ ID NO. 5205

STRAIN M732

AGCGATACCTTTAAATTTTGATATTGACCAAATTGCAGAC
 AATGCTATCACTAAAACAGATAAAAACAGAAATTTATTTCCAACCAGAC
 AACAGGCCAACTGGGCAAAATGGCTTTTTTGAAAAACTAAACCAGCAC
 AAAAACTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACTTTTGTG
 GGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGT
 TAATACTACTGTTAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTC
 CTCAGTTGATGATTTACTAAAAATGCTAATCGCGAACTAAATGGATT
 ATTGCCAAATATAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAAA
 CTTGATTCAAAAAATTATTCAAAACAAAGCAAGACCTCGCTACAGGAATTT
 ATTTTGACTCACAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAAT
 GTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGCTGAAAT
 GCTCATTGAAGATAATACTAAATCTATTGAAAAATTTGGTTGGAGTTATTG
 CTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
 CAACAAGAAATTTAGCATTAGATAGCCAAACGTCGGAATATCAAAATTA
 AAGTAACCAATTAGCCCAATGACTGAAGTTATCAATACCCTCGAACAGC
 AACATACGGAATATGTCAGCCGTCTCTACGTTGCATGGGCAACAACCA
 CAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGG
 TAGTGTACGTCGAAATACCAATCCAACAATGAACTCTCAATCGCTCAGT
 TAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATT
 GTCAACGCTAATAATGCAGCATTGCAAAATGCTGGCTGAAACTAGTAAAGA
 AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTA
 AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATT
 ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAATCTGC
 TGTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAAATTCGTGATA
 AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA
 G

SEQ ID NO. 5206

STRAIN COH1

CTAAAAACAGATAAAAACACAGAAATTTTCCAACCAGACAACAAGCCAA
 ACTGGGCAAAATGGCTTTTTTGAAAAACTAACACCAGCACAAAAGTCTGC
 TWCTCTGAAAAAACACCAAGCTTTGGTAGATACTTTTGTGGTGACCAAA
 ATGCGCTCCTTGATTTTGGACAATCCGCGTAGAAGGCGTTAATACTACT
 GTTAAATCATATCTTGTCTGAGCAGAAAAAAATTCAAATTCCTCAAGTTGA
 TGATTTACTAAAAATGCTAATCGCGAACTAAATGGATTATTGGCCAAAT
 ATAAAGATGCTACTCCGGCAGAAATTAGAGAAAAAACCAAACTTGATTCAA
 AATATTCTCAAAACAAAGCAAGACCTCGCTACAGGAATTTATTTTGACTC
 ACAAAACATCGAGCAAAAAATGGATATGATGGCAGCAAAATGTTGTCAAAC
 AAGAAGTACTTTGGCAAGAAATATCGTCTCTGCTGAAATGCTCATTGAA
 GATAATACTAAATCTATTGAAAAATTTGGTTGGAGTTATTGCTTTTATTGA
 ATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTACAACAAGAA
 TTCTAGCaATTAGATAGCCAAACGTCGGAATATCAAAATTAAGTAACCAA
 TTAGCCCGAATGACTGAaGTTATCaTaCCCTCGAACAGCAACATACGGA
 aTATGTCAGCCGTCTCTACGTTGCATGGGCAACAACCAACAGATGCGAA
 ACTTGGTCAAAGTATCGTCAGATATGCGTCAGAACTTGGTATGTTACGT
 CGAAATACCAATCCAACAATGAAACTCTCAATCGCTCAGTTAGGCATGAT
 GCAACAATCTGTCAAATCCGGTGTCACTGCTGATGCTATTGTCAACGCTA
 ATAATGCAGCATTGCAAATGCTGGCTGAACTAGTAAAGAAGCGATTCCG
 ATGTTAGAGAAGACCGCACAAAGCCCACTGTTTCTATTAAATCTGTCAC

Table 52: Comparative Sequences relating to SAG 1823

TGCATTAGCTGAAAGCTTAGTGGCTCAAATAATGGTATTATCGCTGCCA
TAGACAAAGGACGTAAGGAACGTGCCCAATTAGAATCTGCTGTTATTAA
TCGGCTGAAACAATCAATGATTCTGTCAAATTCGTGATAAAAAAATAGT
TGAAGCCCTACTCAaCGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGT
CT

SEQ ID NO. 5207

STRAIN M781

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA
CAACAGAAATTAATTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGTGACCAAAATGGCGTCTCTTGATT
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTAAATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTATTGCGCAATATAAGATGCTACTC
CGGCAGAATTAGAGAAAAACCAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTTGAAGATAAATACTAAATCT
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCCAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCGGAATATCAAATTAAGTAACCAATTAGCCCGAATGACT
GAAGTTATCAATACCCCTCGAACAGCAACATACGGAATATGTCAGCCGCTCT
CTACGTTGATGGGCAACAACACCACAGATGCGAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAACTTGGTATGTTACGTCGAAATACCATTCGA
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AAATGCTGGCTGAACTAGTAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCAATTAGCTGAAAG
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCAATTAGAATCTGCTGTTTAAATCGGCTGAAACAATC
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5208

STRAIN CJB110

TTTTGATATTGACCAAATTCAGACAATGCTATCACTAAAAACAGATAAAA
CAACAGAAATTAATTCCAACCAGACAACAAGCCAACTGGGCAAAATGGCC
TTTTTTGAAAACTAACACCAGCACAAAAGTCTGCTATCTCTGAAAAAAC
ACCAGCTTTGGTAGATACTTTTGTGGCGATCAAATGCGCTCCTTGATT
TTGGACAATCCGCGAGTAGAAGGCGTTAATACTACTGTAAATCATATCTTG
TCTGAGCAGAAAAAATTCAAATTCCTCAAGTTGATGATTTACTAAAAAA
TGCTAATCGCGAACTAAATGGATTATTGCGCAATATAAGATGCTACTC
CGGCAGAATTAGAGAAAAACCAACTTGATTCAAAAATTATTCAAACAA
AGCAAGACCTCGCTACAGGAATTTTATTTTGACTCACAAAACATCGAGCA
AAAAATGGATATGATGGCAGCAAAATGTTGTCAAACAAGAAGATACTTTGG
CAAGAAATATCGTCTCTGCTGAAATGCTCATTTGAAGATAAATACTAAATCT
ATTGAAAAATTGGTTGGAGTTATTGCTTTTATTGAATCGAGTCAAGCCGA
GGCTGCTAATCGTGCAAGCCACTTACAACAAGAAATCTAGCATTAGATA
GCCAAACGTCGAGTATCAAATTAAGTAACCAATTAGCTCGAATGACT
GAAGTTATCAATACCCCTCGAACAGCAaCATACTGAATATGTCAGCCGCTCT
CTACGTTGATGGGCaCaACACCACAGATGCGAACTTGGTCAAAGTAT
CGTCAGATATGCGTCAGAACTTGGCATGTTACGTCGAAATACCATTCGA
ACAATGAACTCTCAATCGCTCAGTTAGGCATGATGCAACAATCTGTCAA
ATCCGGTGTCACTGCTGATGCTATTGTCAACGCTAATAATGCAGCATTGC
AGATGCTGGCTGAACTAGTAAGAAGCGATTCCGATGTTAGAGAAGACC
GCACAAAGCCCCACTGTTTCTATTAATCTGTCACTGCAATTAGCTGAAAG
CTTAGTGGCTCAAATAATGGTATTATCGCTGCCATAGACAAAGGACGTA
AGGAACGTGCCCAATTGGAATCTGCTGTTTAAATCGGCTGAAACAATC
AATGATTCTGTCAAATTCGTGATAAAAAAATAGTTGAAGCCTTACTCAA
CGAAGGTAAATCTACCCAAGAAAAAGTTGATGAGTCT

SEQ ID NO. 5209

STRAIN 1169NT

GCAGACAATGCTATCACTAAAAACAGATAAAACAACAGAAATTAATTCCAA
CCAGACAACAAGCCAACTGGGCAAAATGCGCTTTTGGAAAACTAACAC
CAGCACAAAAGTCTGCTATCTCTGAAAAAACACCAGCTTTGGTAGATACT
TTTGTGGTGACCAAAATGCGCTCCTTGATTTTGGACAATCCGCGAGTAGA
AGGCGTTAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATTC
AAATTCCTCAAGTTGATGATTTACTAAAAAATGCTAATCGCGAACTAAAT
GGATTATTGCGCAATATAAGATGCTACTCCGGCAGAATTAGAGAAAAA
ACCAACTTGATCCAAAAATTATTCAAACAAGCAAGACCTCACTACAGG
AATTTTATTTTGACTCACAAAACATCGAGCAAAAATGGATATGATGGCA
GCAAAATGTTGTCAAACAAGAAGATACTTTGGCAAGAAATATCGTCTCTGC
TGAATGCTCATTTGAAGATAATACTAAATCTATTGAAATTTGGTTGGAG
TTATTGCTTTTATTGAATCGAGTCAAGCCGAGGCTGCCAATCGTGCAAGC
CACTTACAACAAGAAATTTAGCATTAGATAGCCAAACGTCGAGTATCA
AATTAAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCCCTCG
AaCAGCAACATACTGAATATGTCAGCCGCTCTCTACGTTGATGGGCAACA
aCACCACAGATGCGAACTTGGTCAAAGTATCGTCAGATATGCGTCAAAA
ACTTGGCATGTTACGTCGAAATACCAATTCCAACAATGAACTCTCAATCG
CTCAGTTAGGCATGATGCAACAATCTGTCAAATCCGGTGTCACTGCTGAT
GCTATTGTCAACGCTAATAATGCAGCATTCAGATGCTGGCTGAAACTAG

Table 52: Comparative Sequences relating to SAG 1823

TAAAGAAGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTT
CTATTAAATCTGTCACTGCATTAGCTGAAAGCTTAGTGCGCTCAAATAAT
GGTATTATCGCTGCCATAGACAAAGGACGTAAGGAACGTGCCCAATTAGA
ATCTGCTGTTATTAAATCGGCTGAAACAATCAATGATTCTGTCAAATTC
GTGATAAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAA
GAAAAAGTTGATGAGTCT

SEQ ID NO. 5210

STRAIN JM9130013

AGCGATACCTTTAATTTTGATATTGACCAAATTGCAGAC
AATGCTATCACTAAACAGATAAAACAACAGAAATTATTTCCAACCAGAC
AACAAGCCAAACTGGGCAAAATTGCCTTTTTTGAAAACTAACACCAGCAC
AAAAGTCTGCTATCTCTGAAAAAACACCAAGCTTTGGTAGATACCTTTGTC
GGTGACCAAAATCGGCTCCTTGATTTTGGACAATCGCAGTAGAAGGCGT
TAATACCACTGTTAATCATATCTTGTCTGAGCAGAAAAAATCAAATTC
CTCAAGTTGATGATTACTAAAAATGCTAATCGCGAACTAAATGGATT
ATTGCCAAATATAAAGATGCTACTCGGCAGAAATTAGAGAAAAAACCAA
CTTGATTCAAAAAATTATCAAACAAGCAGACCTCGCTACAGGAATTTT
ATTTTGAATCAAAAACATCGAGCAAAAAATGGATATGATGGCAGCGAAT
GTTGTCAAACAAGAGATACCTTGGCAAGAAATATCGTCTCTGCTGAAAT
GCTCAITGAAGATAATACTAAATCTATTGAAAAATTGGTTGGAGTTATTG
CTTTTATTGAATcGAGTCAAGCCGAGGCTGCCAATCGTGCAAGCCACTTA
CAACAAGAAATTCTAGCATTAGATAGCCAAACGTCGAGTATCAAATTA
AAGTAACCAATTAGCTCGAATGACTGAAGTTATCAATACCTCGAACAGC
AACATACCTGAATATGTGAGCGCTCTACGTTGCATGGGCAACAACCCA
CAGATGCGAACTTTGGTCAAAGTATCGTCAGATATGCGTCAAAAACTGG
CATGTTACGTCGAAATACCATCCAACAATGAACTCTCAATCGCTCAGT
TAGGCATGATGCAACAATCTGTCAAATCCGCTGTCAGTCTGATGCTATT
GTCAACGCTAATAATGACGATGTCAGATGCTGGCTGAAACTAGTAAAGA
AGCGATTCCGATGTTAGAGAAGACCGCACAAAGCCCCACTGTTTCTATTA
AATCTGTCACTGCATTAGCTGAAAGCTTAGTGGCTCAAAATAATGTTATT
ATCGCTGCCATAGACAAAGGACGTAAGGAACGTCGCCAATTAGAACTCTGC
TGTTATTAAATCCGCTGAAACAATCAATGATTCTGTCAAATCTGTGATA
AAAAAATAGTTGAAGCCTTACTCAACGAAGGTAAATCTACCCAAGAAAAA
GTTGATGAGTCT

SEQ ID NO. 5211

STRAIN 2603

agcgatacctttaattttgatattgaccaaattgcagacaatgctatcac
taaaacagataaaaacaacagaaattttccaaccagacaacaagccaaa
ctgggcaaatgtcctttttgaaaaactaacaccagcacaaaagtctgct
atctctgaaaaaacaccagcttttgtagatacttttgcggcgatcaaaa
tgcgctccttgattttggacaatccgcagtagaaggcggttaataaccactg
ttaatcatatcttgtctgagcagaaaaaattcaaatcctcaagttgat
gatttactaaaaaatgctaatcggaactaaatggatttattgccaata
taaaagtgctactccggcagaatttagagaaaaaaccaacttgattcaaa
aattattcaaacaaagcaagacctcgctacaggaattttattttgactca
caaacatcgagcaaaaaatggatatgatggcagcgaatgtgtcaaca
agaagatactttggcaagaaatctgctctgctgaaatgctcattgaag
ataatactaaatctattgaaaatttggttgagttattgcttttattgaa
tcgagtcgaagcgaaggctgctaatcgtagcagcacttacaacaagaaat
tctagcattagatagccaaacgtccgagatcaaatataaagtaaccaat
tagctcgaatgactgaagttatcaataccctcgaacagcaacatcctgaa
tatgtcagcgtctctacgttgcatgggcaacaacaccacagatgcgaaa
cttggtcaaaagtatcgtagatagcgtcagaaacttggtgattacgtc
gaaataccattccaacaatgaaactctcaatcgctcagttaggcatgatg
caacaatctgtcaaatccggtgtcactgctgattgtcaacgctaa
taatgcagcatttgagatgctggtgaaactagtaaaagagcattccga
tgtagagaagaccgcacaaagccccactgtttctattaaatctgtcact
gcattagctgaaagcttagtggtcctcaaaataatggattatcgctgccat
agacaaaggacgtaagggaacgtgcccattggaatctgctgtattaaat
cggctgaaacaatcaatgattctgtcaaaatctgtgataaaaaatagtt
gaagccttactcaacgaaggttaattaccaccaagaaaagttgatgagtc
t

PRETTY of: /biotmp/msa13607.2{*} April 22, 2002 03:55 ..

	1				50
msa13607.2{201_COH1}	-----	-----	-----	-----	-----C
msa13607.2{201_M781}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_090}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_CJB110}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_18RS21}	-----	TTTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_2603}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_A909}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_H36B}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_JM9130013}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
msa13607.2{201_1169NT}	-----	-----	-----	GCAGACA	ATGCTATCAC
msa13607.2{201_M732}	AGCGATACCT	TTAATTTTGA	TATTGACCAA	ATTGCAGACA	ATGCTATCAC
Consensus	*****	*****	*****	*****	*****

Table 52: Comparative Sequences relating to SAG 1823

	51		100
msa13607.2{201_COH1}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_M781}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_090}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_CJB110}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_18RS21}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_2603}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_A909}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_H36B}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_JM9130013}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_1169NT}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
msa13607.2{201_M732}	TAAACAGAT	AAAACAACAG	AAATTATTTTC
Consensus	*****	*****	*****
	101		150
msa13607.2{201_COH1}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_M781}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_090}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_CJB110}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_18RS21}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_2603}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_A909}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_H36B}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_JM9130013}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_1169NT}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
msa13607.2{201_M732}	CTGGGCAAAT	TGCCTTTTTT	GAAAACTAA
Consensus	*****	*****	*****
	151		200
msa13607.2{201_COH1}	wTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_M781}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_090}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_CJB110}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_18RS21}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_2603}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_A909}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_H36B}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_JM9130013}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_1169NT}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
msa13607.2{201_M732}	aTCTCTGAAA	AAACACCAGC	TTTGGTAGAT
Consensus	-*****	*****	*****
	201		250
msa13607.2{201_COH1}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_M781}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_090}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_CJB110}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_18RS21}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_2603}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_A909}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_H36B}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_JM9130013}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_1169NT}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
msa13607.2{201_M732}	TGCGCTCCTT	GATTTTGGAC	AATCCGCAGT
Consensus	*****	*****	*****
	251		300
msa13607.2{201_COH1}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_M781}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_090}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_CJB110}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_18RS21}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_2603}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_A909}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_H36B}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_JM9130013}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_1169NT}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
msa13607.2{201_M732}	TTAATCATAT	CTTGTCTGAG	CAGAAAAAAA
Consensus	*****	*****	*****
	301		350
msa13607.2{201_COH1}	GATTTACTAA	AAAATGCTAA	TCGCGAATA
			AATGGATTAA
			TTGCCAAATA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M781}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_090}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_CJB110}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_18RS21}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_2603}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_A909}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_H36B}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_JM9130013}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_1169NT}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
msa13607.2{201_M732}	GATTACTAA	AAAATGCTAA	TCGCGAACTA	AATGGATTTA	TTGCCAAATA
Consensus	*****	*****	*****	*****	*****
351					
msa13607.2{201_COH1}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M781}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_090}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_CJB110}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_18RS21}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_2603}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_A909}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_H36B}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_JM9130013}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_1169NT}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
msa13607.2{201_M732}	TAAAGATGCT	ACTCCGGCAG	AATTAGAGAA	AAAACCAAAC	TTGATtCAAA
Consensus	*****	*****	*****	*****	*****-****
401					
msa13607.2{201_COH1}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M781}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_090}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_CJB110}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_18RS21}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_2603}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_A909}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_H36B}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_JM9130013}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_1169NT}	AATTATTCAA	ACAAAGCAAG	ACCTCaCTAC	AGGAATTTTA	TTTTGACTCA
msa13607.2{201_M732}	AATTATTCAA	ACAAAGCAAG	ACCTCgCTAC	AGGAATTTTA	TTTTGACTCA
Consensus	*****	*****	*****-****	*****	*****
451					
msa13607.2{201_COH1}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M781}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_090}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_CJB110}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_18RS21}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_2603}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_A909}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_H36B}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_JM9130013}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_1169NT}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
msa13607.2{201_M732}	CAAAACATCG	AGCAAAAAAT	GGATATGATG	GCAGCaAATG	TTGTCAAACA
Consensus	*****	*****	*****	*****-****	*****
501					
msa13607.2{201_COH1}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M781}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_090}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_CJB110}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_18RS21}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_2603}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_A909}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_H36B}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_JM9130013}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_1169NT}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
msa13607.2{201_M732}	AGAAGATACT	TTGGCAAGAA	ATATCGTCTC	TGCTGAAATG	CTCATTGAAG
Consensus	*****	*****	*****	*****	*****
551					
msa13607.2{201_COH1}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M781}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_090}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_CJB110}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_18RS21}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_2603}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_A909}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAwTGC	TTTTATTGAA
msa13607.2{201_H36B}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_JM9130013}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_1169NT}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
msa13607.2{201_M732}	ATAATACTAA	ATCTATTGAA	AATTTGGTTG	GAGTTAtTGC	TTTTATTGAA
Consensus	*****	*****	*****	*****-***	*****
601					
msa13607.2{201_COH1}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M781}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_090}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_CJB110}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_18RS21}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_2603}	TCGAGTCAAG	CCGAGGCTGC	taATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_A909}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_H36B}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_JM9130013}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_1169NT}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
msa13607.2{201_M732}	TCGAGTCAAG	CCGAGGCTGC	caATCGTGCA	AGCCACTTAC	AACAAGAAAT
Consensus	*****	*****	-*****	*****	*****
651					
msa13607.2{201_COH1}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M781}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_090}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_CJB110}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_18RS21}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_2603}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_A909}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_H36B}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_JM9130013}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_1169NT}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
msa13607.2{201_M732}	TCTAGCATTa	GATAGCCAAA	CGTCCGAaTA	TCAAATTAAA	AGTAACCAAT
Consensus	*****	*****	*****-**	*****	*****
701					
msa13607.2{201_COH1}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_M781}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
msa13607.2{201_090}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_CJB110}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_18RS21}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_2603}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATcCtGAA
msa13607.2{201_A909}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_H36B}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_JM9130013}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_1169NT}	TAGCtCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCtGAA
msa13607.2{201_M732}	TAGCcCGAAT	GACTGAAGTT	ATCAATACCC	TCGAACAGCA	ACATaCgGAA
Consensus	****-*****	*****	*****	*****	****-***
751					
msa13607.2{201_COH1}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M781}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_090}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_CJB110}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_18RS21}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_2603}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_A909}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_H36B}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_JM9130013}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_1169NT}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
msa13607.2{201_M732}	TATGTCAGCC	GTCTCTACGT	TGCATGGGCA	ACAACACCAC	AGATGCGAAA
Consensus	*****	*****	*****	*****	*****
801					
msa13607.2{201_COH1}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_M781}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
msa13607.2{201_090}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_CJB110}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_18RS21}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_2603}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC
msa13607.2{201_A909}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGc	ATGTTACGTC

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_H36B}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_JM9130013}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_1169NT}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	aaAACTTGGc	ATGTTACGTC
msa13607.2{201_M732}	CTTGGTCAAA	GTATCGTCAG	ATATGCGTCA	gAAACTTGGt	ATGTTACGTC
Consensus	*****	*****	*****	-*****-	*****
	851				900
msa13607.2{201_COH1}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M781}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_090}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_CJB110}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_18RS21}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_2603}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_A909}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_H36B}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_JM9130013}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_1169NT}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
msa13607.2{201_M732}	GAAATACCAT	TCCAACAATG	AAACTCTCAA	TCGCTCAGTT	AGGCATGATG
Consensus	*****	*****	*****	*****	*****
	901				950
msa13607.2{201_COH1}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M781}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_090}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_CJB110}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_18RS21}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_2603}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_A909}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_H36B}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_JM9130013}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_1169NT}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
msa13607.2{201_M732}	CAACAATCTG	TCAAATCCGG	TGTCAGTCTG	GATGCTATTG	TCAACGCTAA
Consensus	*****	*****	*****	*****	*****
	951				1000
msa13607.2{201_COH1}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M781}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_090}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_CJB110}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_18RS21}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_2603}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_A909}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_H36B}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_JM9130013}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_1169NT}	TAATGCAGCA	TTGCAgATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
msa13607.2{201_M732}	TAATGCAGCA	TTGCAaATGC	TGGCTGAAAC	TAGTAAAGAA	GCGATTCCGA
Consensus	*****	*****-*****	*****	*****	*****
	1001				1050
msa13607.2{201_COH1}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M781}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_090}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_CJB110}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_18RS21}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_2603}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_A909}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_H36B}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_JM9130013}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_1169NT}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
msa13607.2{201_M732}	TGTTAGAGAA	GACCGCACAA	AGCCCCACTG	TTTCTATTAA	ATCTGTCACT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa13607.2{201_COH1}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_M781}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_090}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_CJB110}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_18RS21}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_2603}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_A909}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_H36B}	GCATTAtCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_JM9130013}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
msa13607.2{201_1169NT}	GCATTAgCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT

Table 52: Comparative Sequences relating to SAG 1823

msa13607.2{201_M732}	GCATTAGCTG	AAAGCTTAGT	GGCTCAAAAT	AATGGTATTA	TCGCTGCCAT
Consensus	*****_***	*****	*****	*****	*****
	1101				1150
msa13607.2{201_COH1}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M781}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_090}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_CJB110}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_18RS21}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_2603}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	gGAATCTGCT	GTTATTAAAT
msa13607.2{201_A909}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_H36B}	AGACAAAGGA	CGTAAaGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_JM9130013}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_1169NT}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
msa13607.2{201_M732}	AGACAAAGGA	CGTAAgGAAC	GTGCCCAATT	aGAATCTGCT	GTTATTAAAT
Consensus	*****	*****_****	*****	*****	*****
	1151				1200
msa13607.2{201_COH1}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M781}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_090}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_CJB110}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_18RS21}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_2603}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_A909}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_H36B}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_JM9130013}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_1169NT}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
msa13607.2{201_M732}	CGGCTGAAAC	AATCAATGAT	TCTGTCAAAA	TTCGTGATAA	AAAAATAGTT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa13607.2{201_COH1}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M781}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_090}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_CJB110}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_18RS21}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_2603}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_A909}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_H36B}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_JM9130013}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_1169NT}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
msa13607.2{201_M732}	GAAGCCTTAC	TCAACGAAGG	TAAATCTACC	CAAGAAAAAG	ttgatgagtc
Consensus	*****	*****	*****	*****	-----
	1251				
msa13607.2{201_COH1}	t				
msa13607.2{201_M781}	t				
msa13607.2{201_090}	t				
msa13607.2{201_CJB110}	t				
msa13607.2{201_18RS21}	t				
msa13607.2{201_2603}	t				
msa13607.2{201_A909}	t				
msa13607.2{201_H36B}	t				
msa13607.2{201_JM9130013}	t				
msa13607.2{201_1169NT}	t				
msa13607.2{201_M732}	~				
Consensus	-				

SEQ ID NO. 5212

STRAIN_090 frame: 1

SDTFNFDIDQIADNATTKDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIKAKYKDA
TPAELEKPNLQKLFQKSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSYQIKSNQLARMTEV
INTLEQQHTEYVSRLVAVWATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAIVNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLESAAVSKAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 52013

STRAIN_A909 frame: 1

SDTFNFDIDQIADNATTKDKTTEIISNQTTSQTGQIAFFEKLTPAQKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIKAKYKDA
TPAELEKPNLQKLFQKSKTSLQEFYFDSQNIIEQKMDMMAANVVKQEDTLARNIVSAEM

Table 52: Comparative Sequences relating to SAG 1823

LIEDNTKSIENLVGVXAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5214

STRAIN H36B frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5215

STRAIN 18RS21 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHPEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5216

STRAIN M732 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVD
TFVGDQNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDA
TPAELEKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEV
INTLEQQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEK

SEQ ID NO. 5217

STRAIN COH1 frame: 3

KTDKTEIISNQTTCQTGQIAFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAI VNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5218

STRAIN COH1 frame: 3

KTDKTEIISNQTTCQTGQIAFFEKLTAPAKSAXSEKTPALVDTFVGDQNALLDGQSAV
EGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLIQKLFK
QSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEYVSRLYV
AVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTADAI VNAN
NALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGRKERAQ
LES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5219

STRAIN M781 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5220

STRAIN CJB110 frame: 2

FDIDQIADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVDTFVGD
QNALLDGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAEL
EKKPNLIQKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLE
QQHTEYVSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVK
SGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIA
AIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5221

STRAIN 1169NT frame: 1

ADNAITKTDKTEIISNQTTSQTGQIAFFEKLTAPAKSAISEKTPALVDTFVGDQNALLD
FGQSAVEGVNTTVNHILSEQKKIQIPQVDDLLKNANRELNGFIAKYKDATPAELEKKPNLI
QKLFQSKTSLQEFYFDSQNI EQKMDMMAANVVKQEDTLARNIVSAEM
LIEDNTKSIENLVGVIAFIESSQAEANRASHLQOEILALDSQTSEYQIKSNQLARMTEVINTLEQQHTEY
VSRLYVAVATTPOMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMMQQSVKSGVTAD
AI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQNNGIIAAIDKGR

Table 52: Comparative Sequences relating to SAG 1823

KERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5222

STRAIN JM9130013 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTTPAQKSAISEKTPALVD
 TFVGDQNALDQFQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA
 TPAELEKKPNLIQKLFQKSKTSQEFYFDSQNIQKMDMMANVVKQEDTLARNIVSAEM
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
 INTLEQQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

SEQ ID NO. 5223

STRAIN 2603 frame: 1

SDTFNFDIDQIADNAITKTDKTEIISNQTTSTGTGQIAFFEKLTTPAQKSAISEKTPALVD
 TFVGDQNALDQFQSAVEGVNTTVNHILSEQKKIIPQVDDLLKNANRELNGFIAKYKDA
 TPAELEKKPNLIQKLFQKSKTSQEFYFDSQNIQKMDMMANVVKQEDTLARNIVSAEM
 LIEDNTKSIENLVGVIAFIESSQAEANRASHLQQEILALDSQTSEYQIKSNQLARMTEV
 INTLEQQHPEYVSRLYVAWATTPQMRNLVKVSSDMRQKLGMLRRNTIPTMKLSIAQLGMM
 QQSVKSGVTADAI VNANNAALQMLAETSKEAIPMLEKTAQSPTVSIKSVTALAESLVAQN
 NGIIAAIDKGRKERAQLES AVIKSAETINDSVKIRDKKIVEALLNEGKSTQEKVDES

PRETTY of: /biotmp/msa28369.2{*} April 22, 2002 04:27 ..

	1				50
msa28369.2{201_090}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_1169NT}	-----	-adnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_A909}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_JM9130013}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_COH1}	-----	-----KTD	KTTEIISNQT	TcQTGQIAFF	EKLTPAQKSA
msa28369.2{201_CJB110}	-----fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M781}	-----fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_2603}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_H36B}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_18RS21}	-----fdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
msa28369.2{201_M732}	sdtfnfdidq	iadnaitKTD	KTTEIISNQT	TsQTGQIAFF	EKLTPAQKSA
Consensus	-----	-----*	*****	*-----	*****
	51				100
msa28369.2{201_090}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_1169NT}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_A909}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_JM9130013}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_COH1}	xSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_CJB110}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M781}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_2603}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_H36B}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_18RS21}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
msa28369.2{201_M732}	iSEKTPALVD	TFVGDQNAL	DFGQSAVEGV	NTTVNHILSE	QKKIQIPQVD
Consensus	-*****	*****	*****	*****	*****
	101				150
msa28369.2{201_090}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_1169NT}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_A909}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_JM9130013}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_COH1}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_CJB110}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M781}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_2603}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_H36B}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_18RS21}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
msa28369.2{201_M732}	DLLKNANREL	NGFIAKYKDA	TPAELEKKPN	LIQKLFQKSK	TSLQEFYFDS
Consensus	*****	*****	*****	*****	*****
	151				200
msa28369.2{201_090}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_1169NT}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_A909}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_JM9130013}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_COH1}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_CJB110}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M781}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_2603}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_H36B}	QNIQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE

Table 52: Comparative Sequences relating to SAG 1823

msa28369.2{201_18RS21}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
msa28369.2{201_M732}	QNIEQKMDMM	AANVVKQEDT	LARNIVSAEM	LIEDNTKSIE	NLVGVIAFIE
Consensus	*****	*****	*****	*****	*****
msa28369.2{201_090}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_1169NT}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_A909}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_JM9130013}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_COH1}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_CJB110}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M781}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_2603}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_H36B}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_18RS21}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
msa28369.2{201_M732}	SSQAEAAANRA	SHLQQEILAL	DSQTSEYQIK	SNQLARMTEV	INTLEQQHtE
Consensus	*****	*****	*****	*****	*****
msa28369.2{201_090}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_1169NT}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_A909}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_JM9130013}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_COH1}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_CJB110}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M781}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_2603}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_H36B}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_18RS21}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
msa28369.2{201_M732}	YVSRLYVAWA	TTPQMRNLVK	VSSDMRQKLG	MLRRNTIPTM	KLISIAQLGMM
Consensus	*****	*****	*****	*****	*****
msa28369.2{201_090}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_1169NT}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_A909}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_JM9130013}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_COH1}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_CJB110}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M781}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_2603}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_H36B}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_18RS21}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
msa28369.2{201_M732}	QOSVKSQVTA	DAIVNANNAA	LQMLAETSKE	AIPMLEKTAQ	SPTVSIKSVT
Consensus	*****	*****	*****	*****	*****
msa28369.2{201_090}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_1169NT}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_A909}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_JM9130013}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_COH1}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_CJB110}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M781}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_2603}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_H36B}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_18RS21}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
msa28369.2{201_M732}	ALaESLVAQN	NGIIAAIDKG	RKERAQLESA	VIKSAETIND	SVKIRDKKIV
Consensus	*****	*****	*****	*****	*****
msa28369.2{201_090}	EALLNEGKST	QEKvdes			
msa28369.2{201_1169NT}	EALLNEGKST	QEKvdes			
msa28369.2{201_A909}	EALLNEGKST	QEKvdes			
msa28369.2{201_JM9130013}	EALLNEGKST	QEKvdes			
msa28369.2{201_COH1}	EALLNEGKST	QEKvdes			
msa28369.2{201_CJB110}	EALLNEGKST	QEKvdes			
msa28369.2{201_M781}	EALLNEGKST	QEKvdes			
msa28369.2{201_2603}	EALLNEGKST	QEKvdes			
msa28369.2{201_H36B}	EALLNEGKST	QEKvdes			
msa28369.2{201_18RS21}	EALLNEGKST	QEKvdes			
msa28369.2{201_M732}	EALLNEGKST	QEKvdes			
Consensus	*****	*****			

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5301

STRAIN 2603

acaaataactttgaaaaaagaatttagttgaagctaaaaagacaattccatc
cgtaaaagcttcaaaagtaccgcaaaaatcaacatcatcgaaagataaag
agtttgttcttaaacgattatcgatgtctctggttggcaacttcctaag
gagattgattacgatacgctttcaaaaaatatttcaggtgtgttatttcg
tgtctttggtggatcaaagatatctaaagactaataacgctgcttataca
ctggaatcgataaatacggtttaagaccatatacaagaatttcaaaagcga
aatatcccagtagctgtctacagttatgcacttgggttcaagtggttaaaga
aatgaaagaagaggctcagatatatttataagaatgcagctccttacaac
caactttttattggattgacgtagaagaggagacaatgtctaactgaat
aaaggtgtccaagcattccgaaagaattaaaaagacttgggtgctaaaaa
tggtggtatctacattgggtacttactttatgactgagcaaggcatctctg
taaaaggatttgacgctgttttggtatccaacttatggtagcgattctgga
tactatgaagcggtccgcaaaactgaacttaaatacgatttacaccaata
cacctctcaaggttatctaccaggawtcaatcaaccgcttgatttaaatc
aaattgcagttataaagacaagaagaaaacttatgagaaacttttggga
aaagtaaaagag

SEQ ID NO. 5302

STRAIN 090

ACAAATACTTTGAAAAAAGAATTAG
TTGAAGCTAAAAAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAAGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC
CCATATCAAGAATTTCAAAGCGAATATCCAGTAGCTGTCTACAGTT
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAAGATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT
TCCAACCTTATGGTAGCGATTCTGGATACATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5303

STRAIN A909

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA
AGACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCA
TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTG
GCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAATAATTTTCA
GTGTTGTATTATTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
GCTGCTTATACAACTGGAATCGATAAATCGTTTAAGACCCATATCAAAGA
ATTTCAAAGCGAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT
CAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTTTATAAGAAATGCA
GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAAT
GTCTAAGATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATTAAGAAGAC
TTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAG
CAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGATTCCAACCTTATGG
TAGCGATTCTGGATACATGAAGCGGCTCCGCAAACTGAACCTTAAATACG
ATTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
CTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAACCTATGA
GAAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5304

STRAIN H36B

ACAAATACTTTGAAAAAAGAATTAG
TTGAAGCTAAAAAGACAATCCATCCGTAAAAGCTTCAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGA
TGTCTCTGTTGGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAAGTGTGTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAGAC
CCATATCAAGAATTTCAAAGCGAATATCCAGTAGCTGTCTACAGTT
ATGCACCTTGGTTCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAAGATGCAGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAAGGATTGACGCTGTTTGGAT
TCCAACCTTATGGTAGCGATTCTGGATACATGAAGCGGCTCCGCAAACTG
AACTTAAATACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTAAATCAAATTGCAGTTAATAAAGACAAGAA
GAAACCTTATGAGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5305

STRAIN 18R521

ACAAATACTTTGAAAAAAGAATTAGTTGAAGCTAAAA
GACAAATCCATCCGTAAAAGCTTCAAAGTACCGCAAAATCAACATCAT
CGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGTTGG
CAACTTCTAAGGAGATTGATTACGATACGCTTTCAAATAATATTTCAGG
TGTTGTTATTCGTGTCTTTGGTGGATCAAAGATATCTAAGACTAATAACG

Table 53: Comparative Sequences relating to SAG 0755

CTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGAA
 TTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTC
 AAGTGTAAAGAAATGAAAGAAGAGGCTCAGATAATTTATAAGAAATGCAG
 CTCCTTACAAACCAACTTTTATTTGGATTGACGTAGAAGAGGAGACAATG
 TCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAAATAAAAAGACT
 TGGTGCTAAAAATGTTGGTATCTACATTGGTACTTACTTTATGACTGAGC
 AAGGCATCTCTGTAAGAGGATTGACGCTGTTGGATTCCAACCTTATGGT
 AGCGAATTCGGATACTATGAAGCGGCTCCGCAAACTGAACTTAAATACGA
 TTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGC
 TTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTATGAG
 AAACCTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5306
 STRAIN M732

ACAAATACCTTTGAAAAAAGAATTAGTTGAAGCTAAA
 AAGACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
 GGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA
 GGTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATAATTTATAAGAATGC
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
 GCAAGGTATCTCTGTAAAGGATTGACGCTGTTGGATTCCAACCTTATG
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
 GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5307
 STRAIN COH1

ACAAATACCTTTGAAAAAAGAATTAGTTGAAGCTAAA
 AGACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATCA
 TCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTG
 GCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA
 GTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAAC
 GCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAGA
 ATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTT
 CAAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATAATTTATAAGAATGCA
 GCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAT
 GTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGAC
 TTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAG
 CAAGGTATCTCTGTAAAGGATTGACGCTGTTGGATTCCAACCTTATGG
 TAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATACG
 ATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCG
 CTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATGA
 GAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5308
 STRAIN M781

ACAAATACCTTTGAAAAAAGAATTAGTTGAAGCTAAA
 AAGACAATTCATCCGTAAAAGCTTCAAAGTACCGCAAAAATCAACATC
 ATCGAAAGATAAAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTT
 GGCAACTTCCTAAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCA
 GGTGTTGTTATTCGTATCTTTGGTGGATCAAAGATATCTAAGACTAATAA
 CGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGACCCATATCAAAG
 AATTTCAAAGCGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGT
 TCAAGTGTAAAGAAATGAAAGAAGAGGCTCAGATAATTTATAAGAATGC
 AGCTCCTTACAAACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAA
 TGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAGAGTTAAAAAGA
 CTGGTGCTAAAAATGTTGGTATCTACATCGGTACTTACTTTATGACTGA
 GCAAGGTATCTCTGTAAAGGATTGACGCTGTTGGATTCCAACCTTATG
 GTAGCGATTCTGGATACTATGAAGCAGCTCCACAACTGAACTTAAATAC
 GATTTACACCAATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACC
 GCTTGATTTAAATCAAATTGCAGTTAATAAAGACAAGAAGAAAACCTTATG
 AGAACTTTTGGAAAAGTAAAAGAG

SEQ ID NO. 5309
 STRAIN CJB110

AAATACCTTTGAAAAAAGAATTAGTTGAAGCTAAAAGACAATTCATCCG
 TAAAGCTTCAAAGTACCGCAAAAATCAACATCATCGAAAGATAAAGAG
 TTTGTTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCTAAGGA
 GATTGATTACGATACGCTTTCAAAAAATATTTCAAGGTGTTGTTATTCGTG
 TCTTTGGTGGATCAAAGATATCTAAGACTAATAACGCTGCTTATCAACT
 GGAATCGATAAATCGTTTAAAGACCCATATCAAAGAATTTCAAAGCGGAA
 TATCCCAAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAAAGAAA
 TGAAGAAGAGGCTCAGATAATTTATAAGAATGCAGCTTCTTACAAACCA
 ACTTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATGAATAA
 AGGTGTCGAAGCATTCCGAAAAGAAATTAAGAAAGACTTGGTGCTAAAAATG
 TTGGTATCTACATTTGGTACTTACTTTATGACTGAGCAAGGCATCTCTGTA
 AAAGGATTGACGCTGTTTGGATTCCAACCTTATGGTAGCGATTCTGGATA

Table 53: Comparative Sequences relating to SAG 0755

CTATGAAGCGGCTCCGCAAACTGAACCTAAATACGATTTACACCAATACA
CCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAAATCAA
ATTACAGTTAATAAGACAAGAAGAAACTTTATGAGAAACTTTTGGAAA
AGTAAAGAG

SEQ ID NO. 5310

STRAIN 1169NT

ACAAATACCTTTGAAAAAGAATTAGTTGAAGCTAAAAAGACAATTCC
ATCCGTAAAGCTTCAAAAGTACCGCAAAATCAACATCATCGAAAGATA
AAGAGTTTGTCTTAAACCGATTATCGATGTCTCTGGTTGGCAACTTCCT
AAGGAGATTGATTACGATACGCTTTCAAAAAATATTTCAGGTGTTGTTAT
TCGTGTCTTTGGTGGATCAAGATATCTAAGACTAATAACGCTGCTTATA
CAACTGGAATCGATAAATCCTTTAAGACCCATATCAAGAATTTCAAAAG
CGAAATATCCAGTAGCTGTCTACAGTTATGCACTTGGTTCAAGTGTAA
AGAAATGAAAGAGAGGCTCAGATATTTATAAGATGCAAGCTCCTTACA
AACCAACTTTTATTGGATTGACGTAGAAGAGGAGACAATGTCTAACATG
AATAAAGGTGTCCAAGCATTCCGAAAAGAATTAAAAAGACTTGGCGCTAA
AAATGTTGGTATCTACATCGGTACTTACTTTATGACTGAGCAAGGTATCT
CTGTAAAGGATTGACGCTGTTTGGATTCCAACCTATGGTAGCGATTCT
GGATATCTGAAAGCAGCTCCGCAAACTGAACTTAAATACGATTTACACCA
ATACACCTCTCAAGGTTATCTACCAGGATTCAATCAACCGCTTGATTTAA
ATCAAATTGCAGTTAATAAGACAAGAAGAAACTTTATGAGAACTTTTT
GGAAAAGTAAAGAG

SEQ ID NO. 5311

STRAIN JM9130013

ACAAATACCTTTGAAAAAGAATTAG
TTGAAGCTAAAAAGACAATTCCATCCGTAAAGCTTCAAAAGTACCGCAA
AAATCAACATCATCGAAAGATAAAGAGTTGTTCTTAAACCGATTATCGA
TGTTCTCTGGTTGGCAACTTCTAAGGAGATTGATTACGATACGCTTTCAA
AAAATATTTCAAGGTGTTGTTATTCTGTCTTTGGTGGATCAAAGATATCT
AAGACTAATAACGCTGCTTATACAACTGGAATCGATAAATCGTTTAAAGAC
CCATATCAAAGAATTTCAAAAGCGAAATATCCAGTAGCTGTCTACAGTT
ATGCACCTTGGTTCAAGTGTTAAAGAAATGAAAGAAGAGGCTCAGATATTT
TATAAGAAATGCAGCTCCTTACAAACCACTTTTTATTGGATTGACGTAGA
AGAGGAGACAATGTCTAACATGAATAAAGGTGTCCAAGCATTCCGAAAAG
AATTAAAAAGACTTGGTGCTAAAAATGTTGGTATCTACATTGGTACTTAC
TTTATGACTGAGCAAGGCATCTCTGTAAAGGATTGACGCTGTTTGGAT
TCCAACCTATGGTAGCGATTCTGATACCTATGAAGCGGCTCCGCAAACTG
AATCTAATAACGATTACACCAATACACCTCTCAAGGTTATCTACCAGGA
TTCAATCAACCGCTTGATTTAAATCAAATTGCAGTTAATAAGACAAGAA
GAAACTTATGAGAACTTTTTGGAAAAGTAAAGAG

PRETTY of: /biotmp/msa21441.2{*} January 20, 2003 03:46 ...

	1				50
msa21441.2{206_090}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_18RS21}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_2603}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_A909}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_H36B}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_JM9130013}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_CJB110}	--AAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_COH1}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_M732}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_M781}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
msa21441.2{206_1169NT}	acAAATACCTT	TGAAAAAGA	ATTAGTTGAA	GCTAAAAAGA	CAATTCATC
Consensus	--*****	*****	*****	*****	*****
	51				100
msa21441.2{206_090}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_18RS21}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_2603}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_A909}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_H36B}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_JM9130013}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_CJB110}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_COH1}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M732}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_M781}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
msa21441.2{206_1169NT}	CGTAAAGCT	TCAAAAGTAC	CGCAAAATC	AACATCATCG	AAAGATAAAG
Consensus	*****	*****	*****	*****	*****
	101				150
msa21441.2{206_090}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_18RS21}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_2603}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_A909}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_H36B}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_JM9130013}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_CJB110}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_COH1}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG
msa21441.2{206_M732}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M781}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG		
msa21441.2{206_1169NT}	AGTTTGTCT	TAAACCGATT	ATCGATGTCT	CTGGTTGGCA	ACTTCCTAAG		
Consensus	*****	*****	*****	*****	*****		
msa21441.2{206_090}	151	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	200
msa21441.2{206_18RS21}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_2603}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_A909}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_H36B}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_JM9130013}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_CJB110}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_COH1}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_M732}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_M781}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
msa21441.2{206_1169NT}	GAGATTGATT	ACGATACGCT	TTCAAAAAAT	ATTTTCAGGTG	TTGTTATTTCG	TTGTTATTTCG	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	201	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	250
msa21441.2{206_18RS21}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_2603}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_A909}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_H36B}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_JM9130013}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_CJB110}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_COH1}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_M732}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_M781}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
msa21441.2{206_1169NT}	TgTCTTTGGT	GGATCAAAGA	TATCTAAGAC	TAATAACGCT	GCTTATACAA	GCTTATACAA	
Consensus	*-*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	251	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	300
msa21441.2{206_18RS21}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_2603}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_A909}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_H36B}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_JM9130013}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_CJB110}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_COH1}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_M732}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_M781}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
msa21441.2{206_1169NT}	CTGGAATCGA	TAAATCGTTT	AAGACCCATA	TCAAAGAATT	TCAAAAGCGA	TCAAAAGCGA	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	301	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	350
msa21441.2{206_18RS21}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_2603}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_A909}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_H36B}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_JM9130013}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_CJB110}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_COH1}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_M732}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_M781}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
msa21441.2{206_1169NT}	AATATCCCAG	TAGCTGTCTA	CAGTTATGCA	CTTGGTTCAA	GTGTTAAAGA	GTGTTAAAGA	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	351	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	400
msa21441.2{206_18RS21}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_2603}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_A909}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_H36B}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_JM9130013}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_CJB110}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_COH1}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_M732}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_M781}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
msa21441.2{206_1169NT}	AATGAAAGAA	GAGGCTCAGA	TATTTTATAA	GAATGCAGCT	CCTTACAAAC	CCTTACAAAC	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	401	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	450
msa21441.2{206_18RS21}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_2603}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_A909}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_H36B}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_JM9130013}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_CJB110}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	
msa21441.2{206_COH1}	CAACTTTTAA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT	TAACATGAAT	

Table 53: Comparative Sequences relating to SAG 0755

msa21441.2{206_M732}	CAACCTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT		
msa21441.2{206_M781}	CAACCTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT		
msa21441.2{206_1169NT}	CAACCTTTTTA	TTGGATTGAC	GTAGAAGAGG	AGACAATGTC	TAACATGAAT		
Consensus	*****	*****	*****	*****	*****		
msa21441.2{206_090}	451	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	500
msa21441.2{206_18RS21}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_2603}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_A909}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_H36B}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_JM9130013}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_CJB110}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_COH1}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_M732}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_M781}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
msa21441.2{206_1169NT}	AAAGGTGTCC	AAGCATTCCG	AAAAGAaTTA	AAAAGACTTG	GtGCTAAAAA	GtGCTAAAAA	
Consensus	*****	*****	*****-***	*****	*-*****		
msa21441.2{206_090}	501	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	550
msa21441.2{206_18RS21}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_2603}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_A909}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_H36B}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_JM9130013}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_CJB110}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_COH1}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_M732}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_M781}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
msa21441.2{206_1169NT}	TGTTGGTATC	TACATtGGTA	CTTACTTTAT	GACTGAGCAA	GGcATCTCTG	GGcATCTCTG	
Consensus	*****	*****-***	*****	*****	*****	**-*****	
msa21441.2{206_090}	551	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	600
msa21441.2{206_18RS21}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_2603}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_A909}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_H36B}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_JM9130013}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_CJB110}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_COH1}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_M732}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_M781}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
msa21441.2{206_1169NT}	TAAAAGGATT	TGACGCTGTT	TGGATTCCAA	CTTATGGTAG	CGATTCTGGA	CGATTCTGGA	
Consensus	*****	*****	*****	*****	*****	*****	
msa21441.2{206_090}	601	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	650
msa21441.2{206_18RS21}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_2603}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_A909}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_H36B}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_JM9130013}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_CJB110}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_COH1}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_M732}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_M781}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
msa21441.2{206_1169NT}	TACTATGAAG	CgGCTCCgCA	AACtGAACtT	AAATACGATT	TACACCAATA	TACACCAATA	
Consensus	*****	*-*****-*	*****	*****	*****	*****	
msa21441.2{206_090}	651	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	700
msa21441.2{206_18RS21}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_2603}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_A909}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_H36B}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_JM9130013}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_CJB110}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_COH1}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_M732}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_M781}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
msa21441.2{206_1169NT}	CACCTCTCAA	GGTTATCTAC	CAGGAtTCAA	TCAACCGCTT	GATTtAAATC	GATTtAAATC	
Consensus	*****	*****	*****-****	*****	*****	*****	
msa21441.2{206_090}	701	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	750
msa21441.2{206_18RS21}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	
msa21441.2{206_2603}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	
msa21441.2{206_A909}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	
msa21441.2{206_H36B}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	
msa21441.2{206_JM9130013}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	
msa21441.2{206_CJB110}	AAATTgCAGT	TAATAAAGAC	AAGAAGAAAA	CTTATGAGAA	ACTTTTTGGA	ACTTTTTGGA	

Table 53: Comparative Sequences relating to SAG 0755

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msa21441.2{206_COH1} AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M732} AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_M781} AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
msa21441.2{206_1169NT} AAATTgCAGT TAATAAAGAC AAGAAGAAAA CTTATGAGAA ACTTTTGGGA
Consensus *****-***** ***** ***** ***** ***** *****

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msa21441.2{206_090} 751 762
msa21441.2{206_18RS21} AAAGTAAAAG AG
msa21441.2{206_2603} AAAGTAAAAG AG
msa21441.2{206_A909} AAAGTAAAAG AG
msa21441.2{206_H36B} AAAGTAAAAG AG
msa21441.2{206_JM9130013} AAAGTAAAAG AG
msa21441.2{206_CJB110} AAAGTAAAAG AG
msa21441.2{206_COH1} AAAGTAAAAG AG
msa21441.2{206_M732} AAAGTAAAAG AG
msa21441.2{206_M781} AAAGTAAAAG AG
msa21441.2{206_1169NT} AAAGTAAAAG AG
Consensus ***** **

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SEQ ID NO. 5312
 STRAIN 2603 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGXNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5313
 STRAIN 090 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5314
 STRAIN A909 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5315
 STRAIN H36B frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5316
 STRAIN 18RS21 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5317
 STRAIN M732 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5318
 STRAIN COH1 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

SEQ ID NO. 5319
 STRAIN M781 frame: 1
 TNTLKKELVEAKKTIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEIDYDTLSKN
 ISGVVIRVFGGSKI SKTNNAAYTTGIDKSFKTHIKEFQKRNI PVAVYSYALGSSVKEMKE
 EAQIFYKNAAPYKPTFFYWDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
 GISVKGFDVAVWIPYTGSDSGYYEAPQTELKYDLHQYTSQGYLPGFNQPLDLNQIAVNKD
 KKKTYEKLFGKVKE

Table 53: Comparative Sequences relating to SAG 0755

SEQ ID NO. 5320

STRAIN CJB110 frame: 2

NTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE
AQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQG
ISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQYTSQGYLPGFNQPLDLNQTIVNKDK
KKITYEKLFGKVKE

SEQ ID NO. 5321

STRAIN 1169NT frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQYTSQGYLPGFNQPLDLNQTIVNKD
KKITYEKLFGKVKE

SEQ ID NO. 5322

STRAIN JM9130013 frame: 1

TNTLKKELVEAKKTIIPSVKASKVPQKSTSSKDKFVLKPIIDVSGWQLPKEDYDTLSKNI
ISGVVIRVFGGSKISKTNNAAYTTGIDKSFKTHIKEFQKRNIIPVAVYSYALGSSVKEMKEE
EAQIFYKNAAPYKPTFYWIDVEEETMSNMNKGVAFRKELKRLGAKNVGIYIGTYFMTEQ
GISVKGFDVAVWIPTYGSDSGYEAAPQTELKYLHQYTSQGYLPGFNQPLDLNQTIVNKD
KKITYEKLFGKVKE

PRETTY of: /biotmp/msa21641.2{*} January 20, 2003 03:59 ..

	1		50
msa21641.2{206_090}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_1169NT}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_18RS21}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_2603}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_A909}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_H36B}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_JM9130013}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_COH1}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M732}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_M781}	tNTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
msa21641.2{206_CJB110}	-NTLKKELVE	AKKTIPSVKA	SKVPQKSTSS
Consensus	*****	*****	*****
	51		100
msa21641.2{206_090}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_1169NT}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_18RS21}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_2603}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_A909}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_H36B}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_JM9130013}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_COH1}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M732}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_M781}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
msa21641.2{206_CJB110}	EIDYDTLSKN	ISGVVIRvFG	GSKISKTNNA
Consensus	*****	*****	*****
	101		150
msa21641.2{206_090}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_1169NT}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_18RS21}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_2603}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_A909}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_H36B}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_JM9130013}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_COH1}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M732}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_M781}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
msa21641.2{206_CJB110}	NIPVAVYSYA	LGSSVKEMKE	EAQIFYKNAA
Consensus	*****	*****	*****
	151		200
msa21641.2{206_090}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_1169NT}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_18RS21}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_2603}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_A909}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_H36B}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_JM9130013}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_COH1}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M732}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_M781}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
msa21641.2{206_CJB110}	KGVAFRKEL	KRLGAKNVGI	YIGTYFMTEQ
Consensus	*****	*****	*****

Table 53: Comparative Sequences relating to SAG 0755

	201		250
msa21641.2{206_090}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_1169NT}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_18RS21}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_2603}	YYEAAPQTEL KYDLHQYTSQ GYLPGxNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_A909}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_H36B}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_JM9130013}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_COH1}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M732}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_M781}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
msa21641.2{206_CJB110}	YYEAAPQTEL KYDLHQYTSQ GYLPGFNQPL DLNQIaVNKD KKKTYEKLFG		
Consensus	*****	*****	*****
	251		
msa21641.2{206_090}	KVKE		
msa21641.2{206_1169NT}	KVKE		
msa21641.2{206_18RS21}	KVKE		
msa21641.2{206_2603}	KVKE		
msa21641.2{206_A909}	KVKE		
msa21641.2{206_H36B}	KVKE		
msa21641.2{206_JM9130013}	KVKE		
msa21641.2{206_COH1}	KVKE		
msa21641.2{206_M732}	KVKE		
msa21641.2{206_M781}	KVKE		
msa21641.2{206_CJB110}	KVKE		
Consensus	****		

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5401

STRAIN 2603

TTGACTCACAAAAATATATTATTAACCATTATATTGGATTATTT
 ATGATTATATTATCAGCATGTGGTATGCTAATAAGGAAATGGCTGGTATTGATAATTGG
 GAACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG
 GGATTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGCTAATGCTGTT
 TTTAAAGAAATACGGTATTTCACTGAAATGGCAGCCTATTAAGTGGGATATGAAAGAACT
 GAACCTTAATAATGGTAAATATAGACCTTATTGGAAATGGTATTCAAAAACGGCAGAACGT
 GCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAA
 ACTTCATCAGATATTAAAGTATTAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
 GGTTTCATCTGGTTTGGATGCTTTAAACGCTAAACCTGATATTTTAAAAAAGTTTGTAAAA
 CGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTTTGATTGATTTAAAAATAAC
 CGTATTGATGGTCTTTTGGATTGATGAAGTTTATGCTAACTATTATTTAAAGCAAGAAGGA
 AATATAAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGA
 GCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAACAGCTTCAT
 AATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGTTTATAGTAAA
 GAA

SEQ ID NO. 5402

STRAIN 090

ATTGGGaaCATTATC

AAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTATG
 GGATTGAAAGCCGTTCTGGTGACTATACCGGCTTTGATATTGATTTAGC
 TAATGCTGTTTAAAGAAATACGGTATTTCACTGAAATGGCAGCCTATTA
 ACTGGGATATGAAAGAACTGAACCTTAATAATGGTAAATATAGACCTTATT
 TGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTTAC
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTCATCAC
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCCAGTCG
 GGTTTCATCTGGTTTGGATGCTTTAATGCTAAACCTGATATTTTAAAAA
 GTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACCTTCACTCAGGCTT
 TGATTGATTTAAAAATAACCGTATTGATGGTCTTTTGGATTGATGAAGTT
 TATGCTAACTATTATTAAAGCAAGAAGGAATATAAAAGCTTATTATT
 TGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGCAAAG
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAACAGCTTCAT
 AATAAGGGAATAATTTCAAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
 TTATAGTAAAGAA

SEQ ID NO. 5403

STRAIN A909

ATTGGG

aACATTATCAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTT
 GTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATAT
 TGATTAGCTAATGCTGTTTAAAGAAATACGGTATTTCACTGAAATGGC
 AGCCTATTAACTGGGATATgAAAGAACTGAACCTTAATAATGGTAAATATA
 GACCTTATTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGT
 CGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAA
 CTTTCATCAGATATTAAAGTATTAAAGGATATGAAGGGGAAAAAACTAGGA
 GCCCAGTCGGGTTTCATCTGGTTTGGATGCTTTTAAACGCTAAACCTGATAT
 TTTAAAAAAGTTTGTAAAGGAAAAGAAGCAGTCAATACGATACCTTCA
 CTTAGGCTTTGATTGATTTAAAAATAACCGTATTGATGGTCTTTTGGATT
 GATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATATAAAAGC
 TTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAG
 CTCGTAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAA
 CAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTTACAAATGGTTTGG
 TGAAGATGTTTATAGTAAAGaa

SEQ ID NO. 5404

STRAIN H36B

ATTGGGAACATTATCAAAGGAAAAGAAAATTACTATTGGATT
 TGATAATACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATA
 CCGGCTTTGATATTGATTTAGCTAATGCTGTTTAAAGAAATACGGTATT
 TCAGTGAATGGCAGCCTATTAAGTGGGATATGAAAGAACTGAACCTTAA
 TAATGGTAAATATAGACCTTATTGGAAATGGTTATTCAAAAACGGCAGAAC
 GTGCTAAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTA
 ATTGTTACTAAAACCTCATCAGATATTAAAGTATTAAAGGATATGAAGGG
 GAAAAAACTAGGAGCCCAGTCGGGTTTCATCTGGTTTGGATGCTTTTAAACG
 CTAACCTGATATTTTAAAAAAGTTTGTAAAGGAAAAGAAGCAGTCAAA
 TACGATACCTTCACTCAGGCTTTGATTGATTTAAAAATAACCGTATTGA
 TGGTCTTTTGGATTGATGAAGTCTATGCTAACTATTATTAAAGCAAGAAG
 GAAATATAAAAGCTTATTATTGTGTAAAACTGCTTATCAAGGAGAAAAAT
 TTTGTAGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAA
 CAAAGCTTTCAACAGCTTCATAATAAGGGGAGATTTCAAAAAATCTCTT
 ACAATATGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5405

STRAIN 18RS21

ATTGGGAACATTA

TCAAAAGGAAAAGAAAATTACTATTGGATTGATAATACTTTTGTTCCTA
 TGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTTA
 GCTAATGCTGTTTAAAGAAATACGGTATTTCACTGAAATGGCAGCCTAT
 TAAGTGGGATATGAAAGAACTGAACCTTAATAATGGTAAATATAGACCTTA
 TTTGGAAATGGTTATTCAAAAACGGCAGAACGTGCTAAAAAAGTCGCTTTT
 ACAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACCTTCATC

Table 54: Comparative Sequences relating to SAG0949

ACATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGT
CGGGTTTCATCTGGTTTGTATGCTTTTAAAGCTAAACCTGATATTTAAAA
AAGTTTGTAAAGGAAAAGAAGCAGTTCAATACGATACTTTCACTCAGGC
TTTGATTGATTTAAAAAATAACCGTATTGATGGTCTTTGATTGATGAAG
TTTATGCTAACTATTATTTAAAGCAAGAAGGAAATATAAAAGCTTATTAT
TTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAA
AGTTGATCGTAGACTAATTGAAAAGATTACAAAGCTTTCAAACAGCTTC
ATAATAAGGGGAGATTCAAATAATCTCTTACAAATGGTTTGGTGAAGAT
GTTTATAGTAAAGAA

SEQ ID NO. 5406

STRAIN M732

ATTGGGAACATTATCAAAGGAAAAAGAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
TAATATAGACCTTATTGGAATGGTTATTCAAACCGGCAGAACCGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACCTTCATCACAATATTAAAGTATTAAAGGATATGAAGGGGAAAA
ACTAGGAGCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAAGCTAAAC
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA
TAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTGA
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTCAAATAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5407

STRAIN COH1

ATTGGGAACATTATCAAAGGAAAAAGAAATTACTATTGGATTGATAA
TACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCT
TTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
TAATATAGACCTTATTGGAATGGTTATTCAAACCGGCAGAACCGTGCTA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
ACTAAAACCTTCATCACAATATTAAAGTATTAAAGGATATGAAGGGGAAAA
ACTAGGAGCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAAGCTAAAC
CTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGAT
ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT
TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATA
TAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTGA
GTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGC
TTTCAAACAGCTTCATAATAAGGGGAGATTCAAATAATCTCTTACAAAT
GGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5408

STRAIN M781

ATTGGGAACATTATCAAAGGAAAAAGAAATTACTATTGGATTGATAA
ATACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGC
TTTGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
GAAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGG
GTAATATAGACCTTATTGGAATGGTTATTCAAACCGGCAGAACCGTGCT
AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGT
TACTAAAACTTCATCACAATATTAAAGTATTAAAGGATATGAAGGGGAAAA
AACTAGGAGCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAAGCTAAAC
CCTGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGA
TACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTC
TTTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAAT
ATAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGT
AGTAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAG
CTTTCAAACAGCTTCATAATAAGGGGAGATTCAAATAATCTCTTACAAAT
TGGTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5409

STRAIN CJB110

ATTGGGAACATTATCAAAGGAAAAAGAAATTACTATTGGATTGATAA
ACTTTTGTTCCTATGGGATTGAAAGTCGTTCTGGTGACTATACCGGCTT
TGATATTGATTAGCTAATGCTGTTTTTAAAGAATACGGTATTTCACTG
AATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACCTTAATAATGGT
AATATAGACCTTATTGGAATGGTTATTCAAACCGGCAGAACCGTGCTAA
AAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTTA
CTAAAACCTTCATCACAATATTAAAGTATTAAAGGATATGAAGGGGAAAA
CTAGGAGCCAGTCGGGTTTCATCTGGTTTGTATGCTTTTAAAGCTAAAC
TGATATTTTAAAAAAGTTTGTAAAGGAAAAAGAGCAGTTCAATACGATA
CTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCTT
TTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAAGGAAATAT
AAAAGCTTATTATTTTGTAAAACTGCTTATCAAGGAGAAAAATTTGTAG
TAGGAGCTCGTAAAGTTGATCGTAGACTAATTGAAAAGATTAAACAAAGCT
TTCAAACAGCTTCATAATAAGGGGAGATTCAAATAATCTCTTACAAATG
GTTTGGTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5410

Table 54: Comparative Sequences relating to SAG0949

STRAIN 1169NT
 ATTGGGAACATTATCAAAAGGAAAAGAAAATTACTATTGGATTGATAA
 TACTTTTGTTCCTATGGGATTGAAAAGTCGTTCTGGTGACTATACCGGCT
 TTGATATTGATTAGCTAATGCTGTTTTTAAAGAAATACGGTATTTCAAGTG
 AAATGGCAGCCTATTAACTGGGATATGAAAGAACTGAACTCAATAATGG
 TAATATAGACCTTATTGGGAATGGTTATTCAAAAACGGCAGAACGTCCTA
 AAAAAAGTCGCTTTTACAAACCCATATATGAATAATCATCAAGTAATTGTT
 ACTAAACTTCATCACATATTAAATAGTATTAAAGGATATGAAGGGAAAAA
 ACTAGGAGCCAGTCGGGTTTCATCTGGTTTTGATGCTTTTAATGCTAAAC
 CTGACATTTTAAAAAAGTTTGTAAAGGAAAAGAGCAGTTCAATACGAT
 ACTTTCACTCAGGCTTTGATTGATTAAAAAATAACCGTATTGATGGTCT
 TTTGATTGATGAAGTTTATGCTAACTATTATTAAAGCAAGAGGAAATA
 TAAAAGCTTATTATTGTTTAAACTGCTTATCAAGGAGAAAAATTTGTA
 GTAGGAGCTCGCAAAGTTGATCGTAGACTAATTGAAAAGATTACAAAGC
 TTTCAAACAGCTTCATAATAGGGGAAATTTCAAAAAATCTCTACAAAT
 GGTTCGTTGAAGATGTTTATAGTAAAGAA

SEQ ID NO. 5411
 STRAIN JM9130013
 ATTGGGAACATTATC

AAAAGGAAAAGAAAATTACTATGGATTGATAAATCTTTGTTTCCTATG
 GGATTGAAAAGTCGTTCTGGTGACTATACCGGCTTTGATATTGATTAGC
 TAATGCTGTTTTTAAAGAAATACGGTATTTCAAGTGAATGGCAGCCTATTA
 ACTGGGATATGAAAAGAACTGAACTTAATAATGGTAATATAGACCTTATT
 TGGAAATGGTTATTCAAAACCGGAGAACGTCCTAAAAAAGTCGCTTTTAC
 AAACCCATATATGAATAATCATCAAGTAATTGTTACTAAAACTTCATCAC
 ATATTAAATAGTATTAAAGGATATGAAGGGGAAAAAACTAGGAGCCAGTCG
 GGTTTCATCTGGTTTTGATGCTTTTAAACGCTAAACCTGATATTTAAAAA
 GTTTGTAAAGGAAAAGAGCAGTTCAATACGATACITTTCACTCAGGCTT
 TGATTGATTTAAAAAATAACCGTATTGATGCTTTTGGATTGATGAAGTT
 TATGCTAACTATTATTAAAGCAAGAGGAAATATAAAAGCTTATTATT
 TGTATAAAGCTGCTTATCAAGGAGAAAAATTTGTAGTAGGAGCTCGTAAAG
 TTGATCGTAGACTAATTGAAAAGATTAAACAAAGCTTTCAAACAGCTTCAT
 AATAAGGGGAGATTTCAAAAATCTCTTACAAATGGTTTGGTGAAGATGT
 TTATAGTAAAGAA

PRETTY of: /biotmp/msa39314.2{*} February 18, 2003 11:01 ..

	1				50
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	ttgactcaca	aaaatatatt	attaaccatt	atatttggat	tatttatgat
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa39314.2{225_18RS21}	-----	-----	-----	-----	-----
msa39314.2{225_2603}	tatatattatca	gcatgtggta	tgtctaataa	ggaaatggct	ggatttgata
msa39314.2{225_A909}	-----	-----	-----	-----	-----
msa39314.2{225_CJB110}	-----	-----	-----	-----	-----
msa39314.2{225_COH1}	-----	-----	-----	-----	-----
msa39314.2{225_H36B}	-----	-----	-----	-----	-----
msa39314.2{225_KM9130013}	-----	-----	-----	-----	-----
msa39314.2{225_M732}	-----	-----	-----	-----	-----
msa39314.2{225_M781}	-----	-----	-----	-----	-----
msa39314.2{225_090}	-----	-----	-----	-----	-----
msa39314.2{225_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa39314.2{225_18RS21}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_2603}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_A909}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_CJB110}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_COH1}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_H36B}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_KM9130013}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_M732}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_M781}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_090}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
msa39314.2{225_1169NT}	ATTGGGAACA	TTATCAAAAG	GAAAAGAAAA	TTACTATTGG	ATTGATAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa39314.2{225_18RS21}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT
msa39314.2{225_2603}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGACT	ATACCGGCTT

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_A909}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_CJB110}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_COH1}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_H36B}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_KM9130013}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M732}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_M781}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_090}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
msa39314.2{225_1169NT}	ACTTTTGTTC	CTATGGGATT	TGAAAGtCGT	TCTGGTGA	ATACCGGCTT
Consensus	*****	*****	*****_***	*****	*****
201					
msa39314.2{225_18RS21}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_2603}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_A909}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_CJB110}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_COH1}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_H36B}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_KM9130013}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M732}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_M781}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_090}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
msa39314.2{225_1169NT}	TGATATTGAT	TTAGCTAATG	CTGTTTTTAA	AGAATACGGT	ATTTCAGTGA
Consensus	*****	*****	*****	*****	*****
251					
msa39314.2{225_18RS21}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_2603}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_A909}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_CJB110}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_COH1}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_H36B}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_KM9130013}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M732}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_M781}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_090}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
msa39314.2{225_1169NT}	AATGGCAGCC	TATTAACCTGG	GATATGAAAG	AAACTGAACT	tAATAATGGT
Consensus	*****	*****	*****	*****	*****
301					
msa39314.2{225_18RS21}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_2603}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_A909}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_CJB110}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_COH1}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_H36B}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_KM9130013}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M732}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_M781}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_090}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
msa39314.2{225_1169NT}	AATATAGACC	TTATTTGGAA	TGGTTATTCA	AAAACGGCAG	AACGTGCTAA
Consensus	*****	*****	*****	*****	*****
351					
msa39314.2{225_18RS21}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_2603}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_A909}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_CJB110}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_COH1}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_H36B}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_KM9130013}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M732}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_M781}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_090}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
msa39314.2{225_1169NT}	AAAAGTCGCT	TTTACAAACC	CATATATGAA	TAATCATCAA	GTAATTGTTA
Consensus	*****	*****	*****	*****	*****
401					
msa39314.2{225_18RS21}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_2603}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_A909}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_CJB110}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_COH1}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_H36B}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_KM9130013}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M732}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_M781}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_090}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
msa39314.2{225_1169NT}	CTAAAACTTC	ATCACATATT	AATAGTATTA	AGGATATGAA	GGGGAAAAAA
Consensus	*****	*****	*****	*****	*****
451					
msa39314.2{225_18RS21}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTTT	GATGCTTTTA	AcGCTAAACC

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_2603}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_A909}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_CJB110}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_COH1}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_H36B}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_KM9130013}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M732}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_M781}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_090}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
msa39314.2{225_1169NT}	CTAGGAGCCC	AGTCGGGTTT	ATCTGGTTT	GATGCTTTTA	AcGCTAAACC
Consensus	*****	*****	*****	*****	*****
501					550
msa39314.2{225_18RS21}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_2603}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_A909}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_CJB110}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_COH1}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_H36B}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_KM9130013}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M732}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_M781}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_090}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
msa39314.2{225_1169NT}	TGATATTTTA	AAAAAGTTTG	TAAAAGGAAA	AGAAGCAGTT	CAATACGATA
Consensus	***-*****	*****	*****	*****	*****
551					600
msa39314.2{225_18RS21}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_2603}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_A909}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_CJB110}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_COH1}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_H36B}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_KM9130013}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M732}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_M781}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_090}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
msa39314.2{225_1169NT}	CTTTCACCTCA	GGCTTTGATT	GATTTAAAAA	ATAACCGTAT	TGATGGTCTT
Consensus	*****	*****	*****	*****	*****
601					650
msa39314.2{225_18RS21}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_2603}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_A909}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_CJB110}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_COH1}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_H36B}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_KM9130013}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M732}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_M781}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_090}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
msa39314.2{225_1169NT}	TTGATTGATG	AAGTTTATGC	TAACATTAT	TTAAAGCAAG	AAGGAAATAT
Consensus	*****	*****	*****	*****	*****
651					700
msa39314.2{225_18RS21}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_2603}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_A909}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_CJB110}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_COH1}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_H36B}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_KM9130013}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M732}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_M781}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_090}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
msa39314.2{225_1169NT}	AAAAGCTTAT	TATTTTGTTA	AAACTGCTTA	TCAAGGAGAA	AATTTTGTAG
Consensus	*****	*****	*****	*****	*****
701					750
msa39314.2{225_18RS21}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_2603}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_A909}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_CJB110}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_COH1}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_H36B}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_KM9130013}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M732}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_M781}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_090}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
msa39314.2{225_1169NT}	TAGGAGCTCG	TAAAGTTGAT	CGTAGACTAA	TTGAAAAGAT	TAACAAAGCT
Consensus	*****	*****	*****	*****	*****
751					800

Table 54: Comparative Sequences relating to SAG0949

msa39314.2{225_18RS21}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_2603}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_A909}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_CJB110}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_COH1}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_H36B}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_KM9130013}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M732}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_M781}	TTCAAACAGC	TTCATAATAA	GGGgAgATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_090}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
msa39314.2{225_1169NT}	TTCAAACAGC	TTCATAATAA	GGGgAaATTT	CAAAAAATCT	CTTACAAATG
Consensus	*****	*****	***-*****	*****	*****

	801	828
msa39314.2{225_18RS21}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_2603}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_A909}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_CJB110}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_COH1}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_H36B}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_KM9130013}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M732}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_M781}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_090}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
msa39314.2{225_1169NT}	GTTTGGTGAA	GATGTTTATA GTAAAGAA
Consensus	*****	*****

SEQ ID NO. 5412

STRAIN 2603 frame: 1

LTHKNILLTIIFGLFMIILSACGSMNKEMAGIDNWEHYQKEKKITIGFDNTFVPMGFESR
SGDYTGFDIDLANAVFKEYGISVKWQPINWDMKETLNNGNIDLIWNGYSKTAERAKKVA
FTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQSGSSGFDFAFNAPDILKKFVKGKEAV
QYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQEGNIKAYYFVKITAYQGENFVVGARKVD
RRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYSKE

SEQ ID NO. 5413

STRAIN 090 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5414

STRAIN A909 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5415

STRAIN H36B frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5416

STRAIN 18RS21 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5417

STRAIN M732 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5418

STRAIN COH1 frame: 3

WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHQQIVITKTSSHINSIKDMKGKGLGAQ
SGSSGFDFAFNAPDILKKFVKGKEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLYLKQ
GNIKAYYFVKITAYQGENFVVGARKVDRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

Table 54: Comparative Sequences relating to SAG0949

SEQ ID NO. 5419
STRAIN M781 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ
SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5420
STRAIN CJB110 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ
SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5421
STRAIN 1169NT frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ
SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

SEQ ID NO. 5422
STRAIN JM9130013 frame: 3
WEHYQKEKKITIGFDNTFVPMGFESRSGDYTGFDIDLANAVFKEYGISVKWQPINWDMKE
TELNNGNIDLIWNGYSKTAERAKKVAFTNPYMNHNQVIVTKTSSHINSIKDMKGKGLGAQ
SGSSGDFAFNAKPDILKKFVKGEAVQYDTFTQALIDLKNNRIDGLLIDEVYANYLQKE
GNIKAYYFVKTAQGENFVVGARKVDRRLIEKINKAFKQLHNKGRFQKISYKWFGEDEVYS
KE

PRETTY of: /biotmp/msa45901.2(*) February 19, 2003 03:09 ..

	1				50
msa45901.2{225_090}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_1169NT}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_18RS21}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_2603}	lthknillti	ifglfmiils	acgmsnkema	gidnWEHYQK	EKKITIGFDN
msa45901.2{225_A909}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_CJB110}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_COH1}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_H36B}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_JM9130013}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M732}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
msa45901.2{225_M781}	-----	-----	-----	-----	WEHYQK EKKITIGFDN
Consensus	*****	*****	*****	*****	*****
	51				100
msa45901.2{225_090}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_1169NT}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_18RS21}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_2603}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_A909}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_CJB110}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_COH1}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_H36B}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_JM9130013}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M732}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
msa45901.2{225_M781}	TFVPMGFESR	SGDYTGFDID	LANAVFKEYG	ISVKWQPINW	DMKETELNNG
Consensus	*****	*****	*****	*****	*****
	101				150
msa45901.2{225_090}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_1169NT}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_18RS21}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_2603}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_A909}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_CJB110}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_COH1}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_H36B}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_JM9130013}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M732}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
msa45901.2{225_M781}	NIDLIWNGYS	KTAERAKKVA	FTNPYMNHNQ	VIVTKTSSHI	NSIKDMKGKK
Consensus	*****	*****	*****	*****	*****
	151				200
msa45901.2{225_090}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_1169NT}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_18RS21}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_2603}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_A909}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_CJB110}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGEAV	QYDTFTQALI	DLKNNRIDGL

Table 54: Comparative Sequences relating to SAG0949

msa45901.2{225_COH1}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_H36B}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_JM9130013}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M732}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
msa45901.2{225_M781}	LGAQSGSSGF	DAFNAKPDIL	KKFVKGKEAV	QYDTFTQALI	DLKNNRIDGL
Consensus	*****	*****	*****	*****	*****
201					
msa45901.2{225_090}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_1169NT}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_18RS21}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_2603}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_A909}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_CJB110}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_COH1}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_H36B}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_JM9130013}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M732}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
msa45901.2{225_M781}	LIDEVYANY	LKQEGNIKAY	YFVKTAQGE	NFVVGARKVD	RRLIEKINKA
Consensus	*****	*****	*****	*****	*****
251					
msa45901.2{225_090}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
Consensus	*****	*****	*****		
256					
msa45901.2{225_090}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_1169NT}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_18RS21}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_2603}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_A909}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_CJB110}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_COH1}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_H36B}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_JM9130013}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_M732}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
msa45901.2{225_M781}	FKQLHNKGkF	QKISYKWFG	DVYSKE		
Consensus	*****	*****	*****		

Table 55: Comparative Sequences relating to SAG1592

SEQ ID NO. 5501
STRAIN 2603
ATGCTTAAATCTTTTGTGATTTCTTAGTTCGCTTTTACCAAAAAATATTTCTCCAGCT
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCTTAAGACGTAATAAACGGAT
ATATCAGAT

SEQ ID NO. 5502
STRAIN 090
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTT

SEQ ID NO. 5503
STRAIN A909
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATA

SEQ ID NO. 5504
STRAIN H36B
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5505
STRAIN 18RS21
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5506
STRAIN M732
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5507
STRAIN COH1
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGAAGCTATTCAA
AAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTAATTTGCGATGTCATCCCTTA
GCCACGGAGGAAATGATCCTGTCCCTGATCAITTTAGCT

SEQ ID NO. 5508
STRAIN M781
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5509
STRAIN CJB110
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5510
STRAIN 1169NT
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
TAITTTAGCTTAAGACGTAATAAACGGATATATCAGAT

SEQ ID NO. 5511
STRAIN JM9130013
TTCCCAGCTAGCTGTGCTTATCGTCCAACCTTGCTCTACGTATATGATAGA
AGCTATTCAAAAACATGGTCTAAAAGGTGTGTGATGGGGATTGCACGTA
TTTTGCGATGTCATCCCTTAGCCACGGAGGAAATGATCCTGTCCCTGAT
CATTTTAGCTTAAGACGTAATAAACGGATATATCAGAT

PRETTY of: /biotmp/msa119306.2{*} April 29, 2003 06:23 ..

	1	50
msa119306.2{233_H36B}	-----	-----
msa119306.2{233_JM9130013}	-----	-----

Table 55: Comparative Sequences relating to SAG1592

msa119306.2{233_090}	-----	-----	-----	-----	-----
msa119306.2{233_18RS21}	-----	-----	-----	-----	-----
msa119306.2{233_2603}	atgcttaaat	cttttttgat	tttcttagtt	cgcttttacc	aaaaaaatat
msa119306.2{233_A909}	-----	-----	-----	-----	-----
msa119306.2{233_CJB110}	-----	-----	-----	-----	-----
msa119306.2{233_COH1}	-----	-----	-----	-----	-----
msa119306.2{233_M732}	-----	-----	-----	-----	-----
msa119306.2{233_M781}	-----	-----	-----	-----	-----
msa119306.2{233_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					
msa119306.2{233_H36B}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_JM9130013}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_090}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_18RS21}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_2603}	ttctccagct	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_A909}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_CJB110}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_COH1}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M732}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_M781}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
msa119306.2{233_1169NT}	-----	TTCCAGCTA	GCTGTCGTTA	TCGTCCAAC	TGCTCTACGT
Consensus	*****	*****	*****	*****	*****
101					
msa119306.2{233_H36B}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctTGATGGGG
msa119306.2{233_JM9130013}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	tctTGATGGGG
msa119306.2{233_090}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_18RS21}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_2603}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_A909}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_CJB110}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_COH1}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M732}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_M781}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
msa119306.2{233_1169NT}	ATATGATAGA	AGCTATTCAA	AAACATGGTC	TAAAAGGTGT	gtTGATGGGG
Consensus	*****	*****	*****	*****	-----
151					
msa119306.2{233_H36B}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_JM9130013}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_090}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_18RS21}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_2603}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_A909}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_CJB110}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_COH1}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M732}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_M781}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
msa119306.2{233_1169NT}	ATTGCACGTA	TTTTGCGATG	TCATCCCTTA	GCCCACGGAG	GAAATGATCC
Consensus	*****	*****	*****	*****	*****
201					
msa119306.2{233_H36B}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_JM9130013}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_090}	TGTCCTTGAT	cATTTTAGCT	t-----	-----	-----
msa119306.2{233_18RS21}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_2603}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_A909}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	ata-----
msa119306.2{233_CJB110}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_COH1}	TGTCCTTGAT	cATTTTAGCT	-----	-----	-----
msa119306.2{233_M732}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_M781}	TGTCCTTGAT	cATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
msa119306.2{233_1169NT}	TGTCCTTGAT	tATTTTAGCT	taagacgtaa	taaaacggat	atatcagat
Consensus	*****	*****	-----	-----	-----
249					
SEQ ID NO. 5512					
STRAIN 2603 frame: 1					
MLKSFLIFLVRFYQKNISPAFPASCRRYPTCSTYMIETAIQKHGLKGVLMGIARILRCHPL					
AHGGNDPVPDHFSLRRNKTDISD					
SEQ ID NO. 5513					
STRAIN 090 frame: 1					
FPASCRRYPTCSTYMIETAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5514					
STRAIN A909 frame: 1					
FPASCRRYPTCSTYMIETAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD					
I					
SEQ ID NO. 5515					
STRAIN H36B frame: 1					

Table 55: Comparative Sequences relating to SAG1592

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5516

STRAIN 18RS21 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5517

STRAIN M732 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5518

STRAIN COH1 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD

SEQ ID NO. 5519

STRAIN M781 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5520

STRAIN CJB110 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

SEQ ID NO. 5521

STRAIN 1169NT frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVVMGIARILRCHPLAHGGNDPVPDYFSLRRNKTD
ISD

SEQ ID NO. 5522

STRAIN JM9130013 frame: 1

FPASCRYRPTCSTYMIEAIQKHGLKGVLMGIARILRCHPLAHGGNDPVPDHFSLRRNKTD
ISD

PRETTY of: /biotmp/msa119415.2{*} April 29, 2003 06:25 ..

	1		50
msa119415.2{233_090}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_18RS21}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_COH1}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_A909}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_2603}	mlksfliflv rfyqknispa	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_CJB110}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_H36B}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_JM9130013}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M732}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_M781}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVLMG
msa119415.2{233_1169NT}	-----	FPASCRYRPT	CSTYMIEAIQ KHGLKGVVMG
Consensus	*****	*****	*****-*

	51		83
msa119415.2{233_090}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_18RS21}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_COH1}	IARILRCHPL AHGGNDPVPD	hFS-----	---
msa119415.2{233_A909}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_2603}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_CJB110}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_H36B}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_JM9130013}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_M732}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_M781}	IARILRCHPL AHGGNDPVPD	hFSLRNKT	ISD
msa119415.2{233_1169NT}	IARILRCHPL AHGGNDPVPD	yFSLRNKT	ISD
Consensus	*****	*****	***

Table 56: Comparative Sequences relating to SAG0806

SEQ ID NO. 5601

STRAIN 2603

aagaagcttacttttat ttgggatttagatgggacattaatagattcgta
tgtaccaattttggaagctcttgaaagaacctattcgctcatttgggttaa
tatttgataaagaataatcatgaataattttacaggaatcagtgggg
aaattattgggttaaacctttcagaggaagagcaaatcctcataaaaaact
gaagcattattttcaaaagacaagaagaatcgcgagattctaaatacatt
taatgccatattgcaaaagagattttagaattggaccaagaacaagatc
cccaattttattgtatacacataaaggagcaagctacgcatctcagttgtgga
accttgcagatctctcattatttttgatgaatttttaactggtgtttcgg
gattcgagcgaaaaccacatccacaagggtataattatttgattaaacga
tattctttagataaataatgaatgattattacataggagatcgctcaactga
tttggaggttgctcaaaatgctggtataaaatccataaacttaaggttag
agaattccaagaagaacctataatttttaacgtctcaagatataataatca
cttgatttactcgtttggat

SEQ ID NO. 5602

STRAIN COH1

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAA
TAGATTTCGTATGTACCAATTATGGAAGCTCTGAAGAAACCTATCGTCAT
TTGGCTTAATATTTGATAAAGAATTAATCCATGAATATTTTACAGGA
ATCAGTGGGGCAATTATGGTAAACCTTT CAGAGGAGAGCAAACTCTC
ATGAAAAACTGAAGCATATTTTCAAAAGAACAAGAAAGTCAGATCT
AAAATACATTTAATGCCATATGCAAAAGAGATTTTGAATTTGACCAAAGA
ACAAGATATTTCCCAATTTATGTATACATCAAAAGGCAAGTACGCATT
CAGTGTGTGGAACCTTCGAGATCTCTCATTTTGTATGAAATTTTAAGT
GGTGTTTCCGGATTCGAGCGAAACCAATCACAAAGGGATTAATTTATT
AGTTAAACGATATTTCTTATAGTAATCAATGACTTATCATAGGAGATC
GTCCACTAGATTTGGAGGTTGCTCAAATCTTGGTATATAAATCCATAAC
TTAAGGTTAGAGATACTCAAAGAAACTAATATTTCAAGTCTCAAGA
TATAATATCACTTGATTTCATCGTTTGGAT

SEQ ID NO. 5603

STRAIN A909

STRAIN A309
 AAGAAGCTTACTTTTATTGGGATTAGATGGGACATTAAAT
 AGATTCTGATGTACCAATTATGGAAGCTCTTGAGAACCCTATCGTCATTTTGGTTTAAAT
 ATTGTATAAAGATTAATCCATGATAATATTTTACAGGAATCAGTGGGGAAATATTGGT
 AAACCTTTTCAGAGGAAGAGCAAATCCTCATGAAAAACGTGAAGCATATTTTCAAAAGA
 ACAGAAAGCTCGAGATCTCAAATAACATTTTAAATGCCATATGCAAAAGAGATTTTAAAGAT
 GACCAAAAGAACAGATATCCCCAATTTTATGTATACACATAAAGGAGCGAAGTACGCATTTC
 AGTGTGTGAAACCTTCGAGATCTCTCATTTATTTGATGAAATTTTAACTGGTGTTCCTGGG
 ATTTCGAGCGAAAACCATCCACAAAGGATTAATTAATTTTATGTTAAACGATATCTTTTGA
 TAAATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCT
 TGGTATAAAATCCATAAACTTAAGGTTAGAGAATCCAAAGAAAACTATAATATTTTCAAG
 TCTCAAAGATATAATATCACTGTGATTTCCTCGT

SEQ ID NO. 5604

STRAIN H36B

SGAAGAGCTTACTTCTTATTGTTGGGATTAGATGGGACATTAAATAGATTCCG
 TATGTACCAATTAATGGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATTGTAT
 AAGAATAATATCATCGATAATATTTTACAGAAATCAGTGGGGAAATATTGGTAAACCTT
 TCAGAGGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTCACAAAGAACCAAGAA
 AGTCCAGATTTCTAAATAACATTTTAATGCCATATGCCAAAGAGATTTTAGAATGGACCAA
 AGCCAGATATCCCCAATTTTATGTATACATACAAAGGAGCAAGTACGCATTAGTGTG
 GAAACCTTGCAGATCTCTCATTTTGTGAAATTTTAACTGGTGTTCGGGATTCGAG
 CGAAAACCAATCCACAGGGATTAATTAATTTAGTTAAACGATATTTCTTAGATAAATCA
 ATGACTTTATACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGGTATA
 AATTCCTATAAACTTAAGGTTAGAGAAATCCAAAGAAAACTATAAATTTCAAGTCTCAA
 GATATAATATCACTGTATTTCACTCGTTGGAT

SEQ ID NO. 5605

STRAIN 18RS21

STRAIN 168321
AAGAAGATCTACTTTTATTTGGGATTAGATGGGACATTAAATAGATT
CGTATGTACCAATTTATGAAGACTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATTTG
ATAAAGAATTAATCCATGAATATATTTTACAGGAATCTGGGGGAAATATTGGTAAACC
TTTCAGAGGAAGAGCAATACCTCATGAAAACTGAAAGCATATTTTCAAAAGAAACAAG
AAAGTCGAGATTTCAAATACATTTTAATGCCATCTGCAAAAGAGATTTAGATATGGACCA
AAGAACAGAGATACCCCAATTTTATGTATACATATAAGAGGACGAGTACGCATTCACTGT
TGGAACACCTTGCAGATCTCTCATTTTGTATGAAATTTAACTGGTGTTCGGGATTTG
AGCGAAACACCATCTCCACAGGGATTAATTTAGTTAAACGATATTTCTTAGATATAAT
CAATGACTTTATTACATAGGAGATCTGCTCACTAGATTTGGAGGTTGCTCAAATGCTGGTA
TAAATCCATAAATCTTAGGTTAGAGTAATCCAAAGAAACTATAATATTTCAAGTCTCA
AAGATATAATATCACTTGAGTTCACTCGTTTGGAT

SEO ID NO. 5606

STRAIN M732

STRAIN M752
AAGAAGCTTTACTCTTTTATTGGGATTTAGATGGGACATTAATAGAT
TCGTATGTACCAATTTATGGAAGCTCTTGAAGAAACCATCGTCAATTTGGCTTAATATTT
GATAAGAATTAATCCATGAGATATTTTACAGGAATCAGTGGGGCAATTTTGGTAAAC
CTTTCAGAGGAAGAGCAAAATACCTCATGAAAAAAGTGAAGACATTTTCAAGAAGAACAA
GAAAGTCGAGATCTTAAATACATTTTAAATGCCATATGCAAAAGAGATTTTAGAATGGAC
AAAGAACAAGATATTCCTCAATTTTATGTATACATATAAGGAGCGAAGTACGCAATTCAGT

Table 56: Comparative Sequences relating to SAG0806

TTGGAAACCTTGCAGATCTCTCATTATTTTGTGATAAAATTTAACTGGTGTTCGGGATTTC
GAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTTAGATAAA
TCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGGT
ATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTC
AAGATATAATATCACTTGATTTCACCTCGTTTGGAT

SEQ ID NO. 5607

STRAIN CJB110

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATT
AATAGATTCGTATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTT
AATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGCAATTATT
GGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAA
AGAACAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGATTTTAGA
ATGGACCAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCA
TTCAGTGTGGAAACCTTGCAGATCTCTCATTTATTTGATGAAATTTAACTGGTGTTC
TGGATTTCGAGCGAAAACCATCCACAAGGGATTAAATATTTAGTTAAACGATATCTTT
AGATAAATCAATGACTTATTTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAAA
TGCTGTTATAAAATCCATAAACCTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTT
AAGTCTCAAGGATATAATATCACTTGATTTCACCTCGTT

SEQ ID NO. 5608

STRAIN 1169NT

aAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGTATGTACCAATTA
TAGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTAAATATTTGATAAAGAATTAAATCC
ATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAACCTTTTCAGAGGAAGAGC
AAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTCTA
AAATACATTTTAAATGCCATACGCAAAAGAGATTTAGAATGGACCAAGAACAGATATCC
CCAAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGA
TCTCTCATTTTGTGATAAAATTTAACTGGTGTTCGGGATTTCGAGCGAAAACCATATC
CACAAAGGATTAATTTATTTAGTTAAACGATATCTTTAGATAAATCAATGACTTATTACA
TAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAATGCTGTTATAAAATCCATAAACT
TAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCTCAAGGATATAATATCAC
TTGATTTCACTCGTTTGGAT

SEQ ID NO. 5609

STRAIN JM9130013

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGA
TTGATGTATACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGTTTAAATATT
TGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGGGAAATTATTTGGTAAA
CCCTTTTCAGAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGAAC
AGAAAGTCGAGATTCTAAAATACATTTTAAATGCCATATGCAAAAGAGATTTTAGAATGGAC
CAAAGAACAAGATATCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGT
GTTGGAAACCTTGCAGATCTCTCATTTATTTGATGAAATTTAACTGGTGTTCGGGATT
CGAGCGAAAACCATCCACAAGGATTAATTTAGTTAAACGATATCTTTAGATAAA
ATCAATGACTTATTACATAGGAGATCGTCCACTAGATTTGGAGGTTGCTCAAATGCTGG
TATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATAATATTTCAAGTCT
CAAAGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5610

STRAIN 090

AAGAAGCTTACTTTTATTTGG
GATTTAGATGGGACATTAATAGATTCGTATGTACCAATTATGGAAGCTCT
TGAAGAAACCTATCGTCATTTTGGCTTAAATATTTGATAAAGAATTAAATCC
ATGAATATATTTTACAGGAATCAGTGGGGCAATTATTTGGTAAACCTTTCA
GAGGAAGAGCAAATACCTCATGAAAACTGAAAGCATATTTTACAAAAGA
ACAAAGAAAGTCGAGATTCTAAAATACATTTAATGCCATATGCAAAAGAGA
TTTTAGAAATGGACCAAGAACAAGATATCCCAATTTTATGTATACACAT
AAAGGAGCAAGTACGCATTTCAGTGTGGAAACCTTGCAGATCTCTCATTA
TTTTGATGAAATTTAACTGGTGTTCCTGATTTCGAGCGAAAACCATATC
CACAAAGGATTAATTTATTTAGTTAAACGATATCTTTAGATAAATCAATG
ACTTATTACATAGGAGATCGTCCCTAGATTTGGAGGTTGCTCAAATGCTG
TGGTATAAAATCCATAAACTTAAGGTTAGAGAATTCCAAAGAAAACATA
ATATTTCAAGTCTCAAGGATATAATATCACTTGATTTCACCTCGT

SEQ ID NO. 5611

STRAIN M781

AAGAAGCTTACTTTTATTTGGGATTTAGATGGGACATTAATAGATTCGT
ATGTACCAATTATGGAAGCTCTTGAAGAAACCTATCGTCATTTTGGCTTA
ATATTTGATAAAGAATTAAATCCATGAATATATTTTACAGGAATCAGTGGG
GCAATTTATTTGGTAAACCTTTTCAGAGGAAGAGCAAATACCTCATGAAAAAC
TGAAAGCATATTTTACAAAAGAACAAAGTTCGAGATTyTAAAATACAT
TTAATGCCATATGCAAAAGAGATTTTAGAATGGACCAAGAACAAAGATAT
TCCCAATTTTATGTATACACATAAAGGAGCAAGTACGCATTTCAGTGTGG
AAACCTTGCAGATCTCTCATTTATTTGATGAAATTTAACTGGTGTTCG
GGATTTCGAGCGAAAACCATCCACAAGGATTAATTTATTTAGTTAAACG
ATATTTCTTTAGATAAATCAATGACTTATTACATAGGAGATCGTCCACTAG
ATTTGGAGGTTGCTCAAATGCTGGTATAAAATCCATAAACTTAAGGTTA
GAGAATTTCCAAAGAAAACATAATATTTCAAGTCTCAAGATATAATATC
ACTTGATTTCACTCGT

PRETTY of: /biotmp/msa45163.2{*} January 21, 2003 06:53 ..

Table 56: Comparative Sequences relating to SAG0806

	1				50
msa45163.2{240_18RS21}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_2603}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_A909}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_H36B}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_JM9130013}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_COH1}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M732}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_M781}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_090}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_CJB110}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
msa45163.2{240_1169NT}	AAGAAGCTTA	CTTTTATTTG	GGATTTAGAT	GGGACATTAA	TAGATTCGTA
Consensus	*****	*****	*****	*****	*****
	51				100
msa45163.2{240_18RS21}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_2603}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_A909}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_H36B}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_JM9130013}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_COH1}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_M732}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_M781}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_090}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_CJB110}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
msa45163.2{240_1169NT}	TGTACCAATT	ATGGAAGCTC	TTGAAGAAAC	CTATCGTCAT	TTTGGcTTAA
Consensus	*****	*****	*****	*****	*****
	101				150
msa45163.2{240_18RS21}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_2603}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_A909}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_H36B}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_JM9130013}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_COH1}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M732}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_M781}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_090}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_CJB110}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
msa45163.2{240_1169NT}	TATTTGATAA	AGAATTAATC	CATGAATATA	TTTACAGGA	ATCAGTGGGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa45163.2{240_18RS21}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_2603}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_A909}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_H36B}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_JM9130013}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_COH1}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M732}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_M781}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_090}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_CJB110}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
msa45163.2{240_1169NT}	aAATTATTGG	TAAACCTTTC	AGAGGAAGAG	CAAATACCTC	ATGAAAAACT
Consensus	*****	*****	*****	*****	*****
	201				250
msa45163.2{240_18RS21}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_2603}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_A909}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_H36B}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_JM9130013}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_COH1}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M732}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_M781}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTyT	AAAATACATT
msa45163.2{240_090}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_CJB110}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
msa45163.2{240_1169NT}	GAAAGCATAT	TTTACAAAAG	AACAAGAAAG	TCGAGATTcT	AAAATACATT
Consensus	*****	*****	*****	*****	*****
	251				300
msa45163.2{240_18RS21}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_2603}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_A909}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_H36B}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_JM9130013}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_COH1}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M732}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_M781}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_090}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_CJB110}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
msa45163.2{240_1169NT}	TAATGCCATA	tGCAAAAGAG	ATTTTAGAAT	GGACCAAAGA	ACAAGATATc
Consensus	*****	*****	*****	*****	*****

Table 56: Comparative Sequences relating to SAG0806

msa45163.2{240_18RS21}	301	CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	350
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
msa45163.2{240_1169NT}		CCCAATTTTA	TGTATACACA	TAAAGGAGCA	AGTACGCATT	CAGTGTTCGGA	
Consensus		*****	*****	*****	*****	*****	
msa45163.2{240_18RS21}	351	AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	400
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
msa45163.2{240_1169NT}		AACCTTGCAG	ATCTCTCATT	ATTTTGATGA	AAITTTAACT	GGTGTTCGg	
Consensus		*****	*****	*****	*****	*****	
msa45163.2{240_18RS21}	401	GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	450
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
msa45163.2{240_1169NT}		GATTCGAGCG	AAAACCACAT	CCACAAGGGA	TTAATTATTT	AGTTAAACGA	
Consensus		*****	*****	*****	*****	*****	
msa45163.2{240_18RS21}	451	TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	500
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCaCTAGA	
msa45163.2{240_1169NT}		TATTCCTTAG	ATAAATCAAT	GACTTATTAC	ATAGGAGATC	GTCCcCTAGA	
Consensus		*****	*****	*****	*****	*****	
msa45163.2{240_18RS21}	501	TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	550
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
msa45163.2{240_1169NT}		TTTGGAGGTT	GCTCAAAATG	CTGGTATAAA	ATCCATAAAC	TTAAGGTTAG	
Consensus		*****	*****	*****	*****	*****	
msa45163.2{240_18RS21}	551	AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	600
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
msa45163.2{240_1169NT}		AGAATTCCAA	AGAAAACTAT	AATATTTCAA	GTCTCAAaGA	TATAATATCA	
Consensus		*****	*****	*****	*****	*****	

Table 56: Comparative Sequences relating to SAG0806

Consensus	*****	*****	*****	*****_**	*****
	601		621		
msa45163.2{240_18RS21}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_2603}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_A909}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_H36B}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_JM9130013}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_COH1}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_M732}	CTTGATTTC	CTCGTttgga	t		
msa45163.2{240_M781}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_090}	CTTGATTTC	CTCGT-----	-		
msa45163.2{240_CJB110}	CTTGATTTC	CTCGTt-----	-		
msa45163.2{240_1169NT}	CTTGATTTC	CTCGTttgga	t		
Consensus	*****	*****	-		

SEQ ID NO. 5612

STRAIN 2603 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5613

STRAIN A909 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTR

SEQ ID NO. 5614

STRAIN H36B frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5615

STRAIN 18RS21 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5616

STRAIN M732 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5617

STRAIN COH1 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5618

STRAIN CJB110 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTR

SEQ ID NO. 5619

STRAIN 1169NT frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTRLD

SEQ ID NO. 5620

STRAIN JM9130013 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGKLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO
 ISHYFDEILTGVS GFERKPHPGQGINYL VKRYS LDKSMTYYIGDRPLDLEVAQNAGIKSIN
 LRLENSKENYNISS LKDIISLDFTR

SEQ ID NO. 5621

STRAIN 090 frame: 1

KKLTFIWDLGTLIDSYPIMEALEETRYRHFGLI FDKELIHEYILQESVGQLLVNLSEEE
 QIPHEKLIKAYFTKEQESRDSKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLO

Table 56: Comparative Sequences relating to SAG0806

ISHYFDEILTGVSGFERKPHPGQGINYLKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLNSKENYNISSSKDIISLDFTR

SEQ ID NO. 5622

STRAIN M781 frame: 1

KKLTFIWDLDGTLIDSYPVIMEALEETRYRHFGFLIFDKELIHEYILQESVQGQLLVNLSEEE
QIPHEKLKAYFTKEQESRDXXKIHLMPYAKEILEWTKEQDIPNFMYTHKGASTHSVLETLQ
ISHYFDEILTGVSGFERKPHPGQGINYLKRYSLDKSMTYYIGDRPLDLEVAQNAGIKSIN
LRLNSKENYNISSSKDIISLDFTR

PRETTY of: /biotmp/msa45645.2(*) January 21, 2003 06:57 ..

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1
msa45645.2{240_18RS21} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_A909} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_JM9130013} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_2603} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_H36B} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_090} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_CJB110} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_M781} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_COH1} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_M732} KKLTFIWDLD GTLIDSYPVI mEAL EETRYH FGLIFDKELI HEYILQESVG
msa45645.2{240_1169NT} KKLTFIWDLD GTLIDSYPVI iEAL EETRYH FGLIFDKELI HEYILQESVG
Consensus ***** -*****
50

51
msa45645.2{240_18RS21} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_A909} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_JM9130013} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_2603} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_H36B} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_090} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_CJB110} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_M781} qLLVNLSEEE QIPHEKLKAY FTKEQESRDx KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_COH1} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_M732} qLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
msa45645.2{240_1169NT} KLLVNLSEEE QIPHEKLKAY FTKEQESRDs KIHLMFYAKE ILEWTKEQDI
Consensus -*****
100

101
msa45645.2{240_18RS21} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_A909} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_JM9130013} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_2603} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_H36B} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_090} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_CJB110} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_M781} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_COH1} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_M732} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
msa45645.2{240_1169NT} PNFMYTHKGA STHSVLETLQ ISHYFDEILT GVSGFERKPH PQGINYLKVR
Consensus *****
150

151
msa45645.2{240_18RS21} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_A909} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_JM9130013} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_2603} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_H36B} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_090} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_CJB110} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M781} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_COH1} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_M732} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
msa45645.2{240_1169NT} YSLDKSMTYY IGDRPLDLEV AQNAGIKSIN LRLNSKENY NISSLKDIIS
Consensus *****
200

201
msa45645.2{240_18RS21} LDFTRld
msa45645.2{240_A909} LDFTR--
msa45645.2{240_JM9130013} LDFTR--
msa45645.2{240_2603} LDFTRld
msa45645.2{240_H36B} LDFTRld
msa45645.2{240_090} LDFTR--
msa45645.2{240_CJB110} LDFTR--
msa45645.2{240_M781} LDFTR--
msa45645.2{240_COH1} LDFTRld
msa45645.2{240_M732} LDFTRld
msa45645.2{240_1169NT} LDFTRld
Consensus *****

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Table 57: Comparative Sequences relating to SAG 1488

SEQ ID NO: 5701

STRAIN 2603

ATGCTTATGACAAAAATAATAGGACTGACAGGAGGGATAGCTTCT
 GGAAGTCAACGGTAACAAAAATAATACGAGAATCAGGTTTAAAGTCATAGATGCGGAT
 CAAGTGGTTTCATAAATTGCAAGCTAAGGGTGGGAACTTTACCAAGCTTTATTAGAATGG
 TTGGGTCCCGAGATACCTGATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATG
 ATTTTTGGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATTTTCATGGAT
 ATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTGATGAGATTGGTTGGTATTT
 GTTGATAAAGAAAAACAATTACAAACGATTAAATGGCCCGTAACAACTACAGTCGAGAAGAA
 GCAGAAATACGACTTTACACCAAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTT
 ATTATTGACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTA

SEQ ID NO: 5702

STRAIN 090

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
 TGATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGG
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT
 ATTTTTCGTGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAAACGA
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTA
 ATAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5703

STRAIN A909

AAGTCAACGGTAACAAAAATAATACGAGAATCAG
 GTTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAG
 GGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACT
 TGATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGG
 CTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 CGTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGAT
 ATTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TTGATGAGATTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAAACGA
 TTAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTC
 ACACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTA
 ACAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTT
 CAACGTTTA

SEQ ID NO: 5704

STRAIN H36B

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAAACGAT
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCGGAATTACGACTTTCA
 CACCAAATACCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
 TAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5705

STRAIN 18RS21

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGC
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATT
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATA
 TTTTTCATGGATATTCCCTTTATTGATTGAAGAAAAGTATATAAAATGGT
 TGATGAGATTGGTTGGTATTTGTTGATAAAGAAAAACAATTACAAACGAT
 TAATGGCCCGTAACAACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
 CACCAAATGCCCTTTAACAGATAAAAAAAGTTTCGCTAGTCTTATTATTGA
 CAATAATGGTGATTATAAATCTTTAAAGAGCAAATATTGGATGCTCTTC
 AACGTTTA

SEQ ID NO: 5706

STRAIN M732

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGTT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTTCATAAATTGCAAGCTAAGGGT
 GGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTGA
 TGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGGCTA
 ATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTGCT
 CAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAAACAGAAGAGATATT

Table 57: Comparative Sequences relating to SAG 1488

TTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTTG
 ATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATTA
 ATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTTACA
 CCAAATGCCCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGACA
 ATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCAA
 CGTTTTA

SEQ ID NO: 5707

STRAIN COH1

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGTCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCTG
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT
 TTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT
 AATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTTCA
 ACCAAATGCCCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGAC
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCA
 ACGTTTTA

SEQ ID NO: 5708

STRAIN M781

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGTCT
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCT
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
 CACCAAATGCCCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 CAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCTCTTCA
 AACGTTTTA

SEQ ID NO: 5709

STRAIN CJB110

AAGTCAACGGTAACAAAAATAATACGAGAA
 TCAGGTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGC
 TAAGGGTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGA
 TACTTGATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATT
 TTTGCTAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTAT
 CATTCTGCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAG
 AGATATTTTTCGTTGGATATTCCTTTATTGATTGAAGAAAAGTATATAAA
 TGGTTTGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACA
 ACGATTAAATGGCCCGTAAACAACACTACAGTCGAGAAGAAGCAGAATTACGAC
 TTTTACACCAAATGCCCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATT
 ATTAATAATAATGGTGATTTAATAACTTTAAAAGAGCAAATATTGGATGCT
 TCTTCAACGTTTTA

SEQ ID NO: 5710

STRAIN 1169NT

AAGTCAACGGTAACAAAAATAATACGAGAATCAGG
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGG
 GTGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTT
 GATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGTCT
 TAATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCT
 GTCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATA
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTT
 TGATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGAT
 TAATGGCCCGTAACAACACTACAGTCGAGAAGAAGCAGAATTACGACTTTCA
 CACCAAATACCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGA
 TAATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCA
 AACGTTTTA

SEQ ID NO: 5711

STRAIN JM9130013

AAGTCAACGGTAACAAAAATAATACGAGAATCAGGT
 TTTTAAAGTCATAGATGCGGATCAAGTGGTTCATAAATTGCAAGCTAAGGG
 TGGGAAACTTTACCAAGCTTTATTAGAATGGTTGGGTCCCGAGATACTTG
 ATGCTGATGGTGAGTTGGATAGACCAAGCTTTCTCAAATGATTTTGTCT
 AATCCAGACAATATGAAGACATCAGCTAGGCTACAAAATAGTATCATTCTG
 TCAAGAGTTAGCATGTGAGCGCGACCAATTAAAAACAACAGAAGAGATAT
 TTTTTCATGGATATTCCTTTATTGATTGAAGAAAAGTATATAAAATGGTTT
 GATGAGATTTGGTTGGTATTGTTGATAAAGAAAAACAATTACAACGATT
 AATGGCCCGTAACAACACTACAGTCGAGAAGAAGCGGAATTACGACTTTTCA
 ACCAAATACCTTTAAACAGATAAAAAAGTTTCGCTAGTCTTATTATTGAT
 AATAATGGTGATTTAATAACTTTAAAAGAGCAAATGTTGGATGCTCTTCA
 ACGTTTTA

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221059.2{*} February 10, 2003 07:07 ..

	1				50
msa221059.2{245_H36B}	-----	-----	-----	-----	-----AA
msa221059.2{245_JM9130013}	-----	-----	-----	-----	-----AA
msa221059.2{245_1169NT}	-----	-----	-----	-----	-----AA
msa221059.2{245_090}	-----	-----	-----	-----	-----AA
msa221059.2{245_CJB110}	-----	-----	-----	-----	-----AA
msa221059.2{245_18RS21}	-----	-----	-----	-----	-----AA
msa221059.2{245_2603}	atgctttatga	caaaaataat	aggactgaca	ggaggggatag	cttcttggaAA
msa221059.2{245_A909}	-----	-----	-----	-----	-----AA
msa221059.2{245_COH1}	-----	-----	-----	-----	-----AA
msa221059.2{245_M732}	-----	-----	-----	-----	-----AA
msa221059.2{245_M781}	-----	-----	-----	-----	-----AA
Consensus	*****	*****	*****	*****	*****
	51				100
msa221059.2{245_H36B}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_JM9130013}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_1169NT}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_090}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_CJB110}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_18RS21}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_2603}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_A909}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_COH1}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_M732}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
msa221059.2{245_M781}	GTCAACGGTA	ACAAAAATAA	TACGAGAATC	AGGTTTTTAA	GTCATAGATG
Consensus	*****	*****	*****	*****	*****
	101				150
msa221059.2{245_H36B}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_JM9130013}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_1169NT}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_090}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_CJB110}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_18RS21}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_2603}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_A909}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_COH1}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M732}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
msa221059.2{245_M781}	CGGATCAAGT	GGTTCATAAA	TTGCAAGCTA	AGGGTGGGAA	ACTTTACCAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa221059.2{245_H36B}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_JM9130013}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_1169NT}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_090}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_CJB110}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_18RS21}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_2603}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_A909}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_COH1}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M732}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
msa221059.2{245_M781}	GCCTTATTAG	AATGGTTGGG	TCCCGAGATA	CTTGATGCTG	ATGGTGAGTT
Consensus	*****	*****	*****	*****	*****
	201				250
msa221059.2{245_H36B}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_JM9130013}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_1169NT}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_090}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_CJB110}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_18RS21}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_2603}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_A909}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_COH1}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M732}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
msa221059.2{245_M781}	GGATAGACCA	AAGCTTTCTC	AAATGATTTT	TGCTAATCCA	GACAATATGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa221059.2{245_H36B}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_JM9130013}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_1169NT}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_090}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_CJB110}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_18RS21}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_2603}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_A909}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_COH1}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
msa221059.2{245_M732}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT

Table 57: Comparative Sequences relating to SAG 1488

msa221059.2{245_M781}	AGACATCAGC	TAGGCTACAA	AATAGTATCA	TTCGTCAAGA	GTTAGCATGT
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	301				350
msa221059.2{245_JM9130013}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_1169NT}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_090}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_CJB110}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCg	TGGATATTCC
msa221059.2{245_18RS21}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_2603}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_A909}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_COH1}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M732}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
msa221059.2{245_M781}	CAGCGCGACC	AATTAATAACA	AACAGAAGAG	ATATTTTTCa	TGGATATTCC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	351				400
msa221059.2{245_JM9130013}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_1169NT}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_090}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_CJB110}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_18RS21}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_2603}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_A909}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_COH1}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M732}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
msa221059.2{245_M781}	TTTATTGATT	GAAGAAAAGT	ATATAAAATG	GTTTGATGAG	ATTTGGTTGG
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	401				450
msa221059.2{245_JM9130013}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_1169NT}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_090}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_CJB110}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_18RS21}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_2603}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_A909}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_COH1}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M732}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
msa221059.2{245_M781}	TATTTGTTGA	TAAAGAAAAA	CAATTACAAC	GATTAATGGC	CCGTAACAAC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	451				500
msa221059.2{245_JM9130013}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_1169NT}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TaCCTTTAAC
msa221059.2{245_090}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_CJB110}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_18RS21}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_2603}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_A909}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_COH1}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M732}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
msa221059.2{245_M781}	TACAGTCGAG	AAGAAGCgGA	ATTACGACTT	TCACACCAA	TgCCTTTAAC
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	501				550
msa221059.2{245_JM9130013}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_1169NT}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAtAATAAT	GGTGATTTAA
msa221059.2{245_090}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_CJB110}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TaAtAATAAT	GGTGATTTAA
msa221059.2{245_18RS21}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_2603}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_A909}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_COH1}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M732}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
msa221059.2{245_M781}	AGATAAAAAA	AGTTTCGCTA	GTCCTATTAT	TgAcAATAAT	GGTGATTTAA
Consensus	*****	*****	*****	*****	*****
msa221059.2{245_H36B}	551				591
msa221059.2{245_JM9130013}	TAACTTTAAA	AGAGCAAATg	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_1169NT}	TAACTTTAAA	AGAGCAAATg	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_090}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_CJB110}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_18RS21}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_2603}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_A909}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A
msa221059.2{245_COH1}	TAACTTTAAA	AGAGCAAATa	TTGGATGCCT	TTCAACGTTT	A

Table 57: Comparative Sequences relating to SAG 1488

```

msa221059.2{245_M732} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
msa221059.2{245_M781} TAACTTTAAA AGAGCAAATA TTGGATGCTC TTCAACGTTT A
Consensus *****- *****- *****- *****- *

```

SEQ ID NO: 5712

STRAIN 2603 frame: 1

```

MLMTKIIIGLTGGIASGKSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPET
LDADGELDRPKLSQMI FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI
EEKYIKWFDEIWLWVFDKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNN
GDLITLKEQILDALQRL

```

SEQ ID NO: 5713

STRAIN 090 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5714

STRAIN A909 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5715

STRAIN H36B frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQRL
L

```

SEQ ID NO: 5716

STRAIN 18RS21 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5717

STRAIN M732 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5718

STRAIN COH1 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5719

STRAIN M781 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI IDNNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5720

STRAIN CJB110 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQMPLTDKKS FASLI INNNGDLITLKEQILDALQRL
L

```

SEQ ID NO: 5721

STRAIN 1169NT frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQRL
L

```

SEQ ID NO: 5722

STRAIN JM9130013 frame: 1

```

KSTVTTKI IRESGFKVIDADQVVHKLQAKGGKLYQALLEWLGPETLDADGELDRPKLSQMI
FANPDNMKTSARLQNSI I RQELACQDQLKQTEEFFMDIPLLI EEKYIKWFDEIWLWVFD
DKEKQLQRLMARNNYSREEAELRLSHQIPLTDKKS FASLI IDNNNGDLITLKEQMLDALQRL
L

```

Table 57: Comparative Sequences relating to SAG 1488

PRETTY of: /biotmp/msa221398.2(*) February 10, 2003 07:15 ..

```

1                                     50
msa221398.2{245_090} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_CJB110} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_1169NT} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_H36B} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_JM9130013} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_18RS21} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_2603} mlmtkiiglt ggiasgKSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_A909} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_COH1} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M732} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
msa221398.2{245_M781} -----KSTV TKIIRESGFK VIDADQVVHK LQAKGGKLYQ
Consensus *****

51                                     100
msa221398.2{245_090} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_CJB110} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_1169NT} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_H36B} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_JM9130013} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_18RS21} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_2603} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_A909} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_COH1} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M732} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
msa221398.2{245_M781} ALLEWLGP EI LDADGELDRP KLSQMIFANP DNMKTSARLQ NSIIRQELAC
Consensus *****

101                                    150
msa221398.2{245_090} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_CJB110} QRDQLKQTEE IFFvDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_1169NT} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_H36B} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_JM9130013} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_18RS21} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_2603} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_A909} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_COH1} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M732} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
msa221398.2{245_M781} QRDQLKQTEE IFFmDIPLLI EEKYIKWFDE IWLVFVDKEK QLQRLMARNN
Consensus *****

151                                    197
msa221398.2{245_090} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_CJB110} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_1169NT} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_H36B} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_JM9130013} YSREEAELRL SHQiPLTDKK SFASLIIdNN GDLITLKEQm LDALQRL
msa221398.2{245_18RS21} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_2603} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_A909} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_COH1} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M732} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
msa221398.2{245_M781} YSREEAELRL SHQmPLTDKK SFASLIIdNN GDLITLKEQi LDALQRL
Consensus *****

```

Table 58: Comparative Sequences relating to SAG0182

SEQ ID NO. 5801

STRAIN 2603

ATGTTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGATTTTAGCCCTTTTATTG
 GTAATAATAGTTATTTTAGACAGTTAATTGAAGAGCGGCTAAACGTGAAACGGTAGTC
 CTTGTCAATCATTTTCGGCTGTTTGTATTATATCTAATATAACAGGAATTGAATAAAA
 GGGGATCGAAGTTTGGTCGAGCGCCCTTTCTAACAACGATTCTCATTCTGACTCACTT
 GCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCTCTGGTTGGA
 TCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTCAAGGAAGCTTTTCAGGTTCT
 TTCATATTGTGTCAGTTTCAGTTCTAGTCGGCATTGTTAGCGGAAAGATTGGTGATAAGCTT
 AAGGAAAACCATCTCTACCCCTTCAACAAGCCAAGTTATTTAATTAGTATTAATGCCGAA
 AGTATCCAGATGCTATTGTTGGCAITTTTACAGGATGGGAACCTGTCAAATGATTGTC
 ATTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTGTTGAAACT
 TATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGATGTTCTGAAATTGACT
 CGACAGACTCTGCCCTACCTTAGACAAGGTTTGACACCGCAATCTGCTAGGAGCGTTTGC
 GAAATTTATAAGAGGCATACTAATTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTA
 TTAGCTCATATTGGTGTGGCCATGATCACCATTATGTCAGGACAACCGGTCAAACAGAC
 TTATCTAAAGTGTTATTTTTAAATGCTTATGATGGCGAACCAGAAATGCGCAAGATAAAGCGCGATT
 TCTTGTCCAGATCACAACCTGTGCTAGTTAAATCTGCTATTGTTAGTTCCTCTAAAAATAAAT
 GATAAACTGTGGGTGCCCTTAAATGTAATTTGTCAGGAGATAAGCAATGTCTGAGGTG
 GAGGAAAACCTAGTCTTGGTTTAGCGCAATATTTTTCAGGACAACCTGGCAATGGGGATA
 ACAGAGGAACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAAATC
 AACCTCAATTTCTTCTTTTAAATGCTTAAACACAATTAAGTGCAATTAATCCGTTATTGATTCT
 GATAAAGCAGTTATGCTAGTGCAGTTAAGTACTTTTTTGAAGCAAGTTTTCAGGGT
 GGTCAAGGATCGTGAGGTAACGCTTGAGCAAGAAAATCACATGTGGATGCTTATATGAAT
 GTTGAAAAATTAAGTTTCCCTGATAAATATCAGTTATCTTATGATATTAGTGCACCAGAA
 AAAATGAAGTTACCACTTTTGGTTTACAGGTACTGGTAGAGAAATGCAGTTTCGACATGCT
 TCAAGAAACGTAAGACGGAACAACCATATATTGGTTCAAATAAAGCCAGATGGTCATTAT
 TATTGTTGTTCTGTAGTGAACAATGGACAAGGAATCTCAGATACTATCATTGATAAATTA
 GGTCAAGAAACAGTTGCAGAGAGTAAGGGTACAGGTACTGCTCTAGTTAATCTAAATAAC
 AGGCTGAATTTATTATATGTTAGTGTAAAGTTGCCCTTCAATTTTCAGCGCAAGAATGGT
 ACAAAAGTTTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT
 TCT

SEQ ID NO. 5802

STRAIN 090

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTG
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCAATCATTTTCGGCTTG
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTCATTCTGACTCACTT
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
 CTGGTTGGATCAATTTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTTCA
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCGGCA
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
 TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
 GCTATTGTTGGTATTTTTACAGGATGGGAACCTGTCAAATGATTGTCA
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATT
 TTGAAAACCTTATTGTTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
 AGATGTTCTTGAATGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
 TGACACCGCAATCTGCTAGGAGCGTTTTCGCAAAATTATAAAGAGGCATACT
 AACTTTGATGCTGTAGGATTAAACAGATCGGTCAAACGTTATTAGCTCATAT
 TGGTGTGGCCATGATCACCATTATGTCAGGACAACAGTCAAACAGACC
 TATCTAAAGTGTTATTTTTGTAGGCGAACCAGAAATTGCGCAAGATAAA
 GCGGCGATTCTTGTCCAGATCACAACGTGCTAGTTAAATCTGCTATTGT
 AGTTCCCTCTAAATAAATAATGATAAACTGTGGGTGCCCTTAAATGTTACT
 TTGAGGAGATAAGCAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT
 TTAGCGCAATTTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
 ACCCTCATTTCTCTTAAATGCCATTAAACCAATTAGTGCAATTAATCCGT
 ATTGATTCTGATAAAGCAGTTATGCACTGATGCAAGTTAAGTACTTTTTT
 TAGAACAAGTTTTCAGGTTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAATTAAGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT
 ACCGCTTTTGGTTTACAGGTAAGTTAGGAGAAATGCAAGTTAGACATGCTT
 TCAAGAACGTAAGACGGAACAACCATATATTGGTTCAAATAAAGCCAGAT
 GGTCAATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
 TACTATCAATTGATAAATTAGGTCAAGAAACAGTTGTCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
 AGTGTAAAGTTGCCCTTCAATTTTCAGGCGCAAGAATGGTACAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAT
 CT

SEQ ID NO. 5803

STRAIN A909

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT
 GATTTTAGCCCTTTTATTGGTAAATAATAGTTATTTCAGACAGTTAATTG
 AAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCAATCATTTTCGGCTTG
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
 TTTGGTCGAGCGCCCTTTCTAACAACGATTTCCTCATTCTGACTCACTT
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
 CTGGTTGGATCAATTTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTTTCA
 AGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCGGCA
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT

Table 58: Comparative Sequences relating to SAG0182

TCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGAT
GCTATTTGTTGGCATTTTACAGGATGGGAACCTTGTCAAAATGATTGTCA
TTCCAAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGGGATT
TTGAAACCTTATTTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTT
TGACACCGCAATCTGTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACCT
AACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATAT
TGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACT
TATCTAAAAGTGTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAA
GCCGCGATTTCTGTCCAGATCACAACCTGTCAAGTTAAATCTGCTATTGT
AGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT
TTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAACCTAGTCTTGGT
TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCA
ACCTCATTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCCGT
ATTGATTCTGATAAAGCACGTTATGCACCTGATGCAGTTAAGTACTTTTT
TAGAACCAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAG
AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
GATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTT
ACCACCTTTTGGTTTACAGGTAAGTGTAGAGAAATGCAGTTGCAGATGCTT
TCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
GGTCATTATTATTTGTGTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGGTAAGGGTA
CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGT
AGTGTAAGTTGCCCTTCAATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTG
GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT
CT

SEQ ID NO. 5804

STRAIN H36B

TTGATGGTGTGTTTATTCCAAAGGCTAGGAATTATTATG
ATTTTAGCCCTTTTATGGTAAATAATAGTTATTTAGACAGTTAATTGA
AGAGCGGTCTAAACGTTAAACGTTAGTCTTGTCTCATCTTTTCGGCTTGT
TTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT
TTGGTTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACTTGC
TAATACAGGACTTTAGTTATTACAAACGGAAGTTTGGTTGGTGGACCTC
TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCACTCGCTTTTTCAA
GGAAGCTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
CAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCAGATG
CTATTTGTTGGCATTTTACAGGATGGGAACCTTGTCAAAATGATTGTCTAT
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTT
TGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT
GACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATACTA
ACTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT
GGTGTGGCCATGATCACCATTATGCAGGACAACCGGTCAAACAGACTT
ATCTAAAAGTGTTATTTTGTATGGCGAACCAAGAATTGCGCAAGATAAAG
CGGCGATTTCTTGTCCAGATCACAACCTGTCAAGTTAAATCTGCTATTGTA
GTTCTCTAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACTT
TGCAAGGAGATAAGACAATGTCTGAGGTGGAGGAAACCTAGTCTTGGTT
TAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA
AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAATCAA
CCCTCATTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCCGTA
TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTTT
AGAACAAGTTTGCAGGGTGGTCAAGGATCGTGAGGTAACGCTTGAGCAAGA
AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
ATAAATATCAGTTATCTTATGATATTAGTGCACCAGAAAAATGAAGTTA
CCACCTTTTGGTTTACAGGTAAGTGTAGAGAAATGCAGTTTCGACATGCTTT
CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
ACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTAC
AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
GTGTAAGTTGCCCTTCAATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTG
TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAAATTTTAATT
T

SEQ ID NO. 5805

STRAIN 18RS21

TTGATGGTGTGTTTATTCCAAAGGCTAGGAATTATTATG
ATTTTAGCCCTTTTATGGTAAATAATAGTTATTTAGACAGTTAATTGA
AGAGCGGTCTAAACGTTAAACGTTAGTCTTGTCTCATCTTTTCGGCTTGT
TTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGT
TTGGTTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACTTGC
TAATACAGGACTTTAGTTATTACAAACGGAAGTTTGGTTGGTGGACCTC
TGGTTGGATCAATTTGTTGGTTTATTTGGAGGAGTTTCACTCGCTTTTTCAA
GGAAGCTTTTCAGGTTCTTTCTATATTGTCTAGTTTCTAGTCTCGGCAT
TGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
CAACAAGCCAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGATG
CTATTTGTTGGCATTTTACAGGATGGGAACCTTGTCAAAATGATTGTCTAT
TCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCATTT
TGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAGA
GATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTT

Table 58: Comparative Sequences relating to SAG0182

GACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAGAGGCATACTA
 ACTTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATT
 GGTGTTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGACTT
 ATCTAAAAGTGTATTATTTTGATGGCGAACCAAGATTGCGCAAGATAAAG
 CGGCGATTTCTGTCCAGATCAACAACGTGTCAGTTAAATTCTGCTATTGTA
 GTTCCTCTAAAAATAAATGATAAACTGTGGTGCCTTAAAAATGTACTT
 TGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTGGTT
 TAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAA
 AATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAA
 CCTCATTTCTCTTAAATGCCATTAAACAATTAGTGCATTAAATCCGTA
 TTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT
 AGAACCAAGTTTGACGGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGA
 AAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTG
 ATAAATATCAGTTATCTTATGATATTAGTGCACCGAAGAAATGAAGTTA
 CCACCTTTTGGTTTACAGTACTGGTAGAGAATGCAGTTTCGACATGCTTT
 CAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATG
 GTCATTATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGAT
 ACTATCATTTGATAAATTAGGTCAAGAACAGTTGCAGAGAGTAAGGGTAC
 AGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTA
 GTGTAAGTTGCCTTCATTTTTCGAGCGACAAGATGGTACAAAAGTTTGG
 TATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC
 T

SEQ ID NO. 5806

STRAIN M732

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTATGAT
 TTAGCCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAATTGAAG
 AGCGGCTCAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGCTTGT
 GTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAGTTT
 GGTGCGAGCGCCCTTTTCTAACACAGATTCCCATTCGACTCAGTTGCTA
 ATACAAGGACITTAGTTATTACAACGGCAAGTTGGTTGGTGGACCTCTG
 GTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTTCAAG
 AAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCCGCAATG
 TTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTACCCCTCA
 ACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAGATGCT
 ATTTGTTGGCATTTTTACAGGATGGGAACCTTGTCAAATGATTGTCAATC
 CAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGCGATTTG
 AAAACTTATTGTTCAATGAAAGTCAGTTACGCGCAGTTCAAACGAGAGA
 TGTCTTGAATGACTCGACAGACTCTGCCCTACCTTAGACAAGGTTTGA
 CACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAGAGGCATACTAAC
 TTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCATATTGG
 TATTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAGACTTAT
 CTAAGAGTGTATTATTGATGGCGAACCAGAAATTGCGCAAGATAAAGCG
 GCGAATTCTTGTCCAGATCAACAACGTGTCAGTTAAATTCTGCTATTGTAGT
 TCCCTCTAAAAATAAATGATAAACTGTGTGTCCTTAAAAATGTACTTTG
 CAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGTTTA
 GCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACAAA
 TAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCAAAATCAACC
 CTCATTTCTTCTTAAATGCCATTAAACAATTAGTGCATTAAATCCGTATT
 GATTCTGATAAAGCAGTTATGCACTGATGCAGTTAAGTACTTTTTTTAG
 AACAGTTTGCAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAGAAA
 AATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCTGAT
 AAATATCAGTTATCTTATGATATTAGTGCACCGAAGAAATGAAGTTACC
 GCCTTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGCTTTCA
 AAGAAGCTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGATGGT
 CATATTATTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAGATAC
 TATCATTGATAAATTAGGTCAAGAACAGTTGCAGAGAGTAAGGGGACAG
 GTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGGTAGT
 GTAAGTTGCCCTTCATTTTTCGAGCGACAAGAAATGGTACAAAAGTTTGGTA
 TCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAATTC

SEQ ID NO. 5807

STRAIN COH1

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 TATGATTTTAGCCTTTTATTGGTAAATAATAGTTAATTCAGACAGTTAA
 TTGAAGAGCGGCTCAAACGTGAAACGGTAGTCTTGTTCATCATTTTCGGC
 TTGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCG
 AAGTTTGGTTCGAGCGCCCTTTTCTAACACAGATTCCCATTCGACTCAC
 TTGCTAATACAAGGACITTAGTTATTACAACGGCAAGTTTGGTTGGTGGGA
 CCTCTGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTT
 TCAAGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTCAAGTTCTAGTCTG
 GCATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAAACCATCTCTAC
 CCTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCCGAAAGTATCCA
 GATGCTATTGTTGGCATTTTACAGGATGGGAACCTTGTCAAATGATTG
 TCATTTCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTGGC
 ATTTTGAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAC
 GAGAGATGTTCTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAG
 GTTTGACACCGCAATCTGCTAGGAGCGTTTGCGAAATTATAAAGAGGCAT
 ACTAATTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGTCA
 TATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAACAG
 ACTTATCTAAAAGTGTATTATTGATGGCGAACCAGAAATGCGCAAGAT
 AAAGCGCGGATTCTTGTCCAGATCAACAACGTGTCAGTTAAATCTGCTAT
 TGTAGTTCTCTAAAAATAAATGATAAACTGTGTGTCCTTAAAAATGT

Table 58: Comparative Sequences relating to SAG0182

ACTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCCTT
 GGTTTAGCGCAAAATATTTTCAGGACAACTGGCAATGGGGATAACAGAGGA
 ACAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAA
 TCAACCCTCATTTCTTCTTTAATGCCATTAAACACAATTAGTGCATTAAATC
 CGTATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTT
 TTTTAGAACAAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGC
 AAGAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTC
 CCTGATAAATATCAGTTATCTTATGATATTAGTGACCAGAAAAATGAA
 GTTACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATG
 CTTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCA
 GATGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTC
 AGATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGG
 GGACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATAT
 GGTAGTGAAGTTGCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGT
 TTGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTA
 ATTCT

SEQ ID NO. 5808

STRAIN M781

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTA
 TGATTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATT
 GAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTCTCATCTTTTCGGCTT
 GTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAA
 GTTGGTCGAGCGCCCTTTTCTAACACGATTTCCATTCTGACTCACTT
 GCTAATAACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACC
 TCTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC
 AAGGAAGCTTTTCAGGTTCTTCTATATGTGAGTTCAAGTTCTAGTCGGC
 ATTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCC
 TTCAACAAGCCAAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGA
 TGTATTGTTGGCATTTTACAGGATGGGAACCTGTCAAATGATTGTC
 ATTCCAATGATGATTTAATAAGTTTAGGTTCCACACTTTTCCTTGCGAT
 TTTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAAACGA
 GAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCCTAGACAAGGT
 TTGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATAC
 TAACTTTGATGCTGTGGGATTAACAGATCGGTCAAACGTTATTAGTCTATA
 TTGGTGTGGCCATGATCACCATATTGCGAGCAACCGGTCAAACAGAC
 TTATCTAAAAGTGTATTTTTGATGGCGAACCAGAATTGCGCAAGATAA
 AGCGGCGATTCTTGTCCAGATCACAACTGTGAGTTAAATCTGCTATTG
 TAGTTCCTCTAAAAATAAATGATAAACTGTGTGCTTAAAAATGTAC
 TTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGG
 TTTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAAC
 AAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATC
 AACCCCTCATTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCG
 TATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTT
 TTAGAACAAGTTTGCAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAA
 GAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCC
 TGATAAATATCAGTTATCTTATGATATTAGTGACCAGAAAAAATGAAGT
 TACCGCCTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGCT
 TTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGA
 TGGTCATTATTATTGTGTTTCTGTTAGTGACAATGGACAAGGAATCTCAG
 ATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGG
 ACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
 TAGTGAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTTT
 GGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTAAT
 TCT

SEQ ID NO. 5809

STRAIN CJB110

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATTAT
 GATTTTAGCCTTTTATTGGTAAATAATAGTTATTTTCAGACAGTTAATTG
 AAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTCTCATCTTTTCGGCTTG
 TTTGTTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGAAG
 TTTGGTCGAGCGCCCTTTTCTAACACGATTTCCATTCTGACTCACTTG
 CTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGACCT
 CTGGTTGGATCAATTGTTGGTTTATTGGAGGAGTTTCATCGCTTTTTC
 AGGAAGCTTTTCAGGTTCTTCTATATTGTGAGTTCAAGTTCTAGTCGGCA
 TTGTTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACCCCT
 TCAACAAGCCAAAGTTATTTAATTAGTATTATTGCCGAAAGTATCCAGAT
 GCTATTGTTGGTTATTTTTACAGGATGGGAACCTGTCAAATGATTGTCA
 TTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCCTTGCGATT
 TTGAAAACCTTATTGTCAAATGAAAGTCAGTTACGCGCAGTTCAAACGAG
 AGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTCAGACAAGGTT
 TGACACCGCAATCTGCTAGGAGCGTTTGGGAAATATAAAGAGGCATACT
 AACTTTGATGCTGTAGGATTAACAGATCGGTCAAACGTTATTAGCTCATAT
 TGGTGTGGCCATGATCACCATATTGCGAGCAACCAAGTCAAACAGACC
 TATCTAAAAGTGTATTTTTGTGGCGAACCAGAATTGCGCAAGGATAAA
 GCGGCGATTCTTGTCCAGATCACAACTGTGAGTTAAATCTGCTATTGT
 AGTTCCTCTAAAAATAAATGATAAACTGTGGGTGCCCTTAAAAATGTACT
 TTGCGAGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTTGGT
 TTAGCGCAAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAACA
 AAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAATCA
 ACCCTCATTTTCTTCTTAAATGCCATTAAACACAATTAGTGCATTAAATCGT
 ATTGATTCTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTTTT

Table 58: Comparative Sequences relating to SAG0182

TAGAACAAGTTTTCGAAGGTGGTCAGGATCGTGAGGTAACGCTTGAGCAAG
 AAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCCCT
 GATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAGTT
 ACCGCCCTTTGGTTTACAGGTAAGTGGTAGAATGCAGTTAGACATGCTT
 TCAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAGAT
 GGTCAATTATTTGTTGTTCTGTTAGTGACAATGGACAAGGAATCTCAGA
 TACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGGTA
 CAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATGTT
 AGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGTTACAAAAGTTTG
 GTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAAAT
 CT

SEQ ID NO. 5810

STRAIN 1169NT

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTACTTGTATCATTTTCGGCT
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
 AGTTTGGTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACT
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTGAGTTCTAGTCGG
 CATTTGTGAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT
 CATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG
 AGAGATGTTCTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA
 CTAATTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCAAGTCAAAAACAGA
 CCTATCTAAAAGTGTATTATTGATGGCGAACCAGAAATTGCGCAAGATA
 AAGCGGCGATTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
 CAACCCCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATCC
 GTATTGATTTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA
 AGAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG
 TTACCGCCCTTTGGTTTACAGGTAAGTGGTAGAGAATGCAGTTTCGACATGC
 TTTTAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG
 ATGGTCATTATTATTTGTTTCTGTTAGTGACAATGGACAAGGAATCTCA
 GATACTATCATTGATAAATTAGGTCAAGAAACAGTTGCAGAGAGTAAGGG
 TACAGGTAAGTCTCTAGTTAATCTAATAACAGGCTGAATTTATTATATG
 GTAGTGTAAAGTTGCCCTTCATTTTTCGAGCGACAAGAATGGTACAAAAGTT
 TGGTATCGAATACCTAATAGAATAAGGGAGGATGAGCATGAAAATTTTAA
 TTCT

SEQ ID NO. 5810

STRAIN JM9130013

TTGATGGTGTGTTATTCCAAAGGCTAGGAATTATT
 ATGATTTTAGCCCTTTTATTGGTAATAATAGTTATTTCAGACAGTTAAT
 TGAAGAGCGGTCTAAACGTGAAACGGTAGTCTTGTATCATTTTCGGCT
 TGTTTGTATTATATCTAATATAACAGGAATTGAAATAAAGGGGATCGA
 AGTTTGGTCGAGCGCCCTTTCTAACAACGATTTCTCATTTCTGACTCACT
 TGCTAATACAAGGACTTTAGTTATTACAACGGCAAGTTTGGTTGGTGGAC
 CTCTGGTTGGATCAATTGTTGGTTTTATTGGAGGAGTTTCATCGCTTTTT
 CAAGGAAGCTTTTCAGGTTCTTTCTATATTGTGAGTTGAGTTCTAGTCGG
 CATTTGTAGCGGAAAGATTGGTGATAAGCTTAAGGAAAACCATCTCTACC
 CTTCAACAAGCCAAGTTATTTTAATTAGTATTATTGCGGAAAGTATCCAG
 ATGCTATTTGTTGGCATTTTTACAGGATGGGAACCTGTCAAATGATTGT
 CATTTCCAATGATGATTTTAAATAGTTTAGGTTCCACACTTTTCTTTCGCA
 TTTTGAAAACTTATTGTTCAAAATGAAAGTCAGTTACGCGCAGTTCAAACG
 AGAGATGTTCTTGAATTGACTCGACAGACTCTGCCCTACCTTAGACAAGG
 TTTGACACCGCAATCTGCTAGGAGCGTTTGCAGAAATTATAAAGAGGCATA
 CTAACCTTTGATGCTGTGGGATTAAACAGATCGGTCAAACGTATTAGCTCAT
 ATTGGTGTGGCCATGATCACCATATTGCAGGACAACCGGTCAAAACAGA
 CTTATCTAAAAGTGTATTATTGATGGCGAACCAGAAATTGCGCAAGATA
 AAGCGGCGATTCTTGTCCAGATCACAACGTGTCAGTTAAATTCTGCTATT
 GTAGTTCTCTAAAAATAAATGATAAACTGTGGGTGCCCTAAAAATGTA
 CTTTGCAGGAGATAAGACAATGTCTGAGGTGGAGGAAAACCTAGTCTCTTG
 GTTTAGCGCAAATATTTTCAGGACAACCTGGCAATGGGGATAACAGAGGAA
 CAAAATAAGTTAGCCAGTATGGCAGAGATAAAGGCTTTACAAGCACAAAT
 CAACCCCTCATTTCTCTTTAATGCCATTAAACAATTAGTGCATTATCC
 GTATTGATTTGATAAAGCACGTTATGCACTGATGCAGTTAAGTACTTTT
 TTTAGAACCAAGTTTGCAGGTGGTCAGGATCGTGAGGTAAACGCTTGAGCA
 agAAAAATCACATGTGGATGCTTATATGAATGTTGAAAAATTACGTTTCC
 CTGATAAATATCAGTTATCTTATGATATTAGTGACCCAGAAAAAATGAAG
 TTACCACTTTTGGTTTACAGGTACTGGTAGAGAATGCAGTTTCGACATGC
 TTTCAAAGAACGTAAGACGGACAACCATATATTGGTTCAAATAAAGCCAG

Table 58: Comparative Sequences relating to SAG0182

ATGGTCATTATTATTGTTCTGTTAGTGACAATGGACAAGGAATCTCA
 GATACATCATTCATTGATAAATTAGGCTCAAGAAACAGTTGCGAGAGTAGG
 TACAGGTACTGCTCTAGTTAATCTAAATAACAGGCTGAATTTATTATATG
 GTAGTGTAAAGTTGCTTCTATTTTCGAGCGACAAGAAATGGTACAAAAGTT
 TGGTATCGAATACCTAATAGAATAAGGAGGATGAGCATGAAAATTTTAA
 TTCT

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa442667.2{*} January 13, 2003 06:34 ..

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1                                     50
msa442667.2{248_18RS21} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_2603} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_A909} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_H36B} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_JM9130013} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_COH1} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M781} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_M732} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_090} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_CJB110} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
msa442667.2{248_1169NT} TTGATGGTGT TGTATTCCA AAGGCTAGGA ATTATTATGA TTTTAGCCTT
Consensus *****

51                                     100
msa442667.2{248_18RS21} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_2603} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_A909} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_H36B} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_JM9130013} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_COH1} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M781} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_M732} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_090} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_CJB110} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
msa442667.2{248_1169NT} TTTATTGGTA AATAATAGTT ATTTcAGACA GTTAATTGAA GAGCGGTCTA
Consensus *****

101                                    150
msa442667.2{248_18RS21} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_2603} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_A909} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_H36B} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_JM9130013} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_COH1} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_M781} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_M732} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_090} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_CJB110} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
msa442667.2{248_1169NT} AACGTGAAAC GGTAGTcCTT GTCATCATTT TCGGCTTGTT TGTATTATA
Consensus *****

151                                    200
msa442667.2{248_18RS21} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_2603} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_A909} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_H36B} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_JM9130013} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_COH1} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M781} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_M732} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_090} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_CJB110} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
msa442667.2{248_1169NT} TCTAATATAA CAGGAATTGA AATAAAAGGG GATCGAAGTT TGGTCGAGCG
Consensus *****

201                                    250
msa442667.2{248_18RS21} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_2603} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_A909} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_H36B} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_JM9130013} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_COH1} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M781} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_M732} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_090} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_CJB110} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
msa442667.2{248_1169NT} CCCTTTCTA ACAACGATTT CcCATTCTGA CTCACTTGCT AATACAAGGA
Consensus *****

251                                    300
msa442667.2{248_18RS21} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA
msa442667.2{248_2603} CTTTAGTTAT TACAACGGCA AGTTTGGTTG GTGGACCTCT GGTGGATCA

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Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_A909}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_H36B}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_JM9130013}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_COH1}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M781}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_M732}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_090}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_CJB110}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
msa442667.2{248_1169NT}	CTTTAGTTAT	TACAACGGCA	AGTTTGGTTG	GTGGACCTCT	GGTTGGATCA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_2603}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_A909}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_H36B}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_JM9130013}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_COH1}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M781}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_M732}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_090}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_CJB110}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
msa442667.2{248_1169NT}	ATTGTTGGTT	TTATTGGAGG	AGTTCATCGC	TTTTTCAAG	GAAGCTTTTC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_2603}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_A909}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_H36B}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_JM9130013}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_COH1}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_M781}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_M732}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_090}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_CJB110}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
msa442667.2{248_1169NT}	AGGTTCTTTC	TATATTGTCA	GTTCAAGTCT	AGTCGGCATT	GTtAGCGGAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_2603}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_A909}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_H36B}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_JM9130013}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_COH1}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M781}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_M732}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_090}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_CJB110}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
msa442667.2{248_1169NT}	AGATTGGTGA	TAAGCTTAAG	GAAAACCATC	TCTACCCTTC	AACAAGCCAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_2603}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_A909}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_H36B}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_JM9130013}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_COH1}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M781}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_M732}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_090}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_CJB110}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
msa442667.2{248_1169NT}	GTTATTTTAA	TTAGTATTAT	TGCCGAAAGT	ATCCAGATGC	TATTTGTTGG
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_2603}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_A909}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_H36B}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_JM9130013}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_COH1}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M781}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_M732}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_090}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_CJB110}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
msa442667.2{248_1169NT}	CATTTTACAA	GGATGGGAAC	TTGTCAAAAT	GATTGTCAAT	CCAATGATGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTAAATAG	TTTAGTTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACCTAT
	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_2603}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_A909}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_H36B}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_JM9130013}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_COH1}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M781}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_M732}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_090}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_CJB110}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
msa442667.2{248_1169NT}	TTTTAAATAG	TTTAGGTTCC	ACACTTTTCC	TTGCGATTTT	GAAAACTTAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_2603}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_A909}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_H36B}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_JM9130013}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_COH1}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M781}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_M732}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_090}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_CJB110}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
msa442667.2{248_1169NT}	TTGTCAAATG	AAAGTCAGTT	ACGCGCAGTT	CAAACGAGAG	ATGTTCTTGA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_2603}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_A909}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_H36B}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_JM9130013}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_COH1}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M781}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_M732}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_090}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_CJB110}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
msa442667.2{248_1169NT}	ATTGACTCGA	CAGACTCTGC	CCTACCTTAG	ACAAGGTTTG	ACACCGCAAT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_2603}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_A909}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_H36B}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_JM9130013}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_COH1}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M781}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_M732}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_090}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_CJB110}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
msa442667.2{248_1169NT}	CTGCTAGGAG	CGTTTGCGAA	ATTATAAAGA	GGCATACTAA	CTTTGATGCT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_2603}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_A909}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_H36B}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_JM9130013}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_COH1}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M781}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_M732}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_090}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_CJB110}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
msa442667.2{248_1169NT}	GTGGGATTAA	CAGATCGGTC	AAACGTATTA	GCTCATATTG	GTgTTGGCCA
Consensus	**_*****	*****	*****	*****	**_*****
msa442667.2{248_18RS21}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_2603}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_A909}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_H36B}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_JM9130013}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_COH1}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M781}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_M732}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_090}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_CJB110}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
msa442667.2{248_1169NT}	TGATCACCAT	ATTGCAGGAC	AACCgGTCAA	AACAGAcTA	TCTAAAAGTG
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_2603}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_A909}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_H36B}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_JM9130013}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_COH1}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_M781}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_M732}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_090}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_CJB110}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
msa442667.2{248_1169NT}	TTATTTTGA	TGGCGAACCA	AGAATTGCGC	AAGATAAAGC	GGCGATTCT
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_2603}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_A909}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_H36B}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_JM9130013}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_COH1}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M781}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_M732}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_090}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_CJB110}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
msa442667.2{248_1169NT}	TGTCCAGATC	ACAACGTGTC	GTTAAATTCT	GCTATTGTAG	TTCCTCTAAA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_2603}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_A909}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_H36B}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_JM9130013}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_COH1}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M781}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_M732}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_090}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_CJB110}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
msa442667.2{248_1169NT}	AATAAATGAT	AAAACGTGTC	GTGCCCTTAAA	AATGTACTTT	GCAGGAGATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_2603}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_A909}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_H36B}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_JM9130013}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_COH1}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M781}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_M732}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_090}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_CJB110}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
msa442667.2{248_1169NT}	AGACAATGTC	TGAGGTGGAG	GAAAACCTAG	TCCTTGGTTT	AGCGCAAATA
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_2603}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_A909}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_H36B}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_JM9130013}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_COH1}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M781}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_M732}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_090}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_CJB110}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
msa442667.2{248_1169NT}	TTTTTCAGGAC	AACTGGCAAT	GGGGATAACA	GAGGAACAAA	ATAAGTTAGC
Consensus	*****	*****	*****	*****	*****
msa442667.2{248_18RS21}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_2603}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_A909}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_H36B}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_JM9130013}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_COH1}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M781}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_M732}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_090}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_CJB110}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
msa442667.2{248_1169NT}	CAGTATGGCA	GAGATAAAGG	CTTTACAAGC	ACAAATCAAC	CCTCATTTcT
Consensus	*****	*****	*****	*****	*****

Table 58: Comparative Sequences relating to SAG0182

msa442667.2{248_18RS21}	1151	TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT	1200	TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
		TCTTTAATGC	CATTAACACA	ATTAGTGCAT	TAATCCGTAT		TGATTCGTAT
msa442667.2{248_18RS21}	1201	AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA	1250	GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
		AAAGCACGTT	ATGCACGTAT	GCAGTTAAGT	ACTTTTTTTA		GAACAAGTTT
msa442667.2{248_18RS21}	1251	GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA	1300	AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
		GCAGGGTGGT	CAGGATCGTG	AGGTAACGCT	TGAGCAAGAA		AAATCACATG
msa442667.2{248_18RS21}	1301	TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA	1350	TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
		TGGATGCTTA	TATGAATGTT	GAAAAATTAC	GTTTCCCTGA		TAAATATCAG
msa442667.2{248_18RS21}	1351	TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC	1400	CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
		TTATCTTATG	ATATTAGTGC	ACCAGAAAAA	ATGAAGTTAC		CaCCTTTTGG
msa442667.2{248_18RS21}	1401	TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc	1450	AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA
		TTTACAGGTA	CTGGTAGAGA	ATGCAGTTcG	ACATGCCTTc		AAAGAACGTA

		1451					1550
msa442667.2	{248_18RS21}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_2603}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_A909}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_H36B}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_JM9130013}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_COH1}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_M781}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_M732}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_090}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_CJB110}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
msa442667.2	{248_1169NT}	AGACGGACAA	CCATATATTG	GTTCAAATAA	AGCCAGATGG	TCATTATTAT	
Consensus		*****	*****	*****	*****	*****	
		1501					1551
msa442667.2	{248_18RS21}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_2603}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_A909}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_H36B}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_JM9130013}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_COH1}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_M781}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_M732}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_090}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_CJB110}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
msa442667.2	{248_1169NT}	TGTGTTTCTG	TTAGTGACAA	TGGACAAGGA	ATCTCAGATA	CTATCATTGA	
Consensus		*****	*****	*****	*****	*****	
		1551					1600
msa442667.2	{248_18RS21}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_2603}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_A909}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_H36B}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_JM9130013}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_COH1}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_M781}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_M732}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGgACA	GGTACTGCTC	
msa442667.2	{248_090}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_CJB110}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
msa442667.2	{248_1169NT}	TAAATTAGGT	CAAGAAACAG	TTGCAGAGAG	TAAGGGtACA	GGTACTGCTC	
Consensus		*****	*****	*****	*****-***	*****	
		1601					1650
msa442667.2	{248_18RS21}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	
msa442667.2	{248_2603}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	
msa442667.2	{248_A909}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	
msa442667.2	{248_H36B}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	
msa442667.2	{248_JM9130013}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	
msa442667.2	{248_COH1}	TAGTTAATCT	AAATAACAGG	CTGAATTTAT	TATATGGTAG	TGTAAGTTGC	

Table 58: Comparative Sequences relating to SAG0182

Consensus *****

SEQ ID NO. 5811

STRAIN 2603 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5812

STRAIN 090 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5813

STRAIN A909 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5814

STRAIN H36B frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5815

STRAIN 18RS21 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5816

STRAIN M732 frame: 1

LMVLLFQRLGIIMILAFLLVNNSYFRQLIEERSKRETVVLVIIFGLFVVISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRFFQGSFSGSF
 YIVSSVLVGI VSGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGSSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 I I KRHTNFDAVGLTDRSNVLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHNQCQLNSAIVVPLKINDKTVCALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINTSALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQETVAESKGTGTALVNLNLR
 LNLLYGSVSVCLHFSDDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5817

Table 58: Comparative Sequences relating to SAG0182

STRAIN COH1 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRRFFQGSFSGSF
 YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQGETVAESKGTGTALVNLNRR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5818

STRAIN M781 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRRFFQGSFSGSF
 YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQGETVAESKGTGTALVNLNRR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5819

STRAIN CJB110 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRRFFQGSFSGSF
 YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQGETVAESKGTGTALVNLNRR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5820

STRAIN 1169NT frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRRFFQGSFSGSF
 YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQGETVAESKGTGTALVNLNRR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

SEQ ID NO. 5821

STRAIN JM9130013 frame: 1

LMVLLFQRLGIIMILAFLLVNNYSYFRQLIEERSKRETVVLVLIIFGLFVIIISNITGIEIKG
 DRSLVERPFLTTISHSDSLANTRTLVITTASLVGGPLVGSIVGFIGGVHRRFFQGSFSGSF
 YIVSSVLVGVISGKIGDKLKENHLYPSTSQVILISIIAESIQMLFVGIFTGWELVKMIVI
 PMMILNSLGLSTLFLAILKTYLSNESQLRAVQTRDVLELTRQTLPLYLRQGLTPQSARSVCE
 IIKRHTNFDVAGLTDNRNLAHIGVGHDDHIIAGQPVKTDLSKSVIFDGEPRIAQDKAAIS
 CPDHCNQLNSAIVVPLKINDKTVGALKMYFAGDKTMSEVEENLVGLAQIFSGQLAMGIT
 EEQNKLASMAEIKALQAQINPHFFFNAINITISALIRIDSDKARYALMQLSTFFRTSLQGG
 QDREVTLEQEKSHVDAYMNVKLRFPDKYQLSYDISAPEKMKLPPFGLQVLVENAVRHAF
 KERKTDNHILVQIKPDGHYYCVSVSDNGQGISDTIIDKLQGETVAESKGTGTALVNLNRR
 LNLLYGSVSLHFSSDKNGTKVWYRIPNRIREDEHENFNS

PRETTY of: /biotmp/msa442834.2{*} January 13, 2003 06:47 ..

	1		50
msa442834.2{248_090}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_1169NT}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_18RS21}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_2603}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_A909}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_CJB110}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_H36B}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_JM9130013}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_COH1}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M781}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
msa442834.2{248_M732}	LMVLLFQRLG	IIMILAFLLV NNSYFRQLIE	ERSKRETVVL VIIFGLFVII
Consensus	*****	*****	*****
	51		100
msa442834.2{248_090}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS
msa442834.2{248_1169NT}	SNITGIEIKG	DRSLVERPFL TTISHSDSLA	NTRTLVITTA SLVGGPLVGS

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_18RS21}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_2603}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_A909}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_CJB110}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_H36B}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_JM9130013}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_COH1}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M781}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
msa442834.2{248_M732}	SNITGIEIKG	DRSLVERPFL	TTISHSDSLA	NRTTLVITTA	SLVGGPLVGS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_1169NT}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_18RS21}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_2603}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_A909}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_CJB110}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_H36B}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_JM9130013}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_COH1}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M781}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
msa442834.2{248_M732}	IVGFIGGVHR	FFQGSFSGSF	YIVSSVLVGI	VSGKIGDKLK	ENHLYPSTSQ
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_1169NT}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_18RS21}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_2603}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_A909}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_CJB110}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_H36B}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_JM9130013}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_COH1}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M781}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
msa442834.2{248_M732}	VILISIIAES	IQMLFVGIFT	GWELVKMIVI	PMMILNSLGS	TLFLAILKTY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_1169NT}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_18RS21}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_2603}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_A909}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_CJB110}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_H36B}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_JM9130013}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_COH1}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M781}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
msa442834.2{248_M732}	LSNESQLRAV	QTRDVLELTR	QTLPLYRQGL	TPQSARSVCE	IIKRHTNFDA
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_1169NT}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_18RS21}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_2603}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_A909}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_CJB110}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_H36B}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_JM9130013}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_COH1}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M781}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
msa442834.2{248_M732}	VGLTDRSNVL	AHIGvGHDHH	IAGQPVKTDL	SKSVIFDGEP	RIAQDKAAIS
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_1169NT}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_18RS21}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_2603}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_A909}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_CJB110}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_H36B}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_JM9130013}	CPDHNCQLNS	AIVVPLKIND	KTVgALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_COH1}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M781}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
msa442834.2{248_M732}	CPDHNCQLNS	AIVVPLKIND	KTVcALKMYF	AGDKTMSEVE	ENLVLGLAQI
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD

Table 58: Comparative Sequences relating to SAG0182

msa442834.2{248_1169NT}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_18RS21}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_2603}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_A909}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_CJB110}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_H36B}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_JM9130013}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_COH1}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M781}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
msa442834.2{248_M732}	FSGQLAMGIT	EEQNKLASMA	EIKALQAQIN	PHFFFNAIN	ISALIRIDSD
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_1169NT}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_18RS21}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_2603}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_A909}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_CJB110}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_H36B}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_JM9130013}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_COH1}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_M781}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
msa442834.2{248_M732}	KARYALMQLS	TFFRTSLQGG	QDREVTLEQE	KSHVDAYMNV	EKLRFDPKYY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_1169NT}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_18RS21}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_2603}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_A909}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_CJB110}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_H36B}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_JM9130013}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_COH1}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M781}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
msa442834.2{248_M732}	LSYDISAPEK	MKLPPFGLQV	LVENAVRHAF	KERKTDNHIL	VQIKPDGHYY
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_1169NT}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_18RS21}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_2603}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_A909}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_CJB110}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_H36B}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_JM9130013}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_COH1}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M781}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
msa442834.2{248_M732}	CVSVSDNGQG	ISDTIIDKLG	QETVAESKGT	GTALVNLNLR	LNLLYGSVSC
Consensus	*****	*****	*****	*****	*****
msa442834.2{248_090}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_1169NT}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_18RS21}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_2603}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_A909}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_CJB110}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_H36B}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_JM9130013}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_COH1}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M781}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
msa442834.2{248_M732}	LHFSSDKNGT	KVWYRIPNRI	REDEHENFNS		
Consensus	*****	*****	*****		

Table 59: Comparative Sequences relating to SAG2147

SEQ ID NO. 5901

STRAIN 2603

ATGAATAAAGAGAAATTTATCAAAATTTGAATGTAAAAAACATCATTTAGCTTTATGGA
GCTATCACITTTAGTAGCCCTTTTTCATGTATTTTGGCTGTAAATGGTCATCTTTAAAGT
TCACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCA
AAAAAGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAAACCT
TCTCAGGCATCTAATGAAGCCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAG
CAACAAGTTACTGCGAGTGAAGAGGCAGCTGTAGAACAAGCAGTTGTAAACAGAAAAACCC
CCTGCTACCAAGTCAGGCACAACAAGCTTATGCTGTACTGAGACAACCTTATAGACCTGCT
CAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAATACTGCAGGGGCTATTGGCTCA
GCAGCTGCAGACACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATT
ATTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTT
TTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTTAATTCAGCT
ATTAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTACTAG

SEQ ID NO. 5902

STRAIN JM9130013

AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAAA
AGCAGATAAAGTTTCGCGTAGCCAAAAAATCAAAATGAATAAGGCAACAT
CTAAATCAAAAGTAGAAGGTGTAAAAACAGGCTCCAAAACCAAGTTCTCAA
TCTACAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGC
TGTAGAACAAAGCAGTTGTAAACAGAAAAATACCCCTGCTACCAGTCAAGCAC
AACAAGCTTATGCTGTACTGAGACAACCTTATAGACCTGCTCAACACCAG
CCGAGTGGCCCAAGTATTGAGCAATGGAATACTGCAGGGGTTATTTGGCTC
AGCAGCAGCAGCACAAATGGCTGCTGCAACGGGAGTTCCTCAGTCTACTT
GGGAACATATTATTTGCCCGTGAATCAAATGGTAACTCCTAACGTTGCTAAT
GCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAAC
AGCTACAGTTCAGGATCAAGTTAATCAGCTATTAAAGCTTATCTGCTC
AAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5903

STRAIN 1169NT reverse complement

AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCC
AAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCT
CCAAAACCTTTCTCAGGCATCTAATGAAGTCCCAAATCAAGTTCTCAATCTACAGAAGCT
AATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACA
GAAAATACCCCTGCTACCAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTAC
AAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAATACTGCAGGGGCG
GTCCGATCTGCTGCTGAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTTGG
GAACATATTATTTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCT
TCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGATCAAGTT
AATTACAGCTATTAAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5904

STRAIN 18RS21 reverse complement

AAAAGTTCAACAAGTTACTACTGAATCTTTGTCAAAAGCAGATAAAGTTTC
GCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAAGTAGAAGATGTAA
AACAGGCTCCAAAACCTTTCTCAGGCATCTAATGAAGCCCCCAAATCAAGTTCTCAATCTA
CAGAAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAG
TTGTAAACAGAAAAACCCCTGCTACCAGTCAGGCACAACAAGCTTATGCTGTTACTGAGA
CAACTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAATACTGCA
CAGGGGCTATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGT
CTACTTGGGAACATATTATTTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCT
CAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGG
ATCAAGTTAATTACAGCTATTAAAGCTTATCTGCTCAAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5905

STRAIN 090 reverse complement

TAGCCAAAAAATCAAAAATGATTAAAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAAC
AGGCTCCAAAACCTTTCTCAGGCATCTAATGAAGCCCCCAAATCAAGTTCTCAATCTACAG
AAGCTAATTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAGTTG
TAACAGAAAAACCCCTGCTACCAGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAA
CTTATAGACCTGCTCAACACCAGACGAGTGGCCAAAGTATTGAGTAATGGAATACTGCA
GGGCTATTGGCTCAGCAGCTGCAGCACAATGGCTGCTGCAACAGGAGTCCCTCAGTCTA
CTTGGGAACATATTATTTGCCCGTGAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAG
GAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGGA

SEQ ID NO. 5906

STRAIN A909 reverse complement

AAGGCGACATCTAAATCAAAAGTAGAAGATGTAAAAACAGGCTCCAAAACCTTTCTCAGGCA
TCTAATGAAGCCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTCTCAGCAACAAGTT
ACTGCGAGTGAAGAGGCGAGCTGTAGAACAAGCAGTTGTAAACAGAAAAACCCCTGCTACC
AGTCAGGCACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAG
ACAAGTGGCCAAAGTATTGAGTAATGGAATACTGCAGGGGCTATTGGCTCAGCAGCTGCA
GCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTTGCCCGT
GAATCAAATGGTAACTCCTAATGTTGCTAATGCCTCAGGAGCTTCAGGACTTTTCCAAACG
ATGCCAGGTTGGGGTTCAACAGCTACAGTTCAGAAATCAAGTTAATTCAGCTATTAAAGCT
TATCTGCTCAGGTTTATCA

SEQ ID NO. 5907

STRAIN CJB110 reverse complement

AATCTTTGTCAAAAGCAGATAAAGTTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGA

Table 59: Comparative Sequences relating to SAG2147

CATCTAAATCAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATG
 AAGCCCCAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGA
 GTGAAGAGGCAGCTGTAGAACAAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGG
 CACAACAAGCTTATGCTGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACGAGTG
 GCCAAGTATTGAGTAATGGAAATCTGAGGGGCTATTGGCTCAGCAGCTGCAGCACAAA
 TGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAA
 ATGGTAATCCTAATGTTGCTAATGCCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAG
 GTTGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTG
 CTCAGGTTTATCAGCTTGGGGTTAC

SEQ ID NO. 5908

STRAIN COH1 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTGTCAAAGCAGATAA
 AGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGTAGAAGA
 TGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCA
 ATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACA
 AGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCACAACAACTTATGCTGTTAC
 TGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGCCAAAGTATTGAGCAATGGAAA
 TACTGCGAGGGCGGTCGGATCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCC
 TCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAA
 TGCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGT
 TCAGGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGG
 TTAC

SEQ ID NO. 5909

STRAIN H36B reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTGTCAAAGC
 AGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGT
 AGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAG
 TTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGAGTGT
 AGAACAAGCAGTTGTAAACAGAAAACACCCCTGCTACCAGTCAGGCACAACAAGCTTATGC
 TGTTACTGAGACAACCTTATAGACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGTAA
 TGGAAATACTGCGAGGGCTATTGGCTCAGCAGCTGCAGCACAAATGGCTGCTGCAACAGG
 AGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGT
 TGCTAATGCCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGC
 TACAGTTCAGGATCAAGTTAATTCAGCTATTAAAGCTT

SEQ ID NO. 5910

STRAIN M732 reverse complement

AAAAGTTCACAAGTTACTACTGAATCTTGTCAAAGCAGATAAAGTTCGCGTAGC
 CAAAAAATCAAAAATGACTAAGGCGACATCTAAATCAAAGTAGAAGATGTAAACAGGC
 TCCAAAACCTTCTCAGGCATCTAATGAAGCCCCAAATCAAGTTCTCAATCTACAGAAGC
 TAATTTCTCAGCAACAAGTTACTGCGAGTGAAGAGGCGGCTGTAGAACAAGCAGTTGTAAAC
 AGAAAATACCCCTGCTACCAGTCAGGCACAACAACCTTATGCTGTTACTGAGACAACCTTA
 CAAACCTGCTCAACACCAGACAAGTGGCCAAGTATTGAGCAATGGAAATACTGCGAGGGGC
 GGTGGAATCTGCTGCTGCTGCAGCACAAATGGCTGCTGCAACAGGAGTCCCTCAGTCTACTTG
 GGAACATATTATTGCCCGTGAATCAAATGGTAATCCTAATGTTGCTAATGCCCTCAGGAGC
 TTCAGGACTTTTCCAAACGATGCCAGGTTGGGGTTCAACAGCTACAGTTCAAGATCAAGT
 TAATTCAGCTATTAAAGCTTATCGTGCTCAAGGTTTATCAGCTTGGGGTTA

SEQ ID NO. 5911

STRAIN M781 reverse complement

TCCTTGTCAAAGCAGATAAAGTTCGCGTAGCCAAAAAATCAAAAATGACTAAGGCGACA
 TCTAAATCAAAGTAGAAGATGTAAACAGGCTCCAAAACCTTCTCAGGCATCTAATGAA
 GCCCAAAATCAAGTTCTCAATCTACAGAAGCTAATTTCTCAGCAACAAGTTACTGCGAGT
 GAAGAGGCGGCTGTAGAACAAGCAGTTGTAAACAGAAAATACCCCTGCTACCAGTCAGGCA
 CAACAACTTATGCTGTTACTGAGACAACCTTACAAACCTGCTCAACACCAGACAAGTGGC
 CAAGTATTGAGCAATGGAAATACTGCGAGGGCGGTCGGATCTGCTGCTGCAGCACAAATG
 GCTGCTGCAACAGGAGTCCCTCAGTCTACTTGGGAACATATTATTGCCCGTGAATCAAAT
 GGTAAATCCTAATGTTGCTAATGCCCTCAGGAGCTTCAGGACTTTTCCAAACGATGCCAGG
 TGGGGTTCAACAGCTACAGTTCAAGATCAAGTTAATTCAGCTATTAAAGCTTATCGTGCT
 CAAGGTTTATCAGCTTGGGGTTAC

PRETTY of: /biotmp/msa519780.2{*} March 10, 2003 06:25 ..

	1	50
msa519780.2{25_COH1}	-----	-----
msa519780.2{25_M781}	-----	-----
msa519780.2{25_M732}	-----	-----
msa519780.2{25_1169NT}	-----	-----
msa519780.2{25_18RS21}	-----	-----
msa519780.2{25_A909}	-----	-----
msa519780.2{25_090}	-----	-----
msa519780.2{25_CJB110}	-----	-----
msa519780.2{2603}	atgaataaaa	gaagaaaatt atcaaaattg aatgtaaaaa aacatcattt
msa519780.2{25_H36B}	-----	-----
msa519780.2{25_JM9130013}	-----	-----
Consensus	*****	*****
	51	100
msa519780.2{25_COH1}	-----	-----
msa519780.2{25_M781}	-----	-----
msa519780.2{25_M732}	-----	-----

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	agcttatgga	gctatcactt	tagtagccct	tttttcatgt	attttggctg
msa519780.2{25_H36B}	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	taatgggtcat	ctttaaagt	tcacaagtta	ctactgaatc	tttgtcaaaa
msa519780.2{25_H36B}	-----	-----	-----	-----	-----
msa519780.2{25_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_H36B}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_JM9130013}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
Consensus	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_H36B}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_JM9130013}	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
Consensus	gcagataaag	ttcgcgtagc	caaaaaatca	aaaatgactA	AGGCgACATC
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	TAAATCAAAA	GTAGAAGaTG	TAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_H36B}	TAAATCAAAA	GTAGAAGaTG	TAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_JM9130013}	TAAATCAAAA	GTAGAAGaTG	TAAACAGGC	TCCAAAACct	tctcaggcat
Consensus	TAAATCAAAA	GTAGAAGaTG	TAAACAGGC	TCCAAAACct	tctcaggcat
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_H36B}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_JM9130013}	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
Consensus	ctaatagaagc	cccaaaatCA	AGTTCTCAAT	CTACAGAAGC	TAATTCTCAG
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_H36B}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_JM9130013}	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
Consensus	CAACAAGTTA	CTGCGAGTGA	AGAGGCgGCT	GTAGAACAAG	CAGTTGTAAC
msa519780.2{25_COH1}	-----	-----	-----	-----	-----
msa519780.2{25_M781}	-----	-----	-----	-----	-----
msa519780.2{25_M732}	-----	-----	-----	-----	-----
msa519780.2{25_1169NT}	-----	-----	-----	-----	-----
msa519780.2{25_18RS21}	-----	-----	-----	-----	-----
msa519780.2{25_A909}	-----	-----	-----	-----	-----
msa519780.2{25_090}	-----	-----	-----	-----	-----
msa519780.2{25_CJB110}	-----	-----	-----	-----	-----
msa519780.2{2603}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG
Consensus	AGAAAAACC	CCTGCTACCA	GTCAgGCACA	ACAAaCTTAT	GCTGTTACTG

Table 59: Comparative Sequences relating to SAG2147

msa519780.2{25_M732}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_1169NT}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_18RS21}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_A909}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_090}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_CJB110}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{2603}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_H36B}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
msa519780.2{25_JM9130013}	AGAAAAACC	CCTGCTACCA	GTCAGGCACA	ACAACTTAT	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGc
msa519780.2{25_M781}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGc
msa519780.2{25_M732}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGc
msa519780.2{25_1169NT}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGc
msa519780.2{25_18RS21}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{25_A909}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{25_090}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{25_CJB110}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{2603}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{25_H36B}	AGACAACTTA	CAACCTGCT	CAACACCAGA	CAAGTGGCCA	AGTATTGAGt
msa519780.2{25_JM9130013}	AGACAACTTA	CAACCTGCT	CAACACCAGc	CAAGTGGCCA	AGTATTGAGc
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M781}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_M732}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_1169NT}	AATGGAAATA	CTGCAGGGGc	ggTcGGaTcT	GcTgCtGCAG	CACAAATGGC
msa519780.2{25_18RS21}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_A909}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_090}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_CJB110}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{2603}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_H36B}	AATGGAAATA	CTGCAGGGGc	taTtGGcTcA	GcAgCtGCAG	CACAAATGGC
msa519780.2{25_JM9130013}	AATGGAAATA	CTGCAGGGGt	taTtGGcTcA	GcAgCaGCAG	CACAAATGGC
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M781}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_M732}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_1169NT}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_18RS21}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_A909}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_090}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_CJB110}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{2603}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_H36B}	TGCTGCAACA	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
msa519780.2{25_JM9130013}	TGCTGCAACg	GGAGTcCCTC	AGTCTACTTG	GGAACATATT	ATTGCCCGTG
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M781}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_M732}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_1169NT}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_18RS21}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_A909}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_090}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_CJB110}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{2603}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_H36B}	AATCAAATGG	TAATCCTAAT	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
msa519780.2{25_JM9130013}	AATCAAATGG	TAATCCTAAC	GTTGCTAATG	CCTCAGGAGC	TTCAGGACTT
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M781}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_M732}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_1169NT}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_18RS21}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_A909}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_090}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgA-----
msa519780.2{25_CJB110}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{2603}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_H36B}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
msa519780.2{25_JM9130013}	TTCCAAACGA	TGCCAGGTTG	GGGTTCAACA	GCTACAGTTC	AGgAtcaagt
Consensus	*****	*****	*****	*****	*****
msa519780.2{25_COH1}	taattcagct	attaagactt	atcgtgctca	aggtttatca	gcttgggggtt

Table 59: Comparative Sequences relating to SAG2147

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msa519780.2{25_M781} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_M732} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_1169NT} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_18RS21} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_A909} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_090} -----
msa519780.2{25_CJB110} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{2603} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
msa519780.2{25_H36B} taattcagct attaaagctt -----
msa519780.2{25_JM9130013} taattcagct attaaagctt atcgtgctca aggtttatca gcttgggggtt
Consensus -----

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701
msa519780.2{25_COH1} ac---
msa519780.2{25_M781} ac---
msa519780.2{25_M732} a----
msa519780.2{25_1169NT} ac---
msa519780.2{25_18RS21} ac---
msa519780.2{25_A909} -----
msa519780.2{25_090} -----
msa519780.2{25_CJB110} ac---
msa519780.2{2603} actag
msa519780.2{25_H36B} -----
msa519780.2{25_JM9130013} ac---
Consensus ---***

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SEQ ID NO. 5912

STRAIN 2603 frame: 1

MNKRRLSKLNVKKHLLAYGAITLVALFSCILAVMVI FKSSQVTTESLSKADKVRVAKKS
KMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENT
PATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI
IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAI KAYRAQGLSAWGY

SEQ ID NO. 5913

STRAIN 1169NT frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEVPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5914

STRAIN 18RS21 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5915

STRAIN 2603 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5916

STRAIN 090 frame: 3

AKKSKMIKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVV
TENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQST
WEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQ

SEQ ID NO. 5917

STRAIN A909 frame: 1

KATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTASEEAAVEQAVVTENTPAT
SQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQMAAATGVPQSTWEHI IAR
ESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAI KAYRAQGLS

SEQ ID NO. 5918

STRAIN CJB110 frame: 3

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
EEAAVEQAVVTENTPATSSQAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAI GSAAAAQ
MAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVNSAI KAYRA
QGLSAWGY

SEQ ID NO. 5919

STRAIN COH1 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
SQQQVTASEEAAVEQAVVTENTPATSSQAQQTYAVTETTYKPAQHQTSGQVLSNGNTAGAV
GSAAAAQMAAATGVPQSTWEHI IARESNGNPNVANASGASGLFQTMFGWGSTATVQDQVN
SAIKAYRAQGLSAWGY

SEQ ID NO. 5920

STRAIN H36B frame: 1

Table 59: Comparative Sequences relating to SAG2147

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAV
 GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSANG

SEQ ID NO. 5921

STRAIN M732 frame: 1

KSSQVTTESLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEAN
 SQQQVTASEEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAV
 GSAAAAQMAAATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVN
 SAIKAYRAQGLSANG

SEQ ID NO. 5922

STRAIN M781 frame: 4

SLSKADKVRVAKKSKMTKATSKSKVEDVKQAPKPSQASNEAPKSSSQSTEANSQQQVTAS
 EEAAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGAVGSAAAAQMAA
 AATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRA
 QGLSANGY

SEQ ID NO. 5923

STRAIN JM9130013 frame: 1

KSSQVTTESLSKADKVRVAKKSKMNKATSKSKVEGVKQAPKPSQSTEANSQQQVTASEE
 AAVEQAVVTENTPATSOAQQAYAVTETTYRPAQHQTSGQVLSNGNTAGVIGSAAAAQMAA
 ATGVPQSTWEHIIARESNGNPNVANASGASGLFQTMPGWGSTATVQDQVNSAIKAYRAQ
 LSAWGY

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa519418.2(*) March 10, 2003 06:15 ..

	1				50
msa519418.2{25_090}	-----	-----	-----	-----	-----
msa519418.2{25_H36B}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_COH1}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M781}	-----	-----	-----	-----	-----SLSK
msa519418.2{25_1169NT}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_M732}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_18RS21}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{25_CJB110}	-----	-----	-----	-----	-----SLSK
msa519418.2{25_2603}	-----	-----	-----	-----KS	SQVTTESLSK
msa519418.2{2603}	mnkrrrklsl	nvkhhlayg	aitlvalfsc	ilavmvifks	SQVTTESLSK
msa519418.2{25_A909}	-----	-----	-----	-----	-----
msa519418.2{25_JM9130013}	-----	-----	-----	-----KS	SQVTTESLSK
Consensus	*****	*****	*****	*****	*****
	51				100
msa519418.2{25_090}	-----akks	kmiKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_H36B}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_COH1}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_M781}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_1169NT}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_M732}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_18RS21}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_CJB110}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{2603}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_A909}	ADKVRVakks	kmtKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
msa519418.2{25_JM9130013}	ADKVRVakks	kmiKATSKSK	VEDVKQAPKP	sqasneapks	SSQSTEANSQ
Consensus	*****	*****	*****	*****	*****
	101				150
msa519418.2{25_090}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_H36B}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_COH1}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_M781}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_1169NT}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_M732}	QQVTASEEAA	VEQAVVTENT	PATSOAQQtY	AVTETTYkPA	QHQtSGQVLS
msa519418.2{25_18RS21}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_CJB110}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_2603}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{2603}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_A909}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
msa519418.2{25_JM9130013}	QQVTASEEAA	VEQAVVTENT	PATSOAQQaY	AVTETTYrPA	QHQtSGQVLS
Consensus	*****	*****	*****	*****	*****
	151				200
msa519418.2{25_090}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_H36B}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_COH1}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_M781}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_1169NT}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_M732}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_18RS21}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_CJB110}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL

Table 59: Comparative Sequences relating to SAG2147

msa519418.2{25_2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{2603}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_A909}	NGNTAGaIGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
msa519418.2{25_JM9130013}	NGNTAGviGS	AAAAQMAAAT	GVPQSTWEHI	IARESNGNPN	VANASGASGL
Consensus	*****--**	*****	*****	*****	*****
		201		234	
msa519418.2{25_090}	FQTMPGWGST	ATVQ~-----	-----	----	
msa519418.2{25_H36B}	FQTMPGWGST	ATVQDQVNSA	IKA-----	----	
msa519418.2{25_COH1}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M781}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_1169NT}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_M732}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWG-	
msa519418.2{25_18RS21}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_CJB110}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{2603}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
msa519418.2{25_A909}	FQTMPGWGST	ATVQnQVNSA	IKAYRAQGLS	----	
msa519418.2{25_JM9130013}	FQTMPGWGST	ATVQDQVNSA	IKAYRAQGLS	AWGY	
Consensus	*****	*****	*****	****	

Table 60: Comparative Sequences relating to SAG1945

SEQ ID NO. 6001

STRAIN 2603

ATGAAAGAAAAACAGTCGAAAAGGCTTATTTATATACTACTGGTTGTTTCCATTATTTTT
 ATAAGTGTTTTTACATACAGTATAGCCAGCCTTCTAAACTACTTCCACCAAAGAATTA
 GTTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAA
 AATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGATTA
 AGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGCAATTT
 GAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATGTTCACTACTGTTATCCA
 GACTATATCCATCCAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATT
 GTAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTATACAGCCT
 TCCTTAAAAGGTAAAATTGCTTTGCAGATCCGAATACTTCTCTAGTGCTTTCTCACA
 CTCACATAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACTATGTT
 AAAAAAGCTACAACATAATTAATGCTATCAAATCTTCTAGCTCTTCAGAAAGTTTATCAA
 TCAGTTGCAGAAAGGAAAAATGATGTGGGGCTGACTTACGAAGACCCCTAGTGTCAAATTG
 CAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGTCCCA
 TCTTCGGTTGCAATATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTTATTAAT
 TTTATGCTTTCTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGAGTAACCGACCTATT
 CGTAAAGATGCCCAACGAGTAATGGCATGAAGCTTTAAAGGATATTGCTACTCTTAAA
 GAAGATTATCGCTATGCTACTAAGCATAAAGGCCAAATCCTTAAACCTATAATCGTATT
 CGTAGAAATGCTGAT

SEQ ID NO. 6002

STRAIN 090

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGT
 CCAAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAA
 ATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAG
 ATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTCTTTGGA
 GGAATTTATACGCAATTTGAAAGTCATAGGCATTGTTTGAGTCTTACGT
 ATCAAAGAATGTTCACTACTGTTATTTCCAGACTATATCCATCCAAGTGATA
 CGCGACACCTTTATACTATAAATGGGAGTGCTTGATTGTAATAACGAA
 TTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTC
 CTTAAAAGGTAAAATTGCTTTGCAGATCCGAATACTTCTCTAGTGCTTT
 TCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAATCCA
 AAGCGTGGAACTATGTTAAAAAGCTACAACATAATATTAATGCTATCAA
 ATCTTCTAGCTCTTCAGAAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGA
 TTGTGGGGCTGACTTACGAAGACCCCTAGTGTCATTTGCAAAAAAGTGGT
 GCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGTCCCATC
 TTCGGTTGCAATTTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTAT
 TTATTAATTTTATGCTTTCTTATAGATGTTCAAATGCCTTTGGGCAGTCA
 ACGAGTAACCGACCTATTGCTAAAGATGCCCAACGAGTAATGGCATGAA
 AGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGCTACTA
 AGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTTCGTAGAAATGCT
 GAT

SEQ ID NO. 6003

STRAIN A909

CAGCCTTCTAAACTACTTCCACCAAAGAATTAG
 TTATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCT
 TTTGAGGAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGG
 TCAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATA
 TTTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTT
 GAGTCTTACGTATCAAAGAATATTCACTGTTATTCCAGATTATATCCA
 TCCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGCTTGATTG
 TAAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTA
 TTACAGCCTTCTTAAAAGGTAAAATTGCTTTGCAGATCCGAATACTTC
 CTCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTT
 ACACCAATCCAAAAGCGTGGAACTATGTTAAAAGCTACAACATAATATT
 AATGCTATCAAATCTTCTAGCTCTTCAGAAAGTTATCAATCAGTTGCAGA
 AGGAAAAATGATGTGTGGGGTTGACTTACGAAGACCCCTAGTGTCAAATTGC
 AAAAAAGTGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTT
 TTTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAGA
 AGCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAAATGCCT
 TTGGGCAGTCAACGAGTAACCGACCTATTGTAAGATGCCCAACGAGT
 AATGGCATGAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCG
 CTATGCTACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATT
 GTAGAAATGCTGAT

SEQ ID NO. 6004

STRAIN H36B

TAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAATAGTCAAG
 CCAATTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATACGGTATAAAA
 GTTAAGCTTATTCAAGGTGGGACAGGTCAACTAATAGATAGATTAAAGTAA
 GGAGGGTAAGCAGTTGAAGGCGGATATTTCTTTGGAGGAAATTATACGC
 AATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAAAGAATATT
 CATACTGTTATTCCAGATTATATCCATCCGAGTGATACGGCGACACCTTA
 TACTATAAATGGGAGTGCTTGATTGTAATAACGAATTAGTTAAGGGAC
 TTACCATCAAGAGTTATGAAGATTTATTACAGCCTTCTTAAAAGGTAAA
 ATTGCTTTGCAGATCCGAATACTTCTCTAGTGCTTTCTCACAACCTCAC
 TAATATACTCTTGGCCAAGGGTGGTTACACCAATCCAAAAGCGTGGAACT
 ATGTTAAAAGCTACAACATAATATTAAATGCTATCAAATCTTCTAGCTCT
 TCAGAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGATGTGGGGTTGAC
 TTACGAAGACCCCTAGTGTCATTTGCAAAAAAGTGGTGCCAATGTTTCTA
 TTGTATATCCGACAGAAGGGACAGTTTGTGTCCCATCTTCGGTTGCAATT

Table 60: Comparative Sequences relating to SAG1945

ATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATTAAATTTTAT
GCTTTCTTTAGATGTTCAAATGCTTTTGGGCAGTCAACGAGTAACCGAC
CTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTTTAAAGGAT
ATTGCTACTCTTAAAGAAGATTATCGCTATGTCCTAAGCATAAGGGCCA
AATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6005

STRAIN 18RS21

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATTCTAAGTCCAAA
TAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGGAGAAAAATACG
GTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAGA
TTAAGTAAGGAGGTAAGCAGTTGAAGGCCGATATTTCTTTGGAGGAAA
TTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCAA
AGAATGTTTATACACTGTTATTCCAGACTATATCCATCCAAGTGATACGGCG
ACACCTTATACATAAATGGGAGTGTCTTGATTGTAAATAACGAATTAGC
TAAGGGACTTACCATCAAGAGTTATGAAGATTATACAGCCTTCCCTTAA
AAGGTAAATTTGCTTTGCGAGATCCGAATACTTCTCTAGTGCTTTCTCA
CAACTCATAATATACTCTTGGCCAGGGTGGTTACACCAATCCAAAAGC
GTGGAACCTATGTTAAAGCTACACATAATATTAAATGCTATCAAATCTT
CTAGCTCTTCAGAAATTATCAATCAGTTGAGAAAGGAAAAATGATTGTG
GGGCTGACTTACGAAGACCTTAGTGTCATTTGCAAAAAGTGGTGCCAA
TGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCATCTTCGG
TTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTATT
AATTTATGCTTTCTTTAGATGTTCAAATGCTTTGGGCAGTCAACGAG
TAACCGACCTATTGCTAAAGATGCCCAAACGAGTAATGGCATGAAAGCTT
TAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCCTAAGCAT
AAGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6006

STRAIN M732

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT
TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG
CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATAT
TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTG
AGTCTTACGTATCAAAGAATGTTTACTACTGTTATTCCAGACTATATCCAT
CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
AATAACGAATTAGCTAAGGGAATACCATCAAGAGTTATGAAGATTAT
TACAGCCTTCCCTTAAAGGTAAAATTGCTTTGCGAGATCCGAATACTTCC
TCTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTA
CACCATCCAAAAGCGTGAAGTATGTTAAAGCTACAAACATAATATTA
ATGCTATCAAATCTTCTAGCTCTTCAGAAATTATCAATCAGTTGCGAGAA
GGAAAATGATTGTGGGTTGACTTACGAAGACCTTAGTGTCATTTGCA
AAAAAGTGGTGCCAAATGTTTCTATTGTATACCGACAGAAGGGACAGTTT
TTGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
GCAAAGTTATTTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTT
TGGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTA
ATGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
TATGTCATAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCG
TAGAAATGCTGAT

SEQ ID NO. 6007

STRAIN COH1

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGT
ATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTT
TGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGC
AACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATT
TTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGA
GTCCTACGTATCAAAGAATGTTTACTACTGTTATTCCAGACTATATCCATC
CGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTA
AATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATT
ACAGCCTTCCCTTAAAGGTAAAATTGCTTTGCGAGATCCGAATACTTCCCT
CTAGTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTAC
ACCAATCCAAAAGCGTGAAGTATGTTAAAGCTACAAACATAATATTAA
TGCTATCAAATCTTCTAGCTCTTCAGAAATTATCAATCAGTTGCGAGAAG
GAAAATGATTGTGGGTTGACTTACGAAGACCTTAGTGTCATTTGCAA
AAAAGTGGTGCCAAATGTTTCTATTGTATACCGACAGAAGGGACAGTTT
TGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAG
CAAAGTTATTATTAATTTTATGCTTTCTTTAGATGTTCAAATGCTTTT
GGGCAGTCAACGAGTAACCGACCTATTGCTAAAGATGCCCAAACAGTAA
TGGCATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGC
ATGTCATAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCGT
AGAAATGCTGAT

SEQ ID NO. 6008

STRAIN M781

CAGCCTTCTAAACTACTTCCACCAAAGAATTAGTTATT
CTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGA
GAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAAC
TAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGCGGATATTTC
TTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTC
TTACGTATCAAAGAATGTTTACTACTGTTATTCCAGACTATATCCATCCGA
GTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGTAAAT

Table 60: Comparative Sequences relating to SAG1945

AACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTTATTACA
 GCCTTCCTTAAAGGTTAAATTCCTTTGCAGATCCGAATCTTCCTCTA
 GTGCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACC
 AATCCAAAGCGTGGAACTATGTTAAAGCTACAACATAATATTATGCT
 TATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAAGGAA
 AAATGATGTGGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAA
 AGTGGTGCCAATGTTTCTATTGTATACCCGACAGAAGGGACAGTTTGT
 CCCATCTTCGGTTGCAATTATAAAGATGCTCCTTCTATGAAAGAAGCAA
 AGTTATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGG
 CAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAACAAAGTAATGG
 CATGAAAGCTTTAAAGGATATCGCTACTCTTAAAGAAGATTATCGCTATG
 TCACTAAGCATAAGAGCCAAATCCTTAAACCTATAATCGCATTCTGTAGA
 AATGCTGAT

SEQ ID NO. 6009

STRAIN CJB110

CAGCCTTTTAAACTACTTCCACCAAAAGAATTAGTTATTCT
 AAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGG
 AAAAAATACGGTATAAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTA
 ATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATATTTCTT
 TGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTT
 ACGTATCAAAGAATGTTTCACTACTGTTATTCCAGACTATATCCATCCAAGT
 GATACGGCGACACCTTATCTATATAAATGGGAGTGTCTTGATTGTAATAA
 CGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGC
 CTTCCTTAAAGGTAATAATTCCTTTGCAGATCCGAATACTTCCTCTAGT
 GCTTTCTCACAACCTCACTAATATACTCTTGGCCAAGGGTGGTTACACCAA
 TCCAAAAGCGTGGAACTATGTTAAAGCTACAACATAATATTAATGCTA
 TCAAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAAGGAAA
 ATGATTTGTGGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAAAG
 TGGTGCCAATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCTC
 CATCTTCGGTTGCAATTATAAAGATGCTCCTTCTATGAAAGAAGCAAAG
 TTAATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCA
 GTCACAGGTAACCGACCTATTTCGTAAGATGCCCAACGAGTAATGGCA
 TGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTC
 ACTAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAA
 TGCTGAT

SEQ ID NO. 6010

STRAIN 1169NT

ATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTTTTGAGGAAAAATAC
 GGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGGCAACTAATAGATAG
 ATTAAGTAAGGAGGGTAAGCATTTGAAGGCGGATATTTCTTGGAGGAA
 ATTATACGCAATTTGAAAGTCATAAGGCATTGTTTGAGTCTTACGTATCA
 AAGAATGTTTCACTGTTATTCCAGACTATATCCATCCAAGTGATACGGC
 GACACCTTATCTATAAATGGGAGTGTCTTGATTGTAATAACGAATTAG
 CTAAGGGACTTACCATCAAGAGTTATGAAGATTATTACAGCCTTCCTTA
 AAAGTAAATTCCTTTGCAGATCCGAATACTTCCTCTAGTGCTTTCTC
 ACAACTCACCAATATACTCTTGGCAAAGGGTGGTTACACCAATCCAAAG
 CGTGGAACTATGTTAAAGCTACAACATAATATTAATGCTATCAAATCT
 TCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAAAGGAAAAATGATTGT
 GGGGTTGACTTACGAAGACCCCTAGTGTCAATTTGCAAAAAAGTGGTGCCA
 ATGTTTCTATTGTATATCCGACAGAAGGGACAGTTTGTGCCCATCTTCG
 GTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAAGCAAAGTTATTAT
 TAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTTTGGGCAGTCAACGA
 GTAACCGACCTATTTCGTAAGATGCCCAACGAGTAATGGCATGAAAGCT
 TTAAGGATATTGCTACTCTTAAAGAAGATTATCGCTATGTCATAAGCA
 TAAGGGCCAAATCCTTAAACCTATAATCGTATTCTGTAGAAATGCTGAT

SEQ ID NO. 6011

STRAIN JM91130013

CAGCCTTCTAAACTACTTCCACCAAAAGAATTAGT
 TATTCTAAGTCCAAATAGTCAAGCCATTTTAAACAGGAACGATTCCAGCTT
 TTGAGGAAAAATACGGTATAAAGTTAAGCTTATTCAAGGTGGGACAGGG
 CAACTAATAGATAGATTAAAGTAAGGAGGGTAAGCAGTTGAAGGCGGATGT
 TTTCTTTGGAGGAAATTATACGCAATTTGAAAGTCATAAGGCATTGTTG
 AGTCTTACGTATCAAAGAATGTTTCACTGTTATTCCAGACTATATCCAT
 CCGAGTGATACGGCGACACCTTATACTATAAATGGGAGTGTCTTGATTGT
 AAATAACGAATTAGCTAAGGGACTTACCATCAAGAGTTATGAAGATTAT
 TACAGCCTTCCTTAAAGGTAATAATTCCTTTGCAGATCCGAATACTTCC
 TCTAGTGCTTTCTCACAACCTCACCATATACTCTTGGCAAAGGGTGGTTA
 CACCAATCCAAAAGCGTGGAACTATGTTAAAGCTACAACATAATATTA
 ATGCTATCAAATCTTCTAGCTCTTCAGAAGTTTATCAATCAGTTGCAGAA
 GGCAAAATGATTGTGGGGCTGACTTACGAAGACCCCTAGTGTCAATTTGCA
 AAAAAAGTGGTGCCAATGTTTCTATTGTGTATCCGACAGAAGGGACAGTTT
 TGTCCCATCTTCGGTTGCAATTATAAAGAATGCTCCTTCTATGAAAGAA
 GCAAGCTATTATTAAATTTATGCTTTCTTTAGATGTTCAAAATGCCTT
 TGGGAGTCAACGAGTAACCGACCTATTTCGTAAGATGCCCAACGAGTA
 ATGGCATGAAAGCTTTAAAGGATATTGCTACTCTTAAAGAAGATTATCGC
 TATGTCATAAGCATAAGGGCCAAATCCTTAAACCTATAATCGTATTCTG
 TAGAAATGCTGAT

PRETTY of: /biotmp/msa523010.2{*} April 28, 2003 08:55 ..

Table 60: Comparative Sequences relating to SAG1945

	1				50
msa523010.2{263_COH1}	-----	-----	-----	-----	-----
msa523010.2{263_M732}	-----	-----	-----	-----	-----
msa523010.2{263_M781}	-----	-----	-----	-----	-----
msa523010.2{263_A909}	-----	-----	-----	-----	-----
msa523010.2{263_H36B}	-----	-----	-----	-----	-----
msa523010.2{263_090}	-----	-----	-----	-----	-----
msa523010.2{263_18RS21}	-----	-----	-----	-----	-----
msa523010.2{263_2603}	atgaaagaaa	aacagtcgaa	aaggcttatt	tatatactac	tggttggttc
msa523010.2{263_CJB110}	-----	-----	-----	-----	-----
msa523010.2{263_1169NT}	-----	-----	-----	-----	-----
msa523010.2{263_JM91130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa523010.2{263_COH1}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M732}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_M781}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_A909}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_H36B}	-----	-----	-----	-----taaac	-----
msa523010.2{263_090}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_18RS21}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_2603}	cattattttt	ataagtgtt	ttacatacag	tattagccag	ccttctaaac
msa523010.2{263_CJB110}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_1169NT}	-----	-----	-----	-----cag	ccttctaaac
msa523010.2{263_JM91130013}	-----	-----	-----	-----cag	ccttctaaac
Consensus	*****	*****	*****	*****	-----
	101				150
msa523010.2{263_COH1}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M732}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_M781}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_A909}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_H36B}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_090}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_18RS21}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_2603}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_CJB110}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
msa523010.2{263_1169NT}	-----	-----	-----	-----ATAG	TCAAGCCATT
msa523010.2{263_JM91130013}	tacttccacc	aaaagaatta	gttattctaa	gtccaaATAG	TCAAGCCATT
Consensus	-----	-----	-----	-----****	*****
	151				200
msa523010.2{263_COH1}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M732}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_M781}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_A909}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_H36B}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_090}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_18RS21}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_2603}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_CJB110}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_1169NT}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
msa523010.2{263_JM91130013}	TTAACAGGAA	CGATTCCAGC	TTTTGAGGAA	AAATACGGTA	TAAAAGTTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa523010.2{263_COH1}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M732}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_M781}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_A909}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_H36B}	GCTTATTCAA	GGTGGGACAG	GtCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_090}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_18RS21}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_2603}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_CJB110}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_1169NT}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
msa523010.2{263_JM91130013}	GCTTATTCAA	GGTGGGACAG	GgCAACTAAT	AGATAGATTA	AGTAAGGAGG
Consensus	*****	*****	*****	*****	*****
	251				300
msa523010.2{263_COH1}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M732}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_M781}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_A909}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_H36B}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_090}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_18RS21}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_2603}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_CJB110}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_1169NT}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
msa523010.2{263_JM91130013}	GTAAGCagTT	GAAGGCGGAT	aTTTTCTTTG	GAGGAAATTA	TACGCAATTT
Consensus	*****	*****	*****	*****	*****

Table 60: Comparative Sequences relating to SAG1945

		301			350
msa523010.2{263_COH1}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M732}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_M781}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_A909}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_H36B}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATaTTCATAC
msa523010.2{263_090}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_18RS21}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_2603}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_CJB110}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_1169NT}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
msa523010.2{263_JM91130013}	GAAAGTCATA	AGGCATTGTT	TGAGTCTTAC	GTATCAAAGA	ATgTTCATAC
Consensus	*****	*****	*****	*****	*_*_*_*_*_*_*_*
		351			400
msa523010.2{263_COH1}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M732}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_M781}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_A909}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_H36B}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_090}	TGTTATTCCA	GACTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_18RS21}	TGTTATTCCA	GACTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_2603}	TGTTATTCCA	GACTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_CJB110}	TGTTATTCCA	GACTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_1169NT}	TGTTATTCCA	GACTATATCC	ATCCaAGTGA	TACGGCGACA	CCTTATACTA
msa523010.2{263_JM91130013}	TGTTATTCCA	GACTATATCC	ATCCgAGTGA	TACGGCGACA	CCTTATACTA
Consensus	*****	**_*_*_*_*_*_*	*****	*****	*****
		401			450
msa523010.2{263_COH1}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M732}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_M781}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_A909}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_H36B}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_090}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_18RS21}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_2603}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_CJB110}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_1169NT}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
msa523010.2{263_JM91130013}	TAAATGGGAG	TGTCCTTGATT	GTAATAACG	AATTAGcTAA	GGGACTTACC
Consensus	*****	*****	*****	*****_**	*****
		451			500
msa523010.2{263_COH1}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_M732}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_M781}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_A909}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_H36B}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_090}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_18RS21}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_2603}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_CJB110}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_1169NT}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
msa523010.2{263_JM91130013}	ATCAAGAGTT	ATGAAGATTT	ATTACAGCCT	TCCTTAAAAG	GTAATAATGTC
Consensus	*****	*****	*****	*****	*****
		501			550
msa523010.2{263_COH1}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M732}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_M781}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_A909}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_H36B}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_090}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_18RS21}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_2603}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_CJB110}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_1169NT}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
msa523010.2{263_JM91130013}	CTTTGCAGAT	CCGAATACTT	CCTCTAGTGC	TTTCTCACAA	CTCActAATA
Consensus	*****	*****	*****	*****	*****_****
		551			600
msa523010.2{263_COH1}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M732}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_M781}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_A909}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_H36B}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_090}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_18RS21}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_2603}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_CJB110}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_1169NT}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT
msa523010.2{263_JM91130013}	TACTCTTGCC	cAAGGGTGGT	TACACCAATC	CAAAAGCGTG	GAACtATGTT

Table 60: Comparative Sequences relating to SAG1945

Consensus	*****	*****	*****	*****	*****
	601				650
msa523010.2{263_COH1}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M732}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_M781}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_A909}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_H36B}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_090}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_18RS21}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_2603}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_CJB110}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_1169NT}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
msa523010.2{263_JM91130013}	AAAAAGCTAC	AACATAATAT	TAATGCTATC	AAATCTTCTA	GCTCTTCAGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa523010.2{263_COH1}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M732}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_M781}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_A909}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_H36B}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_090}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_18RS21}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_2603}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_CJB110}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_1169NT}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
msa523010.2{263_JM91130013}	AGTTTATCAA	TCAGTTGCAG	AAGGaAAAAAT	GATTGTGGGG	tTGACTTACG
Consensus	*****	*****	*****	*****	*****
	701				750
msa523010.2{263_COH1}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M732}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_M781}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_A909}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_H36B}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_090}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_18RS21}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_2603}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_CJB110}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_1169NT}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTa
msa523010.2{263_JM91130013}	AAGACCCTAG	TGTCAATTTG	CAAAAAAGTG	GTGCCAATGT	TTCTATTGTg
Consensus	*****	*****	*****	*****	*****
	751				800
msa523010.2{263_COH1}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M732}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_M781}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_A909}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_H36B}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_090}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_18RS21}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_2603}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_CJB110}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_1169NT}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
msa523010.2{263_JM91130013}	TaCCCGACAG	AAGGGACAGT	TTTTGTCCCA	TCTTCGGTTG	CAATTATAAA
Consensus	***	*****	*****	*****	*****
	801				850
msa523010.2{263_COH1}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M732}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_M781}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_A909}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_H36B}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_090}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_18RS21}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_2603}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_CJB110}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_1169NT}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
msa523010.2{263_JM91130013}	GAATGCTCCT	TCTATGAAAG	AAGCAAAGTT	ATTTATTAAT	TTTATGCTTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa523010.2{263_COH1}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M732}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_M781}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_A909}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_H36B}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_090}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_18RS21}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_2603}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_CJB110}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
msa523010.2{263_1169NT}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT

Table 60: Comparative Sequences relating to SAG1945

msa523010.2{263_JM91130013}	CTTTAGATGT	TCAAAATGCC	TTTGGGCAGT	CAACGAGTAA	CCGACCTATT
Consensus	*****	*****	*****	*****	*****
	901				950
msa523010.2{263_COH1}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M732}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_M781}	CGTAAAGATG	CCCAAACaAG	TAATGGCATG	AAAGCTTTAA	AGGATATcGC
msa523010.2{263_A909}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_H36B}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_090}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_18RS21}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_2603}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_CJB110}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_1169NT}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
msa523010.2{263_JM91130013}	CGTAAAGATG	CCCAAACgAG	TAATGGCATG	AAAGCTTTAA	AGGATATtGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa523010.2{263_COH1}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCCAAATCC
msa523010.2{263_M732}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCCAAATCC
msa523010.2{263_M781}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	agCCCAAATCC
msa523010.2{263_A909}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_H36B}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_090}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_18RS21}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_2603}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_CJB110}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_1169NT}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
msa523010.2{263_JM91130013}	TACTCTTAAA	GAAGATTATC	GCTATGTCAC	TAAGCATAAG	gGCCCAAATCC
Consensus	*****	*****	*****	*****	*****
	1001				1035
msa523010.2{263_COH1}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M732}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_M781}	TTAAAACCTA	TAATCGcATT	CGTAGAAATG	CTGAT	
msa523010.2{263_A909}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_H36B}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_090}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_18RS21}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_2603}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_CJB110}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_1169NT}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
msa523010.2{263_JM91130013}	TTAAAACCTA	TAATCGtATT	CGTAGAAATG	CTGAT	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 6012

STRAIN 2603 frame: 1

MKEKQSKRLIYILLVVSIIIFISVFTYSISQPSKLLPPKELVILSPNSQAILTGTIPAFEE
 KYGIKVKLIQGGTGQLIDRLSKEGKQLKADIFFGGNYTQFESHKALFESYVSKNVHTVIP
 DYIHPSDTATPYTINGSVLIVNNELAKGLTIKSYEDLLQPSLKGKIAFADPNTSSSAFSQ
 LTNILLAKGGYTNPKAWNYVKKLQHNINAIKSSSSSEVYQSVAEKMIIVGLTYEDPSVNL
 QKSGANVSIVYPTEGTVPFVSSVAIIKNAPSMKEAKLFINFMLS LDVQNAFGQSTSNRPI
 RKDAQTSNGMKALKDIATLKEDYRYVTKHKGQILKTYNRIIRRNAD

SEQ ID NO. 6013

STRAIN 090 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIIRRNAD

SEQ ID NO. 6014

STRAIN A909 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 DIFFGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
 TIKSYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 IKSSSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNA
 PSMKEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKH
 KGQILKTYNRIIRRNAD

SEQ ID NO. 6015

STRAIN H36B frame: 2

KLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKADIF
 FGGNYTQFESHKALFESYVSKNIHTVIPDYIHPSDTATPYTINGSVLIVNNELVKGGLTIK
 SYEDLLQPSLKGKIAFADPNTSSSAFSQLTNILLAKGGYTNPKAWNYVKKLQHNINA
 SSSSEVYQSVAEKMIIVGLTYEDPSVNLQKSGANVSIVYPTEGTVPFVSSVAIIKNAPSM
 KEAKLFINFMLS LDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKEDYRYVTKHKGQ
 ILKTYNRIIRRNAD

SEQ ID NO. 6016

Table 60: Comparative Sequences relating to SAG1945

STRAIN 18RS21 frame: 1
QPSKLLPPKPELVLSNPSQAILTGTIPAFEEKYGIKVKLIQGGTGQILDRLSKEGKQLKA
DIPFGNGYQFESHKALFESVSKNVHTVIPDYIHPSDTATPYTINGSVLIVNNELAKGL
TISKYEDLQPSLKGKIAFADNPITSSSASQLNTILLLAKGGYTNPKAMNYYVKKLQHNINA
IKSSSSSEVYQSAEKGMI VCLTYEDPSNVLKQSGANVSI VYPTGETVFPVSSVAI I KNA
PSMKEAFLIFNMLSLDVQNAFGQSTSNRPI RKDAQTSNGMKALKDIA TLKEDYRYVYTKH
KGKILKTYNRIIRNAD

SEQ ID NO. 6017

STRAIN M732 frame: 1

QPSKLPPKELVILSPNSQAILTGTIPAFEKEYGIKVKLIQGGTGQLIDRLSIVNKKOLKA
 DIFFGNGYQFESHKALFSPSVKSNVHTVIPDYIHPSDATPTYPINGSRLVNNELAKGL
 TIKSYEDLLQPSKLKGKIAFADPNSTSSAFQSLTNHLLAKGGTYNPKAWNYVKKLQHNIA
 IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSCANVSI VPTEGTVFVPSSVAIKNA
 PSMKEAKLPINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIALTKEDYRYVYTKH
 KSQILTKPYNRINRDV

SEQ ID NO. 6018

STRAIN COH1 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKQLKA
 TIFEGGNYTFQFESHKALFESVYSKNVHTVPIDYIHPSTDATPTYPINGSVLVNNELAKGL
 DTKFSEYDLLOQSKLKGKIAFADNPSTSSAFSLNTLILAKGTYPNKAPWNVKKLOHNI
 IKSSSSSEVYQSAEKGKIMVGLTYEDPSVNLQKSGANVSIYVTEGTVFVPESSVAIKNA
 PSMKEAKLPINFMLSLDVQNAFGQSTSNRPIRKDAQTSNGMKALKDIATLKDEYRYVTKH
 KSOILKTYNRIIRDNA

SEQ ID NO. 6019

STRAIN M781 frame: 1

QPSKLLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGQLIDRLSKGKOLKA
LDFFGNGYQFQSHKALPESYVSNHVHTIPDYIHPSDTPATPYINGSVLVNNELAKGL
TTKSYEDLLQPSKLGKIAFADPENTSSAFSOLTNLILAKGGTYNPKAWNYVKKLQHNI
IKSSSSSEVYQSVAECKMIVGLTYEDPSVNLQKSGANVSI VPTYEGTVFPVSSVAIKNA
PSMKEAKLFINFMLSVDQNAFGQSTSNRP IRKDAQTSNGMKALKDIATLKEDYRYVTKH
KSOILKTYKNIRNAD

SEO ID NO. 6020

STRAIN CJB110 frame: 1

QPKFLPPKELVILSPNSQAILTGTIPAFEEKYGIKVKLIQGGTGLDRLSKEGKOLKA
DIFPGNGYQFESHLKALFESVSKNVNIPDYIHPSDTPATPYTNGSVLIVNNEALGL
TIKSYEDLLQPSHLKGKIAFADNPSTSSAFQSLNTLILAKGGYTNKPAWYVKLQHNINA
IKSSSSSEVYQSVAEKGMIVGLTYEDPSVNLQKSGANVSI VYPTEGTVPVPSSVAIIKNA
PMKEAKLFINFMLSLDVQNAFGQSTSNRP IRKDAQTSNGMKALKDIATLKDEDYRYVTKH
KGOILKTYNRIRRND

SEQ ID NO. 6021

STRAIN 1169NT frame: 3

STAILTGTTPAFEEKYGIKVKLIQGGTGQLIDRLSKEGKHLKADIFFGGNYTQFESHKAL
FESYVSKNVHTVTPDYIHPSDTATPYTINGSVLIVNNELAKGLTISKYEDLLQPSLKGGKI
AFADPNTSSSAFSQLNILLAKGGYTNPKAWNYVVKLOHINAINIKSSSSSEVYQSVABEG
MIVGLTYEDPSQLNQLKSGANVSIYVPTGTGTFVFPSSVAIKNAPSMKEAKLFINFMLSL
VONAFGOSTSNRPIKDAOTSGNMKALKDIATLKEDYRYVTKHGQILKTYNRI RNAD

SEQ ID NO. 6022

STRAIN JM91130013 frame: 1

STRAIN 361/1506 = strain 1
QPSKLPPKELVILSPNSQAALLGTIPAFEEKYKGIKVKLIQGGTGQLIDRLSKEGKQLKA
DVFFGGNYQFESHKALFESYVSKNVHTIYDPDIHSPDATPYTNGSVLIVNNELAKGL
TKISYEDLLQPSLKGKIAFADNPSTSSAFSOLTNILLAKGGYTNPKAWYVKVLLQHNINA
IKSSSSSEVYQSAEGKMIIVGLTYEDPSVNLQKSGANVSIIVYPTGTVFVPSVAIIKNA
PSMKEAKLFINFMLSLDVQNAFGQSTSNRP1RKDAQTSNMGMAKLDIATLKEDYRYVTKH
KGOTIKTYNNRISLAD

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PRETTY of: /biotmp/msa523117.2{*}    April 28, 2003 08:56  ..
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	1	50
msa523117.2 {263_COH1}	-----q	pskllppkel vilspnSQAI
msa523117.2 {263_M732}	-----q	pskllppkel vilspnSQAI
msa523117.2 {263_M781}	-----q	pskllppkel vilspnSQAI
msa523117.2 {263_1169NT}	-----	-----SQAI
msa523117.2 {263_CJB110}	-----q	pfkllppkel vilapnSQAI
msa523117.2 {263_O90}	-----q	pskllppkel vilapnSQAI
msa523117.2 {263_18RS21}	-----q	pskllppkel vilapnSQAI
msa523117.2 {263_2603}	mkekqskrli yillvvsii	iavfytysisq pskllppkel vilapnSQAI
msa523117.2 {263_A909}	-----q	pskllppkel vilapnSQAI
msa523117.2 {263_JM91130013}	-----q	pskllppkel vilapnSQAI
msa523117.2 {263_H36B}	-----	---kllppkel vilapnSQAI
Consensus	*****	*****

	51	100
msa523117.2{263_COH1}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M732}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_M781}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKqLKAD iFFGGNYTQF	
msa523117.2{263_1169NT}	LTGTIPAFEE KYGIKVKLIQ GGTGQLIDRL SKEGKhLKAD iFFGGNYTQF	

Table 60: Comparative Sequences relating to SAG1945

msa523117.2{263_CJB110}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_090}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_18RS21}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_2603}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_A909}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
msa523117.2{263_JM91130013}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	vFFGGNYTQF
msa523117.2{263_H36B}	LTGTIPAFEE	KYGIKVKLIQ	GGTGQLIDRL	SKEGKqLKAD	iFFGGNYTQF
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M732}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_M781}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_1169NT}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_CJB110}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_090}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_18RS21}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_2603}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_A909}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_JM91130013}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELaKGLT
msa523117.2{263_H36B}	ESHKALFESY	VSKNvHTVIP	DYIHPSDTAT	PYTINGSVLI	VNNELvKGLT
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M732}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_M781}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_1169NT}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_CJB110}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_090}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_18RS21}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_2603}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_A909}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_JM91130013}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
msa523117.2{263_H36B}	IKSYEDLLQP	SLKGKIAFAD	PNTSSSAFSQ	LTNILLAKGG	YTNPKAWNYV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M732}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_M781}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_1169NT}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_CJB110}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_090}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_18RS21}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_2603}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_A909}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_JM91130013}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
msa523117.2{263_H36B}	KKLQHNINAI	KSSSSSEVYQ	SVAEGKMIVG	LTIEDPSVNL	QKSGANVSIV
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M732}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_M781}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_1169NT}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_CJB110}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_090}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_18RS21}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_2603}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_A909}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_JM91130013}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
msa523117.2{263_H36B}	YPTEGTVFVP	SSVAIIKNAP	SMKEAKLFIN	FMLS LDVQNA	FGQSTSNRPI
Consensus	*****	*****	*****	*****	*****
msa523117.2{263_COH1}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M732}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_M781}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_1169NT}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_CJB110}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_090}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_18RS21}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_2603}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_A909}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_JM91130013}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
msa523117.2{263_H36B}	RKDAQTSNGM	KALKDIATLK	EDYRYVTKHK	gQILKTYNRI	RRNAD
Consensus	*****	*****	*****	*****	*****

Table 61: Comparative Sequences relating to SAG1030

SEQ ID NO. 6101

STRAIN 2603

ATGGTAAAAGTTAGTGTAAGTCTGTAGGAACCTCAAGCATCAACAGTAGCTATTTCTATG
 TTTAGTCGTGTATCGGCTTTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGGAACGTTAACT
 CCGATGCTTCAAGGAATGATTCCTTTCTCTGAAACATTGAGTGAGAAATGTACAGAATTA
 CAAACCTTATATGTCTCAATTTGTGGTGATGAGGATTTAGACTCTGTCTGTTTAGAATCA
 AAATTAGCAAGTGATAGGGCATCATTAAGATTTGCTGAAGCACCTTTTAGAGCATCTTAAC
 GATGATCCAGAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAATTTAACGCCCAT
 TCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAACTGTTAACCAAGCACTAGCG
 GCTGTTTCAACAGGATTTTCTGGATATAATAGTAAACCGGAGCTTTTGGAAAAACCAACA
 TCCGGACAGATGGAATGGACAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCC
 AAAGCTGAAGAACTGAAAGTAAAGGCTGAAGAAAGTAAGAAGCTTCAAAAAATTGAA
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAAGCGGCTAAT
 GAAGCGTATAAATTAGGAGAAATAAAAAGATACCTATGAATCAATTATCAGTGGTTTA
 AGTAATGCATCGGCTGCCTTACTTAAAGAGGTAGCTAAATCAAAATTGACTGACACAGCT
 CGGCTATTGATG

SEQ ID NO. 6102

STRAIN 090

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 GCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTGG
 AACGTTAACTCCGATGCTTCAAGGAATGATTTCTTTCTCTGAAACATTGA
 GTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT
 GAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGATAGGGC
 ATCATTAAAGATTGCTGAAGCACCTTTAGAGCATCTTAACGATGATCCAG
 AACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
 TAAGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
 CTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAAT
 AGTAAAAACGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGAC
 AAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG
 AACTGAAAGTAAAAAGGCTGAAGAAAGTAAGAAGCTTCAAAAAATTGAA
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA
 AGCGGCTAATGAAGCGTATAAATTAGGAGAAATAAAAAGATACCTATG
 AATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGAG
 GTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

SEQ ID NO. 6103

STRAIN 18RS21

TTAAATGATGCAATAACAAAACCTATCATCTTTTGCAGAGGCT
 TGCAACTCTTCAAGGGACTGCTTATTCAAATGCAAAAAGCTATGCTACTG
 GAACGTTAACTCCGATGCTTCAAGGAATGATTTCTTTCTCTGAAACATTG
 AGTGAGAAATGTACAGAATTACAAACCTTATATGTCTCAATTTGTGGTGAT
 TGAGGATTTAGACTCTGTCTGTTTAGAATCAAAATTAGCAAGTGATAGGG
 CATCATTAAAGATTGCTGAAGCACCTTTAGAGCATCTTAACGATGATCCA
 GAACCTTCCAAATCTGCCATAAGTTCTACAAAAAGTAATATTAAAAAATTA
 AAAAAACGTATAAAATCTAATCAAAAGAAATTAGACAACCTTAATGAAT
 TTAACGCCCATTCAGCAACAGTATTTGCGGACATTTCTAATGCACAGTCAA
 ACTGTTAACCAAGCACTAGCGGCTGTTTCAACAGGATTTTCTGGATATAA
 TAGTAAAACCGGAGCTTTTGGAAAACCAACATCCGGACAGATGGAATGGA
 CAAAGACAGTTAAGAAGAATTGGAAGAGCGAGAAGACGCCAAAGCTGAAG
 GAAGTGAAGTAAAAAGGCTGAAGAAAGTAAGAAGCTTCAAAAAATTGA
 AATACTACTAAAAAAGTAATGTTTCAGTTGATAAAAAGAAATTAATAAA
 AAGCGGCTAATGAAGCGTATAAATTAGGAGAAATAAAAAGATACCTAT
 GAATCAATTATCAGTGGTTAAGTAATGCATCGGCTGCCTTACTTAAAGA
 GGTAGCTAAATCAAAATTGACTGACACAGCTCGGCTATTGATG

PRETTY of: /biotmp/msa185066.2{*} May 13, 2003 07:01 ..

	1				50
msa185066.2{270_090}	-----	-----	-----	-----	-----
msa185066.2{270_18RS21}	-----	-----	-----	-----	-----
msa185066.2{270_2603}	atggtaaaag	ttagtgtgaag	ttctgttagga	actcaagcat	caacagtagc
Consensus	*****	*****	*****	*****	*****
	51				100
msa185066.2{270_090}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_18RS21}	-----	-----	-----TT	AAATGATGCA	ATAACAAAAC
msa185066.2{270_2603}	tattttctatg	tttagtcgtg	tatcggcttt	AAATGATGCA	ATAACAAAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa185066.2{270_090}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_18RS21}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
msa185066.2{270_2603}	TATCATCTTT	TGCAGAGGCT	GCAACTCTTC	AAGGGACTGC	TTATTCAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa185066.2{270_090}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_18RS21}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT
msa185066.2{270_2603}	GCAAAAAGCT	ATGCTACTGG	AACGTTAACT	CCGATGCTTC	AAGGAATGAT

Table 61: Comparative Sequences relating to SAG1030

Consensus	*****	*****	*****	*****	*****
	201				250
msa185066.2{270_090}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_18RS21}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
msa185066.2{270_2603}	TCTTTTCTCT	GAAACATTGA	GTGAGAAATG	TACAGAATTA	CAAACCTTAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa185066.2{270_090}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_18RS21}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
msa185066.2{270_2603}	ATGTCCTCAAT	TTGTGGTGAT	GAGGATTTAG	ACTCTGTCGT	TTTAGAATCA
Consensus	*****	*****	*****	*****	*****
	301				350
msa185066.2{270_090}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_18RS21}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
msa185066.2{270_2603}	AAATTAGCAA	GTGATAGGGC	ATCATTAAAG	ATTGCTGAAG	CACCTTTAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa185066.2{270_090}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_18RS21}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
msa185066.2{270_2603}	GCATCTTAAC	GATGATCCAG	AACCTTCCAA	ATCTGCCATA	AGTTCTACAA
Consensus	*****	*****	*****	*****	*****
	401				450
msa185066.2{270_090}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_18RS21}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
msa185066.2{270_2603}	AAAGTAATAT	TAAAAAATTA	AAAAAACGTA	TAAATCTAA	TCAAAAGAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa185066.2{270_090}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_18RS21}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
msa185066.2{270_2603}	TTAGACAACC	TTAATGAATT	TAACGCCCAT	TCAGCAACAG	TATTTGCGGA
Consensus	*****	*****	*****	*****	*****
	501				550
msa185066.2{270_090}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_18RS21}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
msa185066.2{270_2603}	CATTTCTAAT	GCACAGTCAA	CTGTTAACCA	AGCACTAGCG	GCTGTTTCAA
Consensus	*****	*****	*****	*****	*****
	551				600
msa185066.2{270_090}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_18RS21}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
msa185066.2{270_2603}	CAGGATTTC	TGGATATAAT	AGTAAACCG	GAGCTTTTGG	AAAACCAACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa185066.2{270_090}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_18RS21}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
msa185066.2{270_2603}	TCCGGACAGA	TGGAATGGAC	AAAGACAGTT	AAGAAGAATT	GGAAAGAGCG
Consensus	*****	*****	*****	*****	*****
	651				700
msa185066.2{270_090}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_18RS21}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
msa185066.2{270_2603}	AGAAGACGCC	AAAGCTGAAG	AACTGAAAAG	TAAAAAGGCT	GAAGAAAGTA
Consensus	*****	*****	*****	*****	*****
	701				750
msa185066.2{270_090}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_18RS21}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
msa185066.2{270_2603}	AGAAAGCTTC	AAAAATTGAA	AATACTACTA	AAAAAAGTAA	TGTTTCAGTT
Consensus	*****	*****	*****	*****	*****
	751				800
msa185066.2{270_090}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_18RS21}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
msa185066.2{270_2603}	GATAAAAAGA	AATTAATAAA	AGCGGCTAAT	GAAGCGTATA	AATTAGGAGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa185066.2{270_090}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_18RS21}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
msa185066.2{270_2603}	AATTAAAAAA	GATACCTATG	AATCAATTAT	CAGTGGTTTA	AGTAATGCAT
Consensus	*****	*****	*****	*****	*****
	851				900
msa185066.2{270_090}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT
msa185066.2{270_18RS21}	CGGCTGCCTT	ACTTAAAGAG	GTAGCTAAAT	CAAAATTGAC	TGACACAGCT

Table 61: Comparative Sequences relating to SAG1030

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msa185066.2{270_2603} CGGCTGCCTT ACTTAAAGAG GTAGCTAAAT CAAAATTGAC TGACACAGCT
Consensus *****
          901          912
msa185066.2{270_090} CGGCTATTGA TG
msa185066.2{270_18RS21} CGGCTATTGA TG
msa185066.2{270_2603} CGGCTATTGA TG
Consensus ***** **

SEQ ID NO. 6104
STRAIN 2603 frame: 1
MVKVSVSSVGTQASTVAISMFSRVSALNDAITKLSSFAEAATLQGTAYSNAKSYATGTLT
PMLQGMILFSETLSEKCTELQTLTVSICGDEDLDSVVLESKLASDRASLKIAEALLEHLN
DDPEPSKSAISSTKSNIKKLKKRIKSNQKKLDNLNEFNAHSATVFADISNAQSTVNQALA
AVSTGFSGYNSKTGAFGKPTSGQMEWTKTVKKNWKEREDAKAEELKSKKAEESKKASKIE
NTTKKSNVSVDDKKKLIKAANEAYKLGEIKKDTYESIISGLSNASAALLKEVAKSKLTDTA
RLLM

SEQ ID NO. 6105
STRAIN 090 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKKLIKAANEAYKLGE
EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM

SEQ ID NO. 6106
STRAIN 18RS21 frame: 1
LNDAITKLSSFAEAATLQGTAYSNAKSYATGTLTPMLQGMILFSETLSEKCTELQTLTVS
ICGDEDLDSVVLESKLASDRASLKIAEALLEHLNDDPEPSKSAISSTKSNIKKLKKRIKS
NQKKLDNLNEFNAHSATVFADISNAQSTVNQALAAVSTGFSGYNSKTGAFGKPTSGQMEW
TKTVKKNWKEREDAKAEELKSKKAEESKKASKIENTTKKSNVSVDDKKKLIKAANEAYKLGE
EIKKDTYESIISGLSNASAALLKEVAKSKLTDARLLM
PRETTY of: /biotmp/msa185181.2{*} May 13, 2003 07:03 ..

          1          50
msa185181.2{270_090} ~~~~~-LND AITKLSSFAEA ATLQGTAYSN
msa185181.2{270_18RS21} ~~~~~-LND AITKLSSFAEA ATLQGTAYSN
msa185181.2{270_2603} mvkvsvssvg tqastvaism fersvaLND AITKLSSFAEA ATLQGTAYSN
Consensus *****

          51          100
msa185181.2{270_090} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_18RS21} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
msa185181.2{270_2603} AKSYATGTLT PMLQGMILFS ETLSEKCTEL QTLVVSICGD EDLDSVVLES
Consensus *****

          101          150
msa185181.2{270_090} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_18RS21} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
msa185181.2{270_2603} KLASDRASLK IAEALLEHLN DDPEPSKSAI SSTKSNIKKL KKRIKSNQKK
Consensus *****

          151          200
msa185181.2{270_090} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_18RS21} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
msa185181.2{270_2603} LDNLNEFNAH SATVFADISN AQSTVNQALA AVSTGFSGYN SKTGAFGKPT
Consensus *****

          201          250
msa185181.2{270_090} SQQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_18RS21} SQQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
msa185181.2{270_2603} SQQMEWTKTV KKNWKEREDA KAEELKSKKA EESKKASKIE NTTKKNVSV
Consensus *****

          251          300
msa185181.2{270_090} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_18RS21} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
msa185181.2{270_2603} DKKKLIKAAN EAYKLGEIKK DYESIISGL SNASAALLKE VAKSKLTDTA
Consensus *****

          301
msa185181.2{270_090} RLLM
msa185181.2{270_18RS21} RLLM
msa185181.2{270_2603} RLLM
Consensus ****

```

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6201

STRAIN 2603

ATGATTTTAAAAATTTGTCGTGCAGCATATAGTTTACAATGGGGAGGTGTTACCAATTA
 GCTTTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATA
 GCTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAACATCTCCTC
 GC AAAAATGTTTCATTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATAT
 AGAGAAGCGGCAGCTACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTAAAGC
 CATACATGTACGATTGAAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCA
 GTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAAGATAAGAGGAATGCTGCTGGA
 GACCTTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATCTCGTTAT
 CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAACAGTAGGT
 TTTAAGCCAGGGGTCAGTTTTCATTTTACTTATCAAGATATCATCAATCATCCTGATTCT
 ATTTTGTATGGTTATCATCCTGCTGCTAAAAATAAAAATCAGCTTCTTTAGCAGAACATTTA
 GTTGCATGTGTTATCCCAAAACATTATCAAGAAAGATTATCAAAGCCTTGTGCCCAATGAC
 TTGAAACACAGGGTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAA
 AAAGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6202

STRAIN 090

TGGATTATCCTCTAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTC
 ATAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACAATGTGACGA
 TAAACATCTCCTCACAAAATGTTTCATTTTAAAAATACAATAGTTTTC
 CTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACTTTAATGAG
 GATGGTATTAGTTTAACTTCTGATTTTAAAGCCATACATGTACGATTGA
 AACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAG
 CCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCT
 GGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACTGGTCAAATAC
 CAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCAT
 CTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGCTTTCATTTT
 AATTATCAAGATATCATCAATCATCCTGATTCTATTTTGTATGGTTATCA
 TCCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACATTTAGTTGCAT
 GTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCTAAT
 GACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGAAACACTTTA
 TGAGTGAATCAAAAAGTTTATGATTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6203

STRAIN A909

TTGCTGGATTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATA
 GGAGCTTTCTAGCTTACGAGAAACAATATAAAAGAAAAATTGAGATACA
 ATGTGACGATAAACATCTCCTCACAAAATGTTTCATTTTAAAAATACA
 ATAGTTTACTTTTCCCTATATTCCCAAATATAGAGAAGCGGCAGCTACT
 TTTAATGAGGATGGTATAGTTTAACTTCTGATTTTAAAGCCATACATG
 TACGATTGAACTGCAAACTAATTTTAAAGAAGGTAAAACTTATCAG
 CAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAGAGG
 AATGCTGCTGGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAACTG
 GTCAAATACCAATCTCGTTTATCGTTTAGTAATGGAAAGATTGTTAGGCA
 AAGCACCATCTGAACAGGAGTTAACAGTAGCTTTTAAAGCCAGGGGTCAGC
 TTTTCATTTTAAATTATCAAGATATCATCAATCATCCTGATTCTATTTTGA
 TGGTTATCATCTGCTGCTAAAATTAAAAATCAACTTTCTTTAGCAGAACAT
 TAGTTGCATGTGTTATCCCAAAACATTATCAAGAAGATTATCAAAGCCTT
 GTGCCCTAATGACTTGAAACACAGAGTTTATTATTTAGATTACTGTAACGA
 AACACTTTATGAGTGGAATCAAAAAGTTTATGATTTCTTTGTCAATTGG
 AAAATAA

SEQ ID NO. 6204

STRAIN H36B

TTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAA
 CAATATAAAAGAAAAATTGAGATACAATGTGACGATAAACATCTCCTCAC
 AAAAATGTTTCATTTTAAAAATACAATAGTTTACTTTTCCCTATATTTC
 CCAAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTA
 ACTTCTGATTTTAAAGCCATACATGTACGATTGAACTGCAAACTAAT
 TTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAGCCTTTAATAAGCCTG
 CTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTTAAAGAT
 TACTTTGACTATGTGATGTTGAACTGGTCAAATACCAATTCTGGTTATCG
 TTTAGTAATGGAAAGATTGTTAGGCAAGCACCATCTGAACAGGAGTTAA
 CAGTAGCTTTTAAAGCCAGGGGTCAGCTTTTCATTTTAAATTATCAAGATATC
 ATCAATCATCCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTA
 AATCAACTTTCTTTAGCAGAACATTTAGTTGCATGTGTTATCCCAAAAC
 ATTATCAAGAAGATTATCAAAGCCTTGTGCCCTAATGACTTGAACACAGA
 GTTTATTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAATCAAAA
 AGTTTATGATTTTCTTTGTCAATTGGAAAAATAA

SEQ ID NO. 6205

STRAIN 18RS21

TTGCTGGATTATCCTCGAATTAAGGCGTT
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAA
 GAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAATGTT
 CATTTTAAAAATACAATAGTTTACTTTTCCCTATATTCCCAAATATAG
 AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTGATT
 TTTTAAAGCCATACATGTACGATTGAACTGCAAACTAATTTTAAAGAA
 GGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
 GGTAAAGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACT
 ATGTGATGTTGAACTGGTCAAATACCAATCTGGTTATCGTTTAGTAATG

Table 62: Comparative Sequences relating to SAG0690

GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAAAAGTTTATGAT
 TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6206

STRAIN M732

TTGCTGGATTATCCTCGAATTAAGGCGTT
 TGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATAAAA
 GAAAAACTGAGATACAATGTGACGATAAACATCTCCTCGCAAAAATTTGTT
 CATTTTAAATAACAATAGTTTACITTTCCCTATATCCCAAAATATAG
 AGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTAACTTCTGATT
 TTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTAAAGAA
 GGTAAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACT
 GGTAAAAGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACT
 ATGTGATGTTGAAGTGGTCAAAATACCAATTCTGGTTATCGTTTAGTAATG
 GAAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGGTTT
 TAAGCCAGGGGTGAGTTTTCATTTTACTTATCAAGATATCATCAATCATC
 CTGATTCTATTTTGTATGGTTATCATCCTGCTAAAATTAAAAATCAGCTT
 TCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCAAGA
 AGATTATCAAAGCCTTGTGCCAATGACTTGAACACAGGGTTTATTATT
 TAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAAAAAGTTTATGAT
 TTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6207

STRAIN COH1

TTGCTGGAT

TATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAGC
 TTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAAC
 ATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTTT
 CCTATATTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATGG
 TATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAAACTG
 CAAACTAATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTTT
 AATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAGA
 CCTAAAGATTACTTTGACTATGTGATGTTGAAGTGGTCAAAATACCAAT
 CTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGAA
 CAGGAGTTAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTTA
 TCAAGATATCATCAATCATCTGATTCTATTTTGTATGGTTATCATCTCG
 CTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGTT
 ATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACTT
 GAAACACAGGGTTTATTATTATGATTACTGTAAACGAAACACTTTATGAGT
 GGAATCAAAAAGTTTATGATTTTCTTTGGCAITTTGGAAAATAAA

SEQ ID NO. 6208

STRAIN M781

TTGCTGGA

TTATCCTCGAATTAAGGCGTTTGAATTGGAAAGGATAGGAGCTTTCATAG
 CTTACGAGAAACAATATAAAAGAAAACTGAGATACAATGTGACGATAAA
 CATCTCCTCGCAAAAATTTGTTTCAITTTTAAATAACAATAGTTTACTTT
 TCCTATATTCCCAATATAGAGAAGCGGCAGCTACTTTAATGAGGATG
 GTATTAGTTTAACTTCTGATTTTTAAAGCCATACATGTACGATTGAACT
 GCAAACTAATTTTAAAGAAGGTAAAATCTTATCAGCAGTTAAAGCCTT
 TAATAAGCCTGCTGAAGTACTGGTAAAAGATAAGAGGAATGCTGCTGGAG
 ACCCTAAAGATTACTTTGACTATGTGATGTTGAAGTGGTCAAAATACCAAT
 TCTGGTTATCGTTTAGTAATGGAAGATTGTTAGGCAAAGCACCATCTGA
 ACAGGAGTTAAACAGTAGGTTTAAAGCCAGGGGTGAGTTTTCATTTTACTT
 ATCAAGATATCATCAATCATCTGATTCTATTTTGTATGGTTATCATCT
 GCTAAAATTAATAATCAGCTTCTTTAGCAGAACATTAGTTGCATGTGT
 TATCCCAAAACATTATCAAGAAGATTATCAAAGCCTTGTGCCCAATGACT
 TGAACACAGGGTTTATTATTATGATTACTGTAAACGAAACACTTTATGAGT
 TGAATCAAAAAGTTTATGATTTTCTTTGTCATTTGGAAAATAAA

SEQ ID NO. 6209

STRAIN CJB110

TTGCTGGATTATCCTCGAATTAAGGC

GTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGAAACAATATA
 AAAGAAAAATTTAGATACAATGTGACGATAAACATCTCCTCACAATAAT
 GTTCATTTTAAATAACAATAGTTTACTTTTCCCTATATCCCAATA
 TAGAGAAGCGGCAGCTACTTTAATGAGGATGGTATTAGTTTAACTTCTG
 ATTTTAAAGCCATACATGTACGATTGAAACTGCAAACTAATTTTAA
 GAAGTAAATCTTATCAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGT
 ACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCTTAAAGATTACTTTG
 ACTATGTGATGTTGAAGTGGTCAAAATACCAATCTGGTTATCGTTTAGTA
 ATGGAAGATTGTTAGGCAAAGCACCATCTGAACAGGAGTTAACAGTAGC
 TTTTAAAGCCAGGGGTGAGTTTTCATTTTAAATATCAAGATATCATCAATC
 ATCCTGATTCTATTTTGTATGGTTATCATCTGCTAAAATTAATAATCA
 CTTTCTTTAGCAGAACATTAGTTGCATGTGTATCCCAAAACATTATCA
 AGAAGATTATCAAAGCCTTGTGCTTAATGACTTGAACACAGAGTTTATT
 ATTTAGATTACTGTAACGAAACACTTTATGAGTGAATCAAAAAGTTTAT
 GATTTCTTTGTCATTTGGAAAATAAA

Table 62: Comparative Sequences relating to SAG0690

SEQ ID NO. 6210
STRAIN 1169NT
AATTAAGCGCTTTGAATTGGAAAGGATAGGAGCTTTCATAGCTTACGAGA
AACAAATATAAAGAAAACTGAGATACAAATGTGACGATAAACATCTCCTC
GCAAAAATTGTTTCAATTTTTTAAATACAAATAGTTTACTTTTCCCTATAT
TCCCAAATATAGAGAAGCGGCGAGCTACITTTAATGAGGATGCTATTAGTT
TAACCTTCTGATTTTTTAAGCCATACATGTACGATTGAAACTGCAAACTA
ATTTTTAAAGAAGGTAAAACTTATCAGCAGTTAAAGCCTTTAATAAGCC
TGCTGAAGTACTGGTAAATGATAAGAGGAATGCTGCTGGAGACCCATAAG
ATTACTTTGACTATGTGATGTTGAAGTGGTCAAATACCAATCTGCTTAT
CGTTTAGTAATGGAAAGATTGTTAGGCAAGCACCCTCTGAACAGGAGTT
AACAGTAGGTTTTAAGCCAGGGGTCAGCTTTCATTTTACTTATCAAGATA
TCATCAATCATCTCTGATTCTATTTTGTATGGTTATCATCCTGCTAAAAAT
AAAAATCAGCTTCTTTAGCAGAACATTAGTTGCGTGTGTATCCCAA
ACATTATCAAGAAGATTATCAAAATCTTGTGCCCAATGACTTGAAACACA
GAGTTTATTTATTTAGATTACTGTAACGAAACACTTTATGAGTGGAAATCAA
AAGTTTATGATTTTCTTTGTCATTTGGAAATAAA

SEQ ID NO. 6211
STRAIN JM9130013
ATAGGAGCTTTTCATAGCTTACGAGAAACAATATAAAGAAAAAATTGAGAT
ACAATGTGACGATAAACATCTCCTCACAATAATTGTTCAATTTTTTAAAT
ACAATAGTTTTACTTTTCCCTATATTTCCCAAATATAGAGAAGCGGCGAGCT
ACTTTTAATGAGGATGGTATTAGTTTAACTTCTGATTTTTTAAGCCATAC
ATGTACGATTGAAACTGCAAACTAAATTTTTAAAGAAGGTAAAACTTAT
CAGCAGTTAAAGCCTTTAATAAGCCTGCTGAAGTACTGGTAAATGATAAG
AGGAATGCTGCTGGAGACCTTAAAGATTACTTTGACTATGTGATGTTGAA
CTGGTCAAATACCAATCTGGTTATCGTTTAGTAATGGAAAGATTGTTAG
GCAAAGCACCCTCTGAAACAGGAGTTAAACAGTAGCTTTAAGCCAGGGGTC
AGCTTTTCAATTTAATTTATCAAGATATCATCAATCATCTGATTCTATTTT
TGATGGTTATCATCTCTGCTAAAAATTAATAATCAACTTTCTTTAGCAGAAC
ATTTAGTTGCAATGTGTTATCCCAAACATTATCAAGAAGATTATCAAAAGC
CTTGTGCTTAATGACTTGAACACAGAGTTTATTTATTTAGATTACTGTAA
CGAAACACTTTATGAGTGAATCAAAAAGTTTATGATTTTCTTTGTCATT
TGAAATAAA

PRETTY of: /biotmp/msa185284.2(*) May 13, 2003 07:08 ..

	1				50
msa185284.2{271_090}	-----	-----	-----	-----	-----
msa185284.2{271_H36B}	-----	-----	-----	-----	-----
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	-----	-----	-----	-----
msa185284.2{271_CJB110}	-----	-----	-----	-----	-----
msa185284.2{271_18RS21}	-----	-----	-----	-----	-----
msa185284.2{271_2603}	atgattttaa	aaatttgtcg	tcagcatat	agtttacaat	ggggagggtgt
msa185284.2{271_M732}	-----	-----	-----	-----	-----
msa185284.2{271_M781}	-----	-----	-----	-----	-----
msa185284.2{271_COH1}	-----	-----	-----	-----	-----
msa185284.2{271_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa185284.2{271_090}	-----	-----	-----	-----	-----
msa185284.2{271_H36B}	-----	-----	-----	-----	-----
msa185284.2{271_JM9130013}	-----	-----	-----	-----	-----
msa185284.2{271_A909}	-----	-----	-----	-----	-----
msa185284.2{271_CJB110}	-----	-----	-----	-----	-----
msa185284.2{271_18RS21}	-----	-----	-----	-----	-----
msa185284.2{271_2603}	ttaccaatta	gctTTGCTgg	attatcctcg	aattaaggcg	tttgaattgg
msa185284.2{271_M732}	-----	-----	-----	-----	-----
msa185284.2{271_M781}	-----	-----	-----	-----	-----
msa185284.2{271_COH1}	-----	-----	-----	-----	-----
msa185284.2{271_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
	101				150
msa185284.2{271_090}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_H36B}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_JM9130013}	-----	ATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA
msa185284.2{271_A909}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_CJB110}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_18RS21}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_2603}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M732}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_M781}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_COH1}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
msa185284.2{271_1169NT}	aaaggATAGG	AGCTTTCATA	GCTTACGAGA	AACAATATAA	AAGAAAAAaT
Consensus	-----	*****	*****	*****	*****
	151				200
msa185284.2{271_090}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_H36B}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_JM9130013}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_A909}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_CJB110}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	aCAAAAATTG	TTCATTTTTT
msa185284.2{271_18RS21}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_2603}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M732}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_M781}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_COH1}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
msa185284.2{271_1169NT}	GAGATACAAT	GTGACGATAA	ACATCTCCTC	gCAAAAATTG	TTCATTTTTT
Consensus	*****	*****	*****	-*****	*****
msa185284.2{271_090}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_H36B}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_JM9130013}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_A909}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_CJB110}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_18RS21}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_2603}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M732}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_M781}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_COH1}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
msa185284.2{271_1169NT}	AAAATACAAT	AGTTTTACTT	TTCCTTATAT	TCCCAAATAT	AGAGAAGCGG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_H36B}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_JM9130013}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_A909}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_CJB110}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_18RS21}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_2603}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_M732}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_M781}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_COH1}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
msa185284.2{271_1169NT}	CAGCTACTTT	TAATGAGGAT	GGTATTAGTT	TAACITCTGA	TTTTTTAAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_H36B}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_JM9130013}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_A909}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_CJB110}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_18RS21}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_2603}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M732}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_M781}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_COH1}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
msa185284.2{271_1169NT}	CATACATGTA	CGATTGAAAC	TGCAAACTA	ATTTTAAAG	AAGGTAAAT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_H36B}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_JM9130013}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_A909}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_CJB110}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_18RS21}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_2603}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M732}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_M781}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_COH1}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
msa185284.2{271_1169NT}	CTTATCAGCA	GTTAAAGCCT	TAAATAAGCC	TGCTGAAGTA	CTGGTAAATG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_H36B}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_JM9130013}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_A909}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_CJB110}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_18RS21}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_2603}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M732}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_M781}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_COH1}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
msa185284.2{271_1169NT}	ATAAGAGGAA	TGCTGCTGGA	GACCCATAAG	ATTACTTTGA	CTATGTGATG
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

msa185284.2{271_090}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_H36B}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_JM9130013}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_A909}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_CJB110}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_18RS21}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_2603}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_M732}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_M781}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_COH1}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
msa185284.2{271_1169NT}	TTGAACCTGGT	CAAATACCAA	TTCTGGTTAT	CGTTTAGTAA	TGGAAGATT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_H36B}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_JM9130013}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_A909}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_CJB110}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGcT	TTTAAGCCAG
msa185284.2{271_18RS21}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_2603}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M732}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_M781}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_COH1}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
msa185284.2{271_1169NT}	GTTAGGCCAA	GCACCATCTG	AACAGGAGTT	AACAGTAGgT	TTTAAGCCAG
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_H36B}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_JM9130013}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_A909}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_CJB110}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_18RS21}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_2603}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M732}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_M781}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_COH1}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
msa185284.2{271_1169NT}	GGGTCAGcTT	TCATTTTAaT	TATCAAGATA	TCATCAATCA	TCCTGATTCT
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_H36B}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_JM9130013}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_A909}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_CJB110}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAaC	TTTCTTTAGC
msa185284.2{271_18RS21}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_2603}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M732}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_M781}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_COH1}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
msa185284.2{271_1169NT}	ATTTTGTGATG	GTTATCATCC	TGCTAAAATT	AAAAATCAgC	TTTCTTTAGC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_H36B}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_JM9130013}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_A909}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_CJB110}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_18RS21}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_2603}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M732}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_M781}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_COH1}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
msa185284.2{271_1169NT}	AGAACATTTA	GTTGCaTGTG	TTATCCCAAA	ACATTATCAA	GAAGATTATC
Consensus	*****	*****	*****	*****	*****
msa185284.2{271_090}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_H36B}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_JM9130013}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_A909}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_CJB110}	AAAgcCTTGT	GCCTAATGAC	TTGAAACACA	GaGTTTATTA	TTTAGATTAC
msa185284.2{271_18RS21}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_2603}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M732}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_M781}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_COH1}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
msa185284.2{271_1169NT}	AAAgcCTTGT	GCCcAATGAC	TTGAAACACA	GgGTTTATTA	TTTAGATTAC
Consensus	*****	*****	*****	*****	*****

Table 62: Comparative Sequences relating to SAG0690

	751	800
msa185284.2{271_090}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_H36B}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_JM9130013}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_A909}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_CJB110}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_18RS21}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_2603}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M732}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_M781}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_COH1}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
msa185284.2{271_1169NT}	TGTAACGAAA CACITTTATGA GTGGAATCAA AAAGTTTATG ATTTTCTTTG	
Consensus	*****	*****
	801	816
msa185284.2{271_090}	tCATTTGGAA AATAAA	
msa185284.2{271_H36B}	tCATTTGGAA AATAAA	
msa185284.2{271_JM9130013}	tCATTTGGAA AATAAA	
msa185284.2{271_A909}	tCATTTGGAA AATAAA	
msa185284.2{271_CJB110}	tCATTTGGAA AATAAA	
msa185284.2{271_18RS21}	tCATTTGGAA AATAAA	
msa185284.2{271_2603}	tCATTTGGAA AATAAA	
msa185284.2{271_M732}	nCATTTGGAA AATAAA	
msa185284.2{271_M781}	tCATTTGGAA AATAAA	
msa185284.2{271_COH1}	gCATTTGGAA AATAAA	
msa185284.2{271_1169NT}	tCATTTGGAA AATAAA	
Consensus	..*****	*****

SEQ ID NO. 6212

STRAIN 2603 frame: 1

MILKICRAAYSLQWGVYQLALLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDKHL
AKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSA
VKAENKPAEVLVVDKRNAGDPKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVG
FKPGVSPHFYQDI INHPDSIFDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPND
LKHRYVYLDYCNETLYEWNQKVYDFLCHLENK

SEQ ID NO. 6213

STRAIN A909 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQCDKHLTKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVVDKRNAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6214

STRAIN H36B frame: 3

KAFELERIGAFIAYEKQYKRKIEIQCDKHLTKIVHFLKYNSTFFPYIPKYREAAATFN
EDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVVDKRNAGDPKDYFDY
VMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSPHFYQDI INHPDSIFDGYHPA
KIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQKVYDFLCH
LENK

SEQ ID NO. 6215

STRAIN 18RS21 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVVDKRNAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6216

STRAIN M732 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVVDKRNAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6217

STRAIN COH1 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQCDKHLAKIVHFLKYNSTFFPYIPKYR
EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVVDKRNAGD
PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSPHFYQDI INHPDSI
FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRYVYLDYCNETLYEWNQK
VYDFLCHLENK

SEQ ID NO. 6218

STRAIN M781 frame: 1

Table 62: Comparative Sequences relating to SAG0690

LLDYPRIKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6219

STRAIN CJB110 frame: 1

LLDYPRIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYR
 EAAATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6220

STRAIN 1169NT frame: 2

IKAFELERIGAFIAYEKQYKRKTEIQDDKHLLAKIVHFLKYNSTFFPYIPKYREAAATF
 NEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVGFKPGVSFHFYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6221

STRAIN JM9130013 frame: 1

IGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREAAATFNEDGISLT
 SDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
 VYDFLCHLENK

SEQ ID NO. 6222

STRAIN 090 frame: 3

DYPLIKAFELERIGAFIAYEKQYKRKIEIQDDKHLLTKIVHFLKYNSTFFPYIPKYREA
 AATFNEDGISLTSDFLSHTCTIETAKLIFKEGKILSAVKAFNKPAEVLVNDKRNAAGD
 PKDYFDYVMLNWSNTNSGYRLVMERLLGKAPSEQELTVAFKPGVSFHFNYQDIINHPDSI
 FDGYHPAKIKNQLSLAEHLVACVIPKHYQEDYQSLVPNDLKHRVYLDYCNETLYEWNQK
 VYDFLCHLENK

PRETTY of: /biotmp/msa185358.2{*} May 13, 2003 07:11 ..

	1		50
msa185358.2{271_090}	-----	---dyplika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_JM9130013}	-----	-----	-----IGAFI AYЕКQYKRKi
msa185358.2{271_H36B}	-----	-----ka	felerIGAFI AYЕКQYKRKi
msa185358.2{271_A909}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_CJB110}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_1169NT}	-----	-----ika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_18RS21}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_2603}	-----	-----	felerIGAFI AYЕКQYKRKi
msa185358.2{271_M732}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_M781}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
msa185358.2{271_COH1}	-----	--LLdyprika	felerIGAFI AYЕКQYKRKi
Consensus	*****	*****	*****
	51		100
msa185358.2{271_090}	EIQDDKHLL	tKIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_JM9130013}	EIQDDKHLL	tKIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_H36B}	EIQDDKHLL	tKIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_A909}	EIQDDKHLL	tKIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_CJB110}	EIQDDKHLL	tKIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_1169NT}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_18RS21}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_2603}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_M732}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_M781}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
msa185358.2{271_COH1}	EIQDDKHLL	akIVHFLKYN	SFTFPYIPKY REAAATFNED GISLTSDFLS
Consensus	*****	*****	*****
	101		150
msa185358.2{271_090}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_JM9130013}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_H36B}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_A909}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_CJB110}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_1169NT}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVnDKRNAAG DPKDYFDYVM
msa185358.2{271_18RS21}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_2603}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_M732}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_M781}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVkDKRNAAG DPKDYFDYVM
msa185358.2{271_COH1}	HTCTIETAKL	IFKEGKILSA VKAFNKPAEV	LVkDKRNAAG DPKDYFDYVM

Table 62: Comparative Sequences relating to SAG0690

Consensus	*****	*****	*****	**-*****	*****
	151				200
msa185358.2{271_090}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_JM9130013}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_H36B}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_A909}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_CJB110}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVa	FKPGVSFHF _n	YQDIINHPDS
msa185358.2{271_1169NT}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_18RS21}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_2603}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_M732}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_M781}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
msa185358.2{271_COH1}	LNWSNTNSGY	RLVMERLLGK	APSEQELTVg	FKPGVSFHF _t	YQDIINHPDS
Consensus	*****	*****	*****-	*****-	*****
	201				250
msa185358.2{271_090}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_JM9130013}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_H36B}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_A909}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_CJB110}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_1169NT}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQnLVPND	LKHRVYYLDY
msa185358.2{271_18RS21}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_2603}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M732}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_M781}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
msa185358.2{271_COH1}	IFDGYHPAKI	KNQLSLAEHL	VACVIPKHYQ	EDYQsLVPND	LKHRVYYLDY
Consensus	*****	*****	*****	*****	*****
	251				272
msa185358.2{271_090}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_JM9130013}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_H36B}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_A909}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_CJB110}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_1169NT}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_18RS21}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_2603}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M732}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_M781}	CNETLYEWNQ	KVYDFLCHLE	NK		
msa185358.2{271_COH1}	CNETLYEWNQ	KVYDFLCHLE	NK		
Consensus	*****	*****	*****		

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6301

STRAIN 2603

ATGAAAAGTCGAAAAAAGATAAATGGTATTGAGGTTAACAACAACACTATTGGTTTTT
GGTTTGGGGTGGGGTTTGGTTTTATAATTATAAAAAATGATAATGTCCGAACCGACAGTCACT
AGTGCAATCGGATCAAACGACGACTTTATTCAAACGATTCTCCAACAGCTATTGAAATT
TCTAAGACCTATGATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCC
AGTGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAATATGACT
CAAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTTCACTATATGATTATGCT
GAGTTAGTATCTAGTCAAAGTATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAG
GATGCTACTGACGCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
AACCAAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6302

STRAIN 090

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
ATGCACTCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6303

STRAIN A909

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
ATGCACTCTGCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6304

STRAIN H36B

GGGGTTTGGTTTTATAATTATAAAAAATGATA
ATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATT
CAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTGA
TGGCTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAAT
CAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAA
TATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGG
CAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTG
CTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCACTCT
GCTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAAC
AGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTA
TTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6305

STRAIN 18RS21

GGGGTTTGGTTTTATAATTATAAAAAATGATAATG
TCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAA
ACGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGC
GTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAG
ATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAAATAT
AAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGATGGGAAAGGCAA
TATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCTGCTT
CACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGTATGCACTGTT
TGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGG
TCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAATTA
AAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6306

STRAIN M732

GGGGTTTGGTTTTATAATTATAA
AAATGATAATGTCCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
CTTTTATTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
GATTTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
TGGACAATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCA
AAGGAGAATATAAAGGTAAATCTGTCCAAATGCCTACTTTAGAAGATGAT
GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
TTATTCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAGT
ATGCACTCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6307

STRAIN COH1

GGGGTTTGGTTTATAATTATAA
 AAATGATAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGA
 CTTTATTCAAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTAT
 GATTGTATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAG
 TGGACAAATCAGATTTGTCTAAGGCTCCTAATTAACCTCTTTGGCATCA
 AAGGAGAATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGAT
 GGGAAAGGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAA
 TTATCTGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGT
 ATGCATCTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCA
 GCTCTAACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTA
 CCAAATTATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6308

STRAIN M781

GGGGTTTGGTTTATAATTATAAAAAATGA
 TAATGTCGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTA
 TTCAAACGATTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGG
 TATGCGTCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACA
 ATCAGATTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAG
 AATATAAAGGTAAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAA
 GGCAATATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTC
 TGCTTCACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTAT
 CTGTTTGGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTA
 ACAGGTCTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAAT
 TATTGAAACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6309

STRAIN CJB110

GGGGTTTGGTTTATAATTATAAAAAATGATAATGT
 CGAACCGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
 CGATTTCTCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCGCTTC
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTATGCTTT
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA
 AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6310

STRAIN 1169NT

GGGGTTTGGTTTATAATTATAAAAAATGATAATGT
 CGAACAGACAGTCACTAGTGCATCGGATCAAACGACGACTTTTATTCAAA
 CGATTTCCCCAACAGCTATTGAAATTTCTAAGACCTATGATTGTATGCG
 TCAGTCTTATTAGCACAAAGCTATTTTGGAAATCATCCAGTGGACAATCAGA
 TTTGTCTAAGGCTCCTAATTATAACCTCTTTGGCATCAAAGGAGAATATA
 AAGGTAATCTGTCCAATGCCTACTTTAGAAGATGATGGGAAAGGCAAT
 ATGACTCAAATCCAAGCTCCTTTTCGCGCCTATCCAAATTATTCGCTTC
 ACTATATGATTATGCTGAGTTAGTATCTAGTCAAAAGTATGCTATGCTTT
 GGAAATCAAATACCTCTTCTTATAAGGATGCTACTGCAGCTCTAACAGGT
 CTTTATGCGACAGATACTGCTTATGCTAGTAAATTAACCAAATATTGA
 AACCTACAGTCTAGATGCTTATGATAAA

SEQ ID NO. 6311

STRAIN JM9130013

TTTGGTTTATAATTATAAAAAATGATAATGTCGAACCGACAGTCACTAGT
 GCATCGGATCAAACGACGACTTTTATTCAAAACGATTTCCCCAACAGCTAT
 TGAATTTCTAAGACCTATGATTGTATGCGTCAGTCTTATTAGCACAAAG
 CTATTTTGGAAATCATCCAGTGGACAATCAGATTTGTCTAAGGCTCCTAAT
 TATAACCTCTTTGGCATCAAAGGAGAATATAAAGGTAATCTGTTCAAAT
 GCCTACTTTAGAAGATGATGGGAAAGGTAATATGACCCAAATCCAAGCTC
 CTTTTCGCGCCTATCCAAATTATTCGCTTCACTATATGATTATGCTGAG
 TTAGTATCTAGTCAAAAGTATGCTATGTTTGGAAATCAAATACCTCTTC
 TTATAAGGATGCTACTGCAGCTCTAACAGGTCTTTATGCGACAGATACTG
 CTTATGCTAGTAAATTAACCAAATATTGAAACTACAGTCTAGATGCT
 TATGATAAA

PRETTY of: /biotmp/msa243324.2{*} February 11, 2003 05:11 ..

	1				50
msa243324.2{275_A909}	-----	-----	-----	-----	-----
msa243324.2{275_H36B}	-----	-----	-----	-----	-----
msa243324.2{275_090}	-----	-----	-----	-----	-----
msa243324.2{275_18RS21}	-----	-----	-----	-----	-----
msa243324.2{275_2603}	atgaaaagtc	gaaaaaaaga	taaatgggta	ttgagggtta	caacaacact
msa243324.2{275_CJB110}	-----	-----	-----	-----	-----
msa243324.2{275_COH1}	-----	-----	-----	-----	-----
msa243324.2{275_M732}	-----	-----	-----	-----	-----

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M781}	-----	-----	-----	-----	-----
msa243324.2{275_1169NT}	-----	-----	-----	-----	-----
msa243324.2{275_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
51					100
msa243324.2{275_A909}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_H36B}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_090}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_18RS21}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_2603}	attggtttttt	gggtttgggtg	gggTTTGGTT	TTATAATTAT	AAAAATGATA
msa243324.2{275_CJB110}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_COH1}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_M732}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_M781}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_1169NT}	-----g	gggTTTGGTT	TTATAATTAT	AAAAATGATA	
msa243324.2{275_JM9130013}	-----	---TTTGGTT	TTATAATTAT	AAAAATGATA	
Consensus	*****	*****	*****	*****	*****
101					150
msa243324.2{275_A909}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_H36B}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_090}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_18RS21}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_2603}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_CJB110}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_COH1}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M732}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_M781}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_1169NT}	ATGTCGAACa	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
msa243324.2{275_JM9130013}	ATGTCGAACc	GACAGTCACT	AGTGCATCGG	ATCAAACGAC	GACTTTTATT
Consensus	*****	*****	*****	*****	*****
151					200
msa243324.2{275_A909}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_H36B}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_090}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_18RS21}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_2603}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_CJB110}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_COH1}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M732}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_M781}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_1169NT}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
msa243324.2{275_JM9130013}	CAAACGATTt	CtCCAACAGC	TATTGAAATT	TCTAAGACCT	ATGATTTGTA
Consensus	*****	*-*****	*****	*****	*****
201					250
msa243324.2{275_A909}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_H36B}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_090}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_18RS21}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_2603}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_CJB110}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_COH1}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M732}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_M781}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_1169NT}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
msa243324.2{275_JM9130013}	TGCGTCAGTC	TTATTAGCAC	AAGCTATTTT	GGAATCATCC	AGTGGACAAT
Consensus	*****	*****	*****	*****	*****
251					300
msa243324.2{275_A909}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_H36B}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_090}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_18RS21}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_2603}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_CJB110}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_COH1}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M732}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_M781}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_1169NT}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
msa243324.2{275_JM9130013}	CAGATTTGTC	TAAGGCTCCT	AATTATAACC	TCITTGGCAT	CAAAGGAGAA
Consensus	*****	*****	*****	*****	*****
301					350
msa243324.2{275_A909}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_H36B}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_090}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_18RS21}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_2603}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_CJB110}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_COH1}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG

Table 63: Comparative Sequences relating to SAG1912

msa243324.2{275_M732}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_M781}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_1169NT}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
msa243324.2{275_JM9130013}	TATAAAGGTA	AATCTGTcCA	AATGCCTACT	TTAGAAGATG	ATGGGAAAGG
Consensus	*****	*****_**	*****	*****	*****
351					
msa243324.2{275_A909}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_H36B}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_090}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_18RS21}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_2603}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_CJB110}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_COH1}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M732}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_M781}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_1169NT}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
msa243324.2{275_JM9130013}	caATATGACT	CAAATCCAAG	CTCCTTTTCG	CGCCTATCCA	AATTATTCTG
Consensus	*****	*****	*****	*****	*****
401					
msa243324.2{275_A909}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_H36B}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_090}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_18RS21}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_2603}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_CJB110}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_COH1}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M732}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_M781}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_1169NT}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
msa243324.2{275_JM9130013}	CTTCACTATA	TGATTATGCT	GAGTTAGTAT	CTAGTCAAAA	GTATGCATCT
Consensus	*****	*****	*****	*****	*****
451					
msa243324.2{275_A909}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_H36B}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_090}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_18RS21}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_2603}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_CJB110}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_COH1}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M732}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_M781}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_1169NT}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
msa243324.2{275_JM9130013}	GcTTGGAAAT	CAAATACcTC	TTCTTATAAG	GATGCTACTG	CAGCTCTAAC
Consensus	**_*****	*****_**	*****	*****	*****
501					
msa243324.2{275_A909}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_H36B}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_090}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_18RS21}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_2603}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_CJB110}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_COH1}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M732}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_M781}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_1169NT}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
msa243324.2{275_JM9130013}	AGGTCTTTAT	GCGACAGATA	CTGCTTATGC	TAGTAAATTA	AACCAAATTA
Consensus	*****	*****	*****	*****	*****
551					
msa243324.2{275_A909}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_H36B}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_090}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_18RS21}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_2603}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_CJB110}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_COH1}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_M732}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_M781}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_1169NT}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
msa243324.2{275_JM9130013}	TTGAAAcCTA	CAGTCTAGAT	GCTTATGATA	AA	
Consensus	*****_***	*****	*****	*****	*****
582					

SEQ ID NO. 6312

STRAIN 2603 frame: 1

MKSRKDKLVRLITTTLLVFLGGVWFYNYKNDNVEPTVTSASDQTTTFIQTFISPTAIEI
 SKTYDLYASVLLAQAILSSSGQSDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMT
 QIQAPFRAYPNYSASLYDYAELVSSQKYASVWKSNTSSYKDATAALTLGLYATDTAYASKL
 NQIETYSLDAYDK

Table 63: Comparative Sequences relating to SAG1912

SEQ ID NO. 6313
STRAIN 090 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6314
STRAIN A909 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6315
STRAIN H36B frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASAWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6316
STRAIN 18RS21 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6317
STRAIN M732 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6318
STRAIN M781 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6319
STRAIN CJB110 frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6320
STRAIN 1169NT frame: 1
GVWFFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQ
SDLSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELV
SSQKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIETYSLDAYDK

SEQ ID NO. 6321
STRAIN JM9130013 frame: 3
WFYNYKNDNVEPTVTSASDQTTTFIQTISPTAIEISKTYDLYASVLLAQAILLESSSGQSD
LSKAPNYNLFGIKGEYKGSVQMPTLEDDGKGNMTQIQAPFRAYPNYSASLYDYAELVSS
QKYASVWKSNTSSYKDATAALTGLYATDTAYASKLNQIIENYSLDAYDK

PRETTY of: /biotmp/msa243476.2{*} February 11, 2003 05:17 ..

	1				50
msa243476.2{275_090}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_18RS21}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_2603}	mksrkkdklv	lrltttllvf	glggvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_CJB110}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_M732}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_M781}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_A909}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_H36B}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_JM9130013}	-----	-----	-----WFYNY	KNDNVEpTVT	SASDQTTTFI
msa243476.2{275_1169NT}	-----	-----	---gvWFFYNY	KNDNVEpTVT	SASDQTTTFI
Consensus	*****	*****	***--*****	*****	*****

	51				100
msa243476.2{275_090}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_18RS21}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_2603}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_CJB110}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M732}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_M781}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_A909}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_H36B}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_JM9130013}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
msa243476.2{275_1169NT}	QTISPTAIEI	SKTYDLYASV	LLAQAILLESS	SGQSDLSKAP	NYNLFGIKGE
Consensus	*****	*****	*****	*****	*****

Table 63: Comparative Sequences relating to SAG1912

	101				150
msa243476.2{275_090}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_18RS21}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_2603}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_CJB110}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M732}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_M781}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_A909}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_H36B}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_JM9130013}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
msa243476.2{275_1169NT}	YKGKSVQMPT	LEDDGKGNMT	QIQAPFRAYP	NYSASLYDYA	ELVSSQKYAS
Consensus	*****	*****	*****	*****	*****
	151				194
msa243476.2{275_090}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_18RS21}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_2603}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_CJB110}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M732}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_M781}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_A909}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_H36B}	awKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_JM9130013}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
msa243476.2{275_1169NT}	vWKSNTSSYK	DATAALTGLY	ATDTAYASKL	NQIIETYSLD	AYDK
Consensus	-*****	*****	*****	*****	****

Table 64: Comparative Sequences relating to SAG 0827

SEQ ID NO. 6401

STRAIN 2603

ATGAACAAGTCTAAGAAAATCGAAAATTATCAATTATTATTACTACAAGCGCAAGCTCTA
TTCTCAGATGAAACAAATGCTCTTGCCAACTTATCAAATGCTTCAGCTATGCTAAATGCT
ATGCTTCCAAATCTGTATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAAATCTT
GGCCCTTTCCAGGGTGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT
GAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGCTAACTAT
ATCTCCTGTGATTTCAAAGCTATGAGTGAAATCGTAGTACCTATGTTTAAAAATGGCAAA
CTTCTAGGAGTTCTAGATTAGATTCTCTTTAGTAGCAGATTATGATGAGATTGATCAA
GAATACTTAGAAAAATTTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATG
TTTGGAGTTGAAAAG

SEQ ID NO. 6402

STRAIN 090

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTAC
AGGCTTTTATTTATTTGATGGAAAGGAGTTAATTCTTGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGAA
TCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTGGAATTTGGATA

SEQ ID NO. 6403

STRAIN A909

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAA
CTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTAT
TTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTCC
CAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGG
TGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGC
ATGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTA
CCTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTCT
TTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTG
TAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTT
GAAAAG

SEQ ID NO. 6404

STRAIN H36B

CTCTATTCTCAGATGAAACAAATGCTCTTGCC
CAACTTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGT
TATTTACAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTT
TTCCAGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGT
TGGTGAATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAA
AGCATGCTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTA
GTACCTATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCT
TTCTTTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAAT
TTGTAGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTT
GTTGAAAAG

SEQ ID NO. 6405

STRAIN 18RS21

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAAGAGTTAATTCTTGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCT
ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6406

STRAIN M732

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACCTTCTAGGAGTTCTAGATTAGATTCTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6407

STRAIN COH1

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
TTATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTT
TACAGGCTTTTATTTATTTGATGGAGAGGAGTTAATTCTTGCCCTTTTC
AGGGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGT

Table 64: Comparative Sequences relating to SAG 0827

GAATCTGCACAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCA
TGCTAACTATATCTCCTGTGATTCAAAAGCTATGAGTGAAATCGTAGTAC
CCATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCT
TTAGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGT
AGGTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTGGAGTTG
AAAAG

SEQ ID NO. 6408

STRAIN M781

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTT
ATCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTA
CAGGCTTTTATTTATTTGATGGAGAGGAGTTAATCTTGGCCCTTTCCAG
GGTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
ATCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATG
CTAACTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCC
ATGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTT
AGTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAG
GTATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAA
AAG

SEQ ID NO. 6409

STRAIN CJB110

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTC
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACCTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6410

STRAIN 1169NT

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTC
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATTGTTGATGATGTTACAAAGCATGC
TAACCTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCCA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAAA
AG

SEQ ID NO. 6411

STRAIN JM9130013

CTCTATTCTCAGATGAAACAAATGCTCTTGCCAACTTA
TCAAATGCTTCAGCTATGCTAAATGCTATGCTTCCAAATCTGTATTTC
AGGCTTTTATTTATTTGATGGAGAGGAGTTAATCTTGGCCCTTTCCAGG
GTGGTGTATCATGTGTGCATATTACTTTAGGAAAAGGTGTTTGTGGTGA
TCTGCACAAACTGCTAAGACGCTGATCGTTGATGATGTTACAAAGCATGC
TAACCTATATCTCCTGTGATTCAAAGCTATGAGTGAAATCGTAGTACCTA
TGTTTAAAAATGGCAAACCTCTAGGAGTTCTAGATTAGATTCTTCTTTA
GTAGCAGATTATGATGAGATTGATCAAGAATACTTAGAAAAATTTGTAGG
TATTCTAGTAGAACATACGATTGGAATTTGGATATGTTTGGAGTTGAAA
AG

PRETTY of: /biotmp/msa236796.2{*} February 11, 2003 02:42 ..

	1				50
msa236796.2{282_COH1}	-----	-----	-----	-----	-----
msa236796.2{282_M732}	-----	-----	-----	-----	-----
msa236796.2{282_M781}	-----	-----	-----	-----	-----
msa236796.2{282_090}	-----	-----	-----	-----	-----
msa236796.2{282_CJB110}	-----	-----	-----	-----	-----
msa236796.2{282_18RS21}	-----	-----	-----	-----	-----
msa236796.2{282_2603}	atgaacaagt	ctaagaaaat	cgaaaattat	caattattat	tactacaagc
msa236796.2{282_A909}	-----	-----	-----	-----	-----
msa236796.2{282_H36B}	-----	-----	-----	-----	-----
msa236796.2{282_JM9130013}	-----	-----	-----	-----	-----
msa236796.2{282_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa236796.2{282_COH1}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M732}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_M781}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_090}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_CJB110}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_18RS21}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG
msa236796.2{282_2603}	gcaagCTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_A909}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_H36B}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_JM9130013}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
msa236796.2{282_1169NT}	-----CTCTA	TTCTCAGATG	AAACAAATGC	TCTTGCCAAC	TTATCAAATG		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	101	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT	150
msa236796.2{282_M732}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_M781}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_090}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_CJB110}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_18RS21}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_2603}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_A909}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_H36B}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_JM9130013}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
msa236796.2{282_1169NT}	CTTCAGCTAT	GCTAAATGCT	ATGCTTCCAA	ATTCTGTATT	TACAGGCTTT		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	151	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT	200
msa236796.2{282_M732}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_M781}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_090}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_CJB110}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_18RS21}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_2603}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_A909}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_H36B}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_JM9130013}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
msa236796.2{282_1169NT}	TATTTATTTG	ATGGAGAgGA	GTTAATTCTT	GGCCCTTTtC	AGGGTGGTGT		
Consensus	*****	*****_**	*****	*****_*	*****		
msa236796.2{282_COH1}	201	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC	250
msa236796.2{282_M732}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_M781}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_090}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_CJB110}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_18RS21}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_2603}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_A909}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_H36B}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_JM9130013}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
msa236796.2{282_1169NT}	ATCATGTGTG	CATATTACTT	TAGGAAAAGG	TGTTTGTGGT	GAATCTGCAC		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	251	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT	300
msa236796.2{282_M732}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_M781}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_090}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_CJB110}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_18RS21}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_2603}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_A909}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_H36B}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_JM9130013}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
msa236796.2{282_1169NT}	AAACTGCTAA	GACGCTGATt	GTTGATGATG	TTACAAAGCA	TGCTAACTAT		
Consensus	*****	*****	*****	*****	*****		
msa236796.2{282_COH1}	301	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA	350
msa236796.2{282_M732}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_M781}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_090}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_CJB110}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_18RS21}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_2603}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_A909}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_H36B}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_JM9130013}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
msa236796.2{282_1169NT}	ATCTCCTGTG	ATTCAAAGC	TATGAGTGAA	ATCGTAGTAC	CcATGTTTAA		
Consensus	*****	*****	*****	*****	*****	*_*****	
msa236796.2{282_COH1}	351	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG	400
msa236796.2{282_M732}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_M781}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_090}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_CJB110}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		
msa236796.2{282_18RS21}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG		

Table 64: Comparative Sequences relating to SAG 0827

msa236796.2{282_2603}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_A909}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_H36B}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_JM9130013}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
msa236796.2{282_1169NT}	AAATGGCAAA	CTTCTAGGAG	TTCTAGATTT	AGATTCTTCT	TTAGTAGCAG
Consensus	*****	*****	*****	*****	*****
401					
msa236796.2{282_COH1}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M732}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_M781}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_090}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_CJB110}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_18RS21}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_2603}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_A909}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_H36B}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_JM9130013}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
msa236796.2{282_1169NT}	ATTATGATGA	GATTGATCAA	GAATACTTAG	AAAAATTGT	AGGTATTCTA
Consensus	*****	*****	*****	*****	*****
451					
msa236796.2{282_COH1}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M732}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_M781}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_090}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_CJB110}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_18RS21}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_2603}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_A909}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_H36B}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_JM9130013}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
msa236796.2{282_1169NT}	GTAGAACATA	CGATTGGAA	TTTGGATAtg	tttggagttg	aaaag
Consensus	*****	*****	*****	*****	*****
495					
SEQ ID NO. 6412					
STRAIN 2603 frame: 1					
MNKSKKIENYQLLLQAQALFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELIL					
GPFQGGVSCVHITLKGKVCGESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGK					
LLGVLDLSSSLVADYDEIDQEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6413					
STRAIN 090 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLD					
SEQ ID NO. 6414					
STRAIN A909 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6415					
STRAIN H36B frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6416					
STRAIN 18RS21 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6417					
STRAIN M732 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6418					
STRAIN COH1 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					
QEYLEKFVGILVEHTIWNLDMPGVEK					
SEQ ID NO. 6419					
STRAIN M781 frame: 3					
LFSDETNALANLSNASAMLNAMLPNSVFTGFYLFDFGGEELILGPFQGGVSCVHITLKGKVC					
GESAQTAKTILVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSSLVADYDEID					

Table 64: Comparative Sequences relating to SAG 0827

QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6420

STRAIN M781 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILIGPFQGGVSCVHITLGKGV
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6421

STRAIN CJB110 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGKEILIGPFQGGVSCVHITLGKGV
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6422

STRAIN 1169NT frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILIGPFQGGVSCVHITLGKGV
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID
 QEYLEKFVGIIVHEHTIWNLD MFGEK

SEQ ID NO. 6423

STRAIN JM9130013 frame: 3

LFSDETNALANLSNASAMLNAMLPSVFTGFYLFDFGEEILIGPFQGGVSCVHITLGKGV
 GESAQTAKTLIVDDVTKHANYISCDKAMSEIVVPMFKNGKLLGVLDLSSLVADYDEID
 QEYLEKFVGIIVHEHTIWNLD MFGEK

PRETTY of: /biotmp/msa237960.2{*} February 11, 2003 02:46 ..

	1		50
msa237960.2{282_1169NT}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_18RS21}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_2603}	mnkskkieny qllllqaqaL	FSDETNALAN	LSNASAMLNA
msa237960.2{282_A909}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_COH1}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_H36B}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_JM9130013}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M732}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_M781}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_090}	-----L	FSDETNALAN	LSNASAMLNA
msa237960.2{282_CJB110}	-----L	FSDETNALAN	LSNASAMLNA
Consensus	*****	*****	*****

	51		100
msa237960.2{282_1169NT}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_18RS21}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_2603}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_A909}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_COH1}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_H36B}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_JM9130013}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M732}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_M781}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_090}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
msa237960.2{282_CJB110}	YLFdGeELIL	GPFQGGVSCV	HITLGKGVCG
Consensus	*****	*****	*****

	101		150
msa237960.2{282_1169NT}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_18RS21}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_2603}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_A909}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_COH1}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_H36B}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_JM9130013}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M732}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_M781}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_090}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
msa237960.2{282_CJB110}	ISCDKAMSE	IVVPMFKNGK	LLGVLDLSS
Consensus	*****	*****	*****

	151	165
msa237960.2{282_1169NT}	VEHTIWNLDm	fgvek
msa237960.2{282_18RS21}	VEHTIWNLDm	fgvek
msa237960.2{282_2603}	VEHTIWNLDm	fgvek
msa237960.2{282_A909}	VEHTIWNLDm	fgvek
msa237960.2{282_COH1}	VEHTIWNLDm	fgvek
msa237960.2{282_H36B}	VEHTIWNLDm	fgvek
msa237960.2{282_JM9130013}	VEHTIWNLDm	fgvek
msa237960.2{282_M732}	VEHTIWNLDm	fgvek
msa237960.2{282_M781}	VEHTIWNLDm	fgvek
msa237960.2{282_090}	VEHTIWNLDm	fgvek
msa237960.2{282_CJB110}	VEHTIWNLDm	fgvek
Consensus	*****	-----

Table 65: Comparative Sequences relating to SAG0231

SEQ ID NO. 6501

STRAIN 2603

ATGAAAAAGAGTACCCAAATAATACTACTAATAGTTGCA
 TTATTCTACTTGTTTTATAGCGGAGGATTTTATATGAAAGAACCAACAAAGAAAAGAGAA
 CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAATTCCTATGAG
 AATATAGAAGAAATAAAATCACACATCCTGTTTCAACTGAAATTCCTGGAGATTGGCAT
 TGTACTGTAAAGATTTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAAT
 TTGGAATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTGAT
 TCAAGAAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6502

STRAIN 090

GGAGGATTTTATATGAAAGAACA
 ACAAAAGAAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6503

STRAIN A909

GGAGGATTTTATATGAAAGAACAACA
 AGAAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAA
 AGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTCA
 TTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATC
 GAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTG
 ATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTCAGAT
 GGTCAGGAGAAGATaCAA

SEQ ID NO. 6504

STRAIN H36B

GGAGGATTTTATATGAAAGAACA
 ACAAAAGAAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAG
 TCAAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 CATCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGAT
 TTCATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGG
 AATCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTT
 TTTGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTC
 AGATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6505

STRAIN 18RS21

GGAGGATTTTATATGAAAGAACAAC
 AAAGAAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCT
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATC
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATT
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
 TCGAAAAAAATTTATAGCGGAAATTTAATGAAAAAAATATGAATTTTT
 TGATTCAAGAAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTCAG
 ATGGTCAGGAGAAGATaCAA

SEQ ID NO. 6506

STRAIN M781

GGAGGATTTTATATGAAAGAACAACAAGAAAA
 GAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATT
 GAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTT
 CAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAAT
 GATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAA
 AAATTATAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAG
 GAATTGGTAAACAAAAAACTATAAAAAATTTATTTTTTCAGATGGTCAG
 GAGAAGATACAA

SEQ ID NO. 6507

STRAIN CJB110

GGAGGATTTTATATGAAAGAACAACAAGAAAAGAA
 CTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAGCATTGAAAAA
 TTCCTATGAGAATATAGAAGAAATAAAATCACACATCCTGTTTCAACTG
 AAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATTTAATGATAAA
 AATCTATTGTTTATAATATTACACATAATTTGGAATCGAAAAAAATTA
 TAGCGGAAATTTAATGAAAAAAATATGAATTTTTTTGATTCAAGAAATTG
 GTAAAACAAAAAACTATAAAAAATTTATTTTTTCAGATGGTCAGGAGAAG
 ATACAA

SEQ ID NO. 6508

STRAIN 1169NT

GGAGGATTTTATATGAAAGAACAACAAG
 AAAAGAAAGAACTAAAACGGAATCGAGAATATGAAGTTAGTCTAGTCAAAG
 CATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAATCACACATCCT

Table 65: Comparative Sequences relating to SAG0231

GTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATTTCATT
 TAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAATCGA
 AAAAAAATTATAGTGGAAAATTTAATGAAAAAATATGAATTTTTTGGAT
 TCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAGATGG
 TCAGGAGAAGATACAA

SEQ ID NO. 6509

STRAIN JM9130013

GGAGGATTTTATATGAAAGAACAAC

AAAGAAAAGAAAGAACTAAACCGGAATCGAGAATATGAAGTTAGTCTAGTC
 AAAGCATTGAAAAATTCCTATGAGAATATAGAAGAAATAAAAATCACACA
 TCCTGTTTCAACTGAAATTCCTGGAGATTGGCATTGTACTGTAAAGATT
 CATTTAATGATAAAAAATCTATTGTTTATAATATTACACATAATTTGGAA
 TCGAAAAAATTTATAGCGGAAAATTTAATGAAAAAATATGAATTTTTT
 TGATTCAAGAAATGGTAAACAAAAAACTATAAAAAATTATTTTTTCAG
 AtGgtCAGGAGAAGATACAA

PRETTY of: /biotmp/msa75400.2{*} March 10, 2003 09:56 ..

	1				50
msa75400.2{286_090}	-----	-----	-----	-----	-----
msa75400.2{286_CJB110}	-----	-----	-----	-----	-----
msa75400.2{286_18RS21}	-----	-----	-----	-----	-----
msa75400.2{286_2603}	atgaaaaaga	gtacccaaat	aataactacta	atagtgtgcat	tatttcatact
msa75400.2{286_A909}	-----	-----	-----	-----	-----
msa75400.2{286_H36B}	-----	-----	-----	-----	-----
msa75400.2{286_JM9130013}	-----	-----	-----	-----	-----
msa75400.2{286_M781}	-----	-----	-----	-----	-----
msa75400.2{286_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa75400.2{286_090}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_CJB110}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_18RS21}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_2603}	tgttttttagc	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_A909}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_H36B}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_JM9130013}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_M781}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
msa75400.2{286_1169NT}	-----	GGAGGATTTT	ATATGAAAGA	ACAACAAAGA	AAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
	101				150
msa75400.2{286_090}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_CJB110}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_18RS21}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_2603}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_A909}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_H36B}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_JM9130013}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_M781}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
msa75400.2{286_1169NT}	TAAAACGGAA	TCGAGAATAT	GAAGTTAGTC	TAGTCAAAGC	ATTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa75400.2{286_090}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_CJB110}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_18RS21}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_2603}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_A909}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_H36B}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_JM9130013}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_M781}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
msa75400.2{286_1169NT}	TCCTATGAGA	ATATAGAAGA	AATAAAAAATC	ACACATCCTG	TTTCAACTGA
Consensus	*****	*****	*****	*****	*****
	201				250
msa75400.2{286_090}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_CJB110}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_18RS21}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_2603}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_A909}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_H36B}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_JM9130013}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_M781}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
msa75400.2{286_1169NT}	AATTCCTGGA	GATTGGCATT	GTACTGTAAA	GATTTTCATT	AATGATAAAA
Consensus	*****	*****	*****	*****	*****
	251				300
msa75400.2{286_090}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_CJB110}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT
msa75400.2{286_18RS21}	AATCTATTGT	TTATAATATT	ACACATAATT	TGGAATCGAA	AAAAAATTAT

Table 65: Comparative Sequences relating to SAG0231

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msa75400.2{286_2603} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_A909} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_H36B} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_JM9130013} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_M781} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
msa75400.2{286_1169NT} AATCTATTGT TTATAATATT ACACATAATT TGGAATCGAA AAAAAATTAT
Consensus *****

301
msa75400.2{286_090} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_CJB110} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_18RS21} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_2603} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_A909} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_H36B} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_JM9130013} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_M781} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
msa75400.2{286_1169NT} AGcGGAAAT TTAATGAAAA AAATATGAAT TTTTGTGATT CAAGAATTGG
Consensus **-*****

351
msa75400.2{286_090} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_CJB110} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_18RS21} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_2603} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_A909} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_H36B} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_JM9130013} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_M781} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
msa75400.2{286_1169NT} TAAAACAAAA AAAACTATAA AAATTATTTT TTCAGATGGT CAGGAGAAGA
Consensus *****

401
msa75400.2{286_090} TACAA
msa75400.2{286_CJB110} TACAA
msa75400.2{286_18RS21} TACAA
msa75400.2{286_2603} TACAA
msa75400.2{286_A909} TACAA
msa75400.2{286_H36B} TACAA
msa75400.2{286_JM9130013} TACAA
msa75400.2{286_M781} TACAA
msa75400.2{286_1169NT} TACAA
Consensus *****

SEQ ID NO. 6510
STRAIN 2603 frame: 1
MKKSTQIILLIVAFILVFSGGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKI
THPVSTEIPGDWHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTK
KTIKIIIFSDGQEKIQ

SEQ ID NO. 6511
STRAIN 090
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ
EKIQ

SEQ ID NO. 6512
STRAIN A909
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
CTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK
IQ

SEQ ID NO. 6513
STRAIN H36B
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGD
WHCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQ
EKIQ

SEQ ID NO. 6514
STRAIN 18RS21
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH
HCTVKISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEK
KIQ

SEQ ID NO. 6515
STRAIN CJB110
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVK
ISFNDKKSIVYNITHNLESKKNYSKGFNEKNMNFDSRIGKTKTIKIIIFSDGQEKIQ

SEQ ID NO. 6516
STRAIN JM9130013
GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWH

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Table 65: Comparative Sequences relating to SAG0231

HCTVKISFNDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQE
KIQ

SEQ ID NO. 6517

STRAIN 1169NT frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

SEQ ID NO. 6518

STRAIN M781 frame: 1

GGFYMKEQQRKEELKRNREYEVSLVKALKNSYENIEEIKITHPVSTEIPGDWHCTVKISF
NDKKSIVYNITHNLESKKNYSGKFNEKNMNFDSRIGTKTKTIKIIFSDGQEKIQ

PRETTY of: /biotmp/msa75376.2{*} March 10, 2003 10:01 ..

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      1                                     50
msa75376.2{286_090} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_1169NT} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_18RS21} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_2603} mkkstqiill ivalfilvfs GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_A909} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_CJB110} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_H36B} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_JM9130013} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
msa75376.2{286_M781} ----- GGFYMKEQQR KEELKRNREY EVSLVKALKN
Consensus *****

      51                                     100
msa75376.2{286_090} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_1169NT} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_18RS21} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_2603} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_A909} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_CJB110} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_H36B} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_JM9130013} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
msa75376.2{286_M781} SYENIEEIKI THPVSTEIPG DWHCTVKISF NDKKSIVYNI THNLESKKNY
Consensus *****

      101                                     135
msa75376.2{286_090} SGnFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_1169NT} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_18RS21} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_2603} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_A909} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_CJB110} SGnFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_H36B} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_JM9130013} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
msa75376.2{286_M781} SGkFNEKNMN FFDSRIGGTK KTIKIIFSDG QEKIQ
Consensus **-*****

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Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6601

STRAIN 2603

TTGACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATG
GAAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAGCAGCGCTT
ACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAG
GATCCTAGATTAACTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGAT
GAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAAATACCA
AAGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGTAAAAGGAAG
GCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATG
TATGGTGAAGAGCGACCTCTCTCGATTTCAGCAAGCCAAGTGTATAAAGTTATTTAGTCAT
TTGCCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTATAGTGGCA
GAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAA
TTAAATAATAAA

SEQ ID NO. 6602

STRAIN 090

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
CAGAACITTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTCAGCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6603

STRAIN A909

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAATG
AAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTTA
GGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTAA
CTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA
CCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC
AGAACITTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATCA
ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGTCT
ACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTAT
TCAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAGC
GACCTCTCTCGATTTCAGCAAGCCAAGTGTATAAAGTTATTTAGTCATTTG
CCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGAT
AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
TCCTTTCTATTGAAGAATTAATAATAAA

SEQ ID NO. 6604

STRAIN H36B

TATAAAAATTTCTATACTAAATTTACAAAATGAAGGAGAGGGAAGTATGG
AAATACTGATTGCAGGTGGTAGTGGTTTTTTAGGAAAGCAGATAATAAAA
GCAGCGCTTACAAAAGGGCATAAAGTGGCTTACTTATCAAGACATGAAGG
TAAAGGTGATATATTAAAGGATCCTAGATTAACTTACATTAGGGGAGATA
TTACAGAAGCTGATAAGATTCAATTTAGAAGACAGAACITTTTGATATATTA
ATTGACTGTATTGGAGCGATTAAAGCCCAATCAACTAGATGAGCTTAACGT
TAAAGCAACCCAAAAGCAGTAGCACTCTGTCAAAAATCAAATACCAA
AGTTAGTTTATATTTAGCCCAACAGCGGCTATTAGCTTACATTAAAAGT
AAAAGGAAGGCAGAGCAGATAATCAAAGCAAGCGGTCTGGATTATCTTTT
TGTAAGACCAGGTTTGATGTATGGTGAAGAGCGACCTCTCTCGATTTC
AAGCCAAAGTGTATAAAGTTATTTAGTCATTTGCCTTTCTTAGGTATTGTT
GTACAAAAGGTCTTTCCAACCTAAGGTTGTATAGTGGCAGAAGCAATCGT
TACTACGCTTAGGAAAAAACCAACCCAAAAATCCTTTCTATTGAAGAAT
TAAATAATAAA

SEQ ID NO. 6605

STRAIN 18RS21

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAAAT
GAAGGAGAGGGAACCTATGGAAATACTGATTGCAGGTGGTAGTGGTTTTTT
AGGAAAGCAGATAATAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTT
ACTTATCAAGACATGAAGGTAAAGGTGATATATTAAAGGATCCTAGATTAA
ACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGA
CAGAACITTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCCAATC
AACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCTGT
CACAAAATCAAATACCAAGTTAGTTTATATTTAGCCCAACAGCGGCTA
TTAGCTTACATTAAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAA
GCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAGAG
CGACCTCTCTCGATTTCAGCAAGCCAAGTGTATAAAGTTATTTAGTCATTT
GCCTTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACCTAAGGTTGTGA
TAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAA
ATCCTTTCTATTGAAGAATTAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6606

STRAIN M732

CAAAATGAAGGAGAGGGAACCTATGgAAATACTGATTGCAGGTGGTAGTGG
 TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGG
 TGGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCT
 AGATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAAT
 AGaACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGC
 CCAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCA
 CTCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAG
 CGGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCA
 AAGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGT
 GAAGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAG
 TCATTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGG
 TTGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACT
 CAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6607

STRAIN COH1

ACAAGGCATATAAAAAATTTCTATACTAAATTTAC
 AAAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGT
 TTTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGT
 GGCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTA
 GATTAACTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTA
 GAACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCC
 CAATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCAC
 TCTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGC
 GGCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA
 AGCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTG
 AAGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGT
 CATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGT
 TGTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTC
 AAAAAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6608

STRAIN M781

ACAAGGCATATAAAAAATTTCTATACTAAATTTaCA
 AAATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTT
 TTCTAGGGAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGGTG
 GCTTACTTATCAAGGCATGAAGGTAAAGGTGATATATTTAAGGATCCTAG
 ATTAACCTTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTTAG
 AACATAGAAATTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCC
 AATCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACT
 CTGTACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAATAGCG
 GCTATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAA
 GCAAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGA
 AGAGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCA
 ATTTGCGCTTCTTAGGTATTGTTGTACAAAAGTCTTTCCAACTAAGGTT
 GTGATAGTGGCAGAAGCAATCGTTACTTCGCTTAGGAAAAACCAACTCA
 AAAAAATCCTTTCTATGAAGAATTAAATAATAAA

SEQ ID NO. 6609

STRAIN 1169NT

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
 TAACCTACATTAAAGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT
 GTCACAAAAATCAAATACCAAAGTTAGTTTACATTTCAGCCAACAGCGGC
 TATTAGCTTACATTAGAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
 AGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCAT
 TTGCCCTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGACAAAACCAACTCAA
 AAATCCTTTCTATTGAAGAATTAAATAATAAA

SEQ ID NO. 6610

STRAIN CJB110

ACAAGGCATATAAAAAATTTCTATACTAAATTTACAAA
 ATGAAGGAGAGGGAACCTATGGAATACTGATTGCAGGTGGTAGTGGTTT
 TTAGGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAGTTGGC
 TTACTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGAT
 TAACCTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAA
 GACAGAACTTTTGATATATTAATTGACTGTATTGGAGCGATTAAAGCCAA
 TCAACTAGATGAGCTTAACGTTAAAGCAACCCAAAAGCAGTAGCACTCT
 GTCACAAAAATCAAATACCAAAGTTAGTTTATATTTCAGCCAACAGCGGC
 TATTAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGC
 AAGCGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGATGTATGGTGAAG
 AGCGACCTCTCTCGATTTCAGCAAGGTGATATAAAATTAATTAGTCAT
 TTGCCCTTCTTAGGTATTGTTGTACAAAAGGTCTTTCCAACTAAGGTTGT
 GATAGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAACCAACTCAA
 AAATCCTTTCTATTGAAGAATTAAATAATAAA

Table 66: Comparative Sequences relating to SAG 0754

SEQ ID NO. 6611

STRAIN JM9130013

ACAAGGCATATAAAATTTCTATACTAAATTTACAAAATG
 AAGGAGGGGAAGTATGGAAATCTGATTGCAGGTGGTAGTGGTTTTTTA
 GGAAAGCAGATAATAAAAGCAGCGCTTACAAAAGGGCATAAAGTGGCTTA
 CTTATCAAGACATGAAGGTAAAGGTGATATATTTAAGGATCCTAGATTAA
 CcTACATTAGGGGAGATATTACAGAAGCTGATAAGATTCAATTTAGAAGAC
 AGAACITTTGATATATTAATTGACTGTATTGGAGCGATTAAGCCCAATCA
 ACTAGATGAGCTTAACGTTAAAGCAACCCAAAAAGCAGTAGCACTCTGTG
 ACAAAAATCAAAATACCAAGTTAGTTTATATTTTCAGCCAACACGGCTAT
 TCAGCTTACATTAAAGTAAAGGAAGGCAGAGCAGATAATCAAAGCAAG
 CGGTCTGGATTATCTTTTGTAAAGACCAGGTTTGTATGTTGGTGAAGAGC
 GACCTCTCTCGATTTTCCAGCCAAGTGTATAAAGTTATTTAGTCATTTG
 CCTTTCTTAgGTATTGTTGTACAAAAGGCTTTCCAACTAAGGTTGTGAT
 AGTGGCAGAAGCAATCGTTACTACGCTTAGGAAAAAACCAACCCAAAAAA
 TCCTTTCTATGAAGAATTAATAATAAA

PRETTY of: /biotmp/msal37119.2{*} April 10, 2003 03:30 ..

	1				50
msal37119.2{303_COH1}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_M732}	-----	-----	-----	-----CAAA	ATGAAGGAGA
msal37119.2{303_m781}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_090}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_18RS21}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_2603}	ttgacaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_A909}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_CJB110}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_H36B}	-----	-tataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_JM9130013}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
msal37119.2{303_1169NT}	---acaagggc	atataaaaaat	ttctatacta	aatttaCAAA	ATGAAGGAGA
Consensus	***-----	-----	-----	-----****	*****

	51				100
msal37119.2{303_COH1}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_M732}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_m781}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	cTAGGgAAGC
msal37119.2{303_090}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_18RS21}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_2603}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_A909}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_CJB110}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_H36B}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_JM9130013}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
msal37119.2{303_1169NT}	GGGAAGCTATG	GAAATACTGA	TTGCAGGTGG	TAGTGGTTTT	tTAGGaaAGC
Consensus	*****	*****	*****	*****	*****

	101				150
msal37119.2{303_COH1}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_M732}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_m781}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_090}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_18RS21}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_2603}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_A909}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_CJB110}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_H36B}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_JM9130013}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
msal37119.2{303_1169NT}	AGATAATAAA	AGCAGCGCTT	ACAAAAGGGC	ATAAagTGGC	TTACTTATCA
Consensus	*****	*****	*****	*****	*****

	151				200
msal37119.2{303_COH1}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_M732}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_m781}	AGgCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_090}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_18RS21}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_2603}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_A909}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_CJB110}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_H36B}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_JM9130013}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
msal37119.2{303_1169NT}	AGaCATGAAG	GTAAGGTGA	TATATTTAAG	GATCCTAGAT	TAACCTACAT
Consensus	***-----	*****	*****	*****	*****

	201				250
msal37119.2{303_COH1}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_M732}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_m781}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	cAtAGAAaTT
msal37119.2{303_090}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_18RS21}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msal37119.2{303_2603}	TAaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_A909}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_CJB110}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_H36B}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_JM9130013}	TagGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
msa137119.2{303_1169NT}	TaaGGGAGAT	ATTACAGAAG	CTGATAAGAT	TCATTTAGAA	gAcAGAAcTT
Consensus	***-*****	*****	*****	*****	-*-*****
msa137119.2{303_COH1}	251				300
msa137119.2{303_M732}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_m781}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_090}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_18RS21}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_2603}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_A909}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_CJB110}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_H36B}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_JM9130013}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
msa137119.2{303_1169NT}	TTGATATATT	AATTGACTGT	ATTGGAGCGA	TTAAGCCCAA	TCAACTAGAT
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	301				350
msa137119.2{303_M732}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_m781}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_090}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_18RS21}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_2603}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_A909}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_CJB110}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_H36B}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_JM9130013}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
msa137119.2{303_1169NT}	GAGCTTAAACG	TTAAAGCAAC	CCAAAAAGCA	GTAGCACTCT	GTCACAAAAA
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	351				400
msa137119.2{303_M732}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_m781}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_090}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_18RS21}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_2603}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_A909}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_CJB110}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_H36B}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_JM9130013}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
msa137119.2{303_1169NT}	TCAAATACCA	AAGTTAGTTT	AcATTTCAGC	CAATAGCGGC	TATTGAGCTT
Consensus	*****	*****	*-*****	***-*****	*****
msa137119.2{303_COH1}	401				450
msa137119.2{303_M732}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_m781}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_090}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_18RS21}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_2603}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_A909}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_CJB110}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_H36B}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_JM9130013}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
msa137119.2{303_1169NT}	ACATTAAAG	TAAAAGGAAG	GCAGAGCAGA	TAATCAAAGC	AAGCGGTCTG
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	451				500
msa137119.2{303_M732}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_m781}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_090}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_18RS21}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_2603}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_A909}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_CJB110}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_H36B}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_JM9130013}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
msa137119.2{303_1169NT}	GATTATCTTT	TTGTAAGACC	AGGTTTGATG	TATGGTGAAG	AGCGACCTCT
Consensus	*****	*****	*****	*****	*****
msa137119.2{303_COH1}	501				550
msa137119.2{303_M732}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTAGTCAT	TTGCCTTTCT
msa137119.2{303_m781}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTAGTCAT	TTGCCTTTCT
msa137119.2{303_090}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTAGTCAT	TTGCCTTTCT
msa137119.2{303_18RS21}	CTCGATTTC	CAAGCCAAGT	GTATAAAaTT	ATTAGTCAT	TTGCCTTTCT

Table 66: Comparative Sequences relating to SAG 0754

msa137119.2{303_2603}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_A909}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_CJB110}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_H36B}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_JM9130013}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
msa137119.2{303_1169NT}	CTCGATTTC	CAAGCCAAGT	GTATAAAGTT	ATTTAGTCAT	TGCGCTTTCT
Consensus	*****	*****	*****_**	*****	*****
551					
msa137119.2{303_COH1}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_M732}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_m781}	TAGGTATTGT	TGTACAAAAa	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_090}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_18RS21}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_2603}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_A909}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_CJB110}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_H36B}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_JM9130013}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
msa137119.2{303_1169NT}	TAGGTATTGT	TGTACAAAAg	GTCTTTCCAA	CTAAGGTTGT	GATAGTGGCA
Consensus	*****	*****_*	*****	*****	*****
601					
msa137119.2{303_COH1}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_M732}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_m781}	GAAGCAATCG	TTACTtCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
msa137119.2{303_090}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_18RS21}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_2603}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_A909}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_CJB110}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_H36B}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_JM9130013}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAACcCAAA	AAATCCTTTC
msa137119.2{303_1169NT}	GAAGCAATCG	TTACTaCGCT	TAGGAaAAAA	CCAActCAAA	AAATCCTTTC
Consensus	*****	*****_****	*****_****	*****_****	*****
651					
msa137119.2{303_COH1}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_M732}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_m781}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_090}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_18RS21}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_2603}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_A909}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_CJB110}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_H36B}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_JM9130013}	TATTGAAGAA	TAAATAATA	AA		
msa137119.2{303_1169NT}	TATTGAAGAA	TAAATAATA	AA		
Consensus	*****	*****	**		
672					

SEQ ID NO. 6612

STRAIN 2603 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRITYIRGDIETADKIHLERDTFDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPKVVIVABAIVITTLRKPTQKILSIEELNNK

SEQ ID NO. 6613

STRAIN 090 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRITYIRGDIETADKIHLERDTFDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPKVVIVABAIVITTLRKPTQKILSIEELNNK

SEQ ID NO. 6614

STRAIN A909 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRITYIRGDIETADKIHLERDTFDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPKVVIVABAIVITTLRKPTQKILSIEELNNK

SEQ ID NO. 6615

STRAIN H36B frame: 2

IKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDIKFD
 PRITYIRGDIETADKIHLERDTFDILIDCIGAIPNQLDELNVKATQKAVALKHNQIPK
 LVYISANSYGSAIYKSKRKAQIIKASGLDYLFVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPKVVIVABAIVITTLRKPTQKILSIEELNNK

SEQ ID NO. 6616

Table 66: Comparative Sequences relating to SAG 0754

STRAIN 18RS21 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6617

STRAIN M732 frame: 1

QNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD PRLTYIKGDIT
 EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPKLVYISANSYS
 AYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH PFLGIVVQKV
 PTKVIVAEIAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6618

STRAIN COH1 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6619

STRAIN M781 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIKGDIT EADKIHLEHRNFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTSLRKKPTQKILSIEELNNK

SEQ ID NO. 6620

STRAIN 1169NT frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKLAYLSRHEGKGDI FKD
 PRLTYIKGDIT EADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTTLRKTPTQKILSIEELNNK

SEQ ID NO. 6621

STRAIN CJB110 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTTLRKKPTQKILSIEELNNK

SEQ ID NO. 6622

STRAIN JM9130013 frame: 1

TRHIKISILNLQNEGEGTMEILIAGGSGFLGKQIIKAALTKGHKVAYLSRHEGKGDI FKD
 PRLTYIRGDI TEADKIHLEDRTFDILIDCIGAIKPNQLDELNVKATQKAVALCHKNQIPK
 LVYISANSYSAYIKSKRKAQEI KASGLDYL FVRPGLMYGEERPLSIFQAKCIKLFSLH
 PFLGIVVQKVFPPTKVVI VAEIAVTTLRKKPTQKILSIEELNNK

PRETTY of: /biotmp/msa137299.2{*} April 10, 2003 03:37 ..

	1				50
msa137299.2{303_COH1}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_M732}	-----	-QNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_M781}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_090}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_18RS21}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_2603}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_A909}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_CJB110}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_JM9130013}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_H36B}	---ikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
msa137299.2{303_1169NT}	trhikisiln	lQNEGEGTME	ILIAGGSGFL	GKQIIKAALT	KGHKVAYLSR
Consensus	-----	*****	*****	*****	*****

	51				100
msa137299.2{303_COH1}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_M732}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_M781}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEh	RnFDILIDCI	GAIKPNQLDE
msa137299.2{303_090}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_18RS21}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_2603}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_A909}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_CJB110}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_JM9130013}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_H36B}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
msa137299.2{303_1169NT}	HEGKGDI FKD	PRLTYIKGDI	TEADKIHLEd	RtFDILIDCI	GAIKPNQLDE
Consensus	*****	*****	*****	*****	*****

Table 66: Comparative Sequences relating to SAG 0754

	101		150
msa137299.2{303_COH1}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_M732}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_M781}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_090}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_18RS21}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_2603}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_A909}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_CJB110}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_JM9130013}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_H36B}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
msa137299.2{303_1169NT}	LNvkATQKAV	ALCHKNQIPK	LVYISANSgy
Consensus	*****	*****	*****
	151		200
msa137299.2{303_COH1}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_M732}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_M781}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_090}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_18RS21}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_2603}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_A909}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_CJB110}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_JM9130013}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_H36B}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
msa137299.2{303_1169NT}	YLFVRPGLMY	GEERPLSIFQ	AKCIKLFSHL
Consensus	*****	*****	*****
	201		223
msa137299.2{303_COH1}	AIvTsLRkKP	TQKILSIEEL	NNK
msa137299.2{303_M732}	AIvTsLRkKP	TQKILSIEEL	NNK
msa137299.2{303_M781}	AIvTsLRkKP	TQKILSIEEL	NNK
msa137299.2{303_090}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_18RS21}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_2603}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_A909}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_CJB110}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_JM9130013}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_H36B}	AIvTtLRkKP	TQKILSIEEL	NNK
msa137299.2{303_1169NT}	AIvTtLRkKP	TQKILSIEEL	NNK
Consensus	*****	*****	***

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6701

STRAIN 090

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGA
 TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAAACCATTTGATGAAAAACCAACAGCACAGTCTTTGT
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
 GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTGTACTGAAG
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGGAAAACGACACGACACGATGATGCAGAAAGTCTTAAATGC
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG
 AAGTTGTTTCAAGGCTGCGGATGATAAAGATATTCTAGTTATGGAATTATCA
 AGTTTTCAGCTAATGGGAGTTAAGGAATTTTCCTCATATTGCGAGTAAT
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT
 TTGGTACTTAATTTAATCAAGGTATTTCTAAGAGTTAGCTAAAACCTAC
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAAGTTGATGGTGCTT
 ACGTACAGACAAGCAACTTTCTATAAAGGGGAGAAATATTATGTTAGTA
 GATGACATTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTCAATCACTCGGTAAAG
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
 CAGGAGGTCCTGATCGCGGTAATGAGTTTGTGAATTGATACCAGATATC
 ACTGGACTTAAACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAA
 ACGTGCTGCACAAAAGCAGGAGTAACCTATAGCGATGCTTTAGATTGTTA
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
 TTGCTAAGTCTTCAAAATGCATCATGGGACATGTATAAGAATTTCAAGT
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6702

STRAIN A909

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGA
 TCTGGAGAAGCTGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
 AGTTAATGATGGCAAACCATTTGATGAAAAACCAACAGCACAGTCTTTGT
 TGGAAAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTA
 GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA
 TCCTATGGTCAAAAAGCATTAGAAAAACAAATCCCTGTTTGTACTGAAG
 TGGAAATTAGCATACTTAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGC
 TCTAACGGGAAAACGACACGACACGATGATGCAGAAAGTCTTAAATGC
 TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTG
 AAGTTGTTTCAAGGCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCA
 AGTTTTCAGCTAATGGGAGTTAAGGAATTTTCCTCATATTGCGAGTAAT
 TACTAATTTAATGCCAACTCAATTAGATTATCATGGGTCTTTTGAAGATT
 ATGTTGCTGCAAAATGGAATATCCAAATCAAATGTCTTCATCTGATTTT
 TTGGTACTTAATTTAATCAAGGTATTTCTAAGAGTTAGCTAAAACCTAC
 TAAAGCAACAATCGTTCCTTCTCTACTACGGAAGTTGATGGTGCTT
 ACGTACAGACAAGCAACTTTCTATAAAGGGGAGAAATATTATGTCAGTA
 GATGACATTGGTGTCCAGGAAGCCATAACGTAAAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTGCGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTTTGGAGGTGTTAAACACCGCTTCAATCACTCGGTAAAG
 GTTCATGGTATTAGTTTCTATAACGACAGCAAGTCAACTAATATATTGGC
 AACTCAAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCCTAATTG
 CAGGAGGTCCTGATCGCGGTAATGAGTTTGTGAATTGATACCAGATATC
 ACTGGACTTAAACATATGGTTGTTTATAGGGGAATCGGCATCTCGAGTAAA
 ACGTGCTGCACAAAAGCAGGAGTAACCTATAGCGATGCTTTAGATTGTTA
 GAGATGCGGTACATAAAGCTTATGAGGTGGCACAACAGGGCGATGTTATC
 TTGCTAAGTCTTCAAAATGCATCATGGGACATGTATAAGAATTTCAAGT
 CCGTGGTGATGAATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6703

STRAIN H36B

GGACGAGTAATGAAAACAATAACAACATTTGAAAAT
 AAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCTGCACG
 TTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACCAT
 TTGATGAAAATCCAAACAGCACAGTCTTTGTGGAAAGAGGGTATTAAAGTG
 GTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTACAT
 GATTAAAAATCCAGGAATACCTTATAACCAATCCTATGGTCAAAAAGCAT
 TAGAAAAACAATAATCCCTGTTTGTAGTGAAGTGAATTAGCATACTTAGTT
 TCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAACGACAA
 GACAACGATGATTGCAGAAAGTCTTAAATGCTGGAGGTGAGAGAGGTTTGT
 TAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTCAAGGCTGCGAAT
 GATAAAGATACTCTAGTTATGGAATATCAAGTTTTCAGCTAATGGGAGT
 TAAGGAATTTCTGCTCATATTGCAAGTAATTAATAATTAAATGCCAACTC
 ATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGAAT
 ATCCAAATCAAATGTCTTCATCTGATTTTGTGTTACTTAATTTAATCA
 AGGTATTTCTAAAGAGTTAGCTAAAACCTACTAAAGCAACAATCGTTCCTT
 TCTCTACTACGGAAGTTGATGGTGCTTACGTACAAGACAAGCAACTT
 TTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGGTGTCCAGG
 AAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACTGG
 CTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGGAGGT
 GTTAAACACCGCTTCAATCACTCGGTAAAGTTTATGGTATTAGTTTCTA
 TAACGACAGCAAG

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6704

STRAIN 18RS21

GGACGAGTAATGAAAAACAATAACAACATTTG
 AAAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCTGCT
 GCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
 ACCATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAA
 AAGTGGTTTGGTGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT
 TACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
 AGCATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGAATTAGCATACT
 TAGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACG
 ACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGG
 TTTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTG
 CGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCTAATG
 GGAGTTAAGGAATTCGTCTCATATTGCAGTAATTACTAATTTAATGCC
 AACTCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAAT
 GGAATATCCAAAAATCAAAATGTCCTCATCTGATTTTGGTACTTAATTTT
 AATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGT
 TCCTTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGC
 AACTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTTGGTGT
 CCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAA
 ACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTG
 GAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGT
 TTCTATAACGACAGCAAGTCACTAATATATTGGCACTCAAAAAGCATT
 ATCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAAGGAGGCTTGATC
 GCGGTAATGAGTTTGTGATGAATTGATACAGATATCACTGGACTTAAACAT
 ATGGTTGTTTGGGGGAATCGGCATCTCGAGTAAAACGTGCTGCACAAAA
 AGCAGGAGTAACCTTAGCGATGCTTTAGATGTTAGAGATGCGGTACATA
 AAGCTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCA
 AATGCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATT
 CATTGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6705

STRAIN M732

GGACGAGTAATGAAAAACAATAACAACATTTGAAA
 ATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTGCA
 CGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAACC
 ATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAAAG
 TGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGTATAC
 ATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAAGC
 ATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGAATTAGCATACTTAG
 TTTGAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGACA
 ACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGTTT
 GTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGCGG
 ATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGGGA
 GTTAAGGAATTTGCTCCTCATATTGCAGTAATTACTAATTTAATGCCAAC
 TCACTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAAATGGA
 ATATCCAAAAATCAAAATGTCCTCATCTGATTTTGGTACTTAATTTAAT
 CAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTTCC
 TTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCAAC
 TTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTTGGTGTCCTCA
 GGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAACT
 AGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTGGAG
 GTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTATGTTATTAGTTTC
 TATAACGACAGCAAGTCACTAATATATTGGCAACTCAAAAAGCATTATC
 TGGCTTTGATAAATACTAAAGTTATCCTAATTGCAAGGAGGCTTGTATCGCG
 GTAATGAGTTTGTGATGAATTGATACAGATATCACTGGACTTAAACATATG
 GTTGTTTTAGGGCAATCGGCATCTCGAGTAAAACGTGCTGCACAAAAAGC
 AGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAAAG
 CTTATGAGGTGGCACAACAGGGCGATGTTATCTTGCTAAGTCTTGCAAAAT
 GCATCATGGGACATGTATAAGAATTTGGAAGTCCGTGGTGATGAATTAT
 TGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6706

STRAIN COH1

GGACGAGTAATGAAAAACAATAACAACATTTGA
 AAATAAAAAAGTTTGTAGTCCTTGGTTTAGCACGATCTGGAGAAGCCGCTG
 CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAA
 CCATTTGATGAAAAATCCAACAGCACAGTCTTGTGGAAGAGGGTATTAA
 AGTGGTTTGTGGTAGTCATCCTTTAGAATTGTTAGATGAGGATTTTGT
 ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAA
 GCATTAGAAAAACAATCCCTGTTTGTGACTGAAGTGAATTAGCATACT
 AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA
 CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGGTT
 TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTGAGGCTGC
 GGAATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG
 GAGTTAAGGAATTTGCTCCTCATATTGCAGTAATTACTAATTTAATGCCA
 ACTCATTTAGATTATCATGGGTCTTTGAAGATTATGTTGCTGCAAAATG
 GAATATCCAAAAATCAAAATGTCCTCATCTGATTTTGGTACTTAATTTTA
 ATCAAGGTATTTCTAAAGAGTTAGCTAAAACTACTAAAGCAACAATCGTT
 CCTTCTCTACTACGGAAAAAGTTGATGGTGCTTACGTACAAGACAAGCA
 ACTTTTCTATAAAGGGGAGAATATTATGTGAGTAGATGACATTTGGTGTC
 CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTGCTAAA

Table 67: Comparative Sequences relating to SAG0475

CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTAGTT
TCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAGCATTA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
CGGTAAAGTGGTGGTGAATTGATACAGATATCACTGGACTTAAACATA
TGGTTCTTTTAGGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTTGCAA
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC
ATTGATACCTTCGAAA

SEQ ID NO. 6707

STRAIN M781

GGACGAGTAATGAAAACAATAACAACATT
TGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCG
CTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGC
AAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTAT
TAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTT
GTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAA
AAAGCATTAGAAAAACAATCCCTGTTTGGACTGAAGTGAATTAGCATA
CTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAA
CGACAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGA
GGTTTGTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTTCAGGC
TGCGGATGATAAAGATAATCTAGTTATGGAATTATCAAGTTTTCAGCTAA
TGGGAGTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATG
CCAATCATTTAGATTATCATGGGTCTTTTGAAGATTATGTTGCTGCAAA
ATGGAAATATCCAAAATCAAATGTCTTCATCTGATTTTTGGTACTTAATT
TTAATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAaCAATC
GTTCTTTCTCTACTACGGAATAAGTTGATGGTGTCTACGTACAAGACAA
GCAACTTTTCTATAAAGGGGAGAATATATGTCACTAGATGACATTGGTG
TCCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTGTCT
AAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAACTTAAAGCAATTT
TGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTA
GTTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAAGCA
TTATCTGGCTTTGATAATACTAAAGTTATCTAATTGCAGGAGGTCTTGA
TCGCGGTAATGAGTTTGATGAATTGATACAGATATCACTGGACTTAAAC
ATATGGTTGTTTtagGGGAATCGGCATCTCGAGTAAACGTGCTGCACAA
AAAGCAGGAGTaaCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACA
TAAAGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTCG
CAAAATGCATCATGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATC
TTCATTGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6708

STRAIN CJB110

GGACGAGTAATGAAAACAATAACAACATTTGA
AAATAAAAAAGTTTGTAGTCTTGGTTTAGCAGGATCTGGAGAAGCCGCTG
CACGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATGGCAAA
CCATTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGTATTAA
AGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTAGATGAGGATTTTGTGTT
ACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCAAAAAA
GCATTAGAAAAACAATCCCTGTTTGGACTGAAGTGAATTAGCATACTT
AGTTTCAGAAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAAAAACGA
CAACGACAACGATGATTGCAGAAGTCTTAAATGCTGGAGGTGAGAGAGGT
TTGTTAGCTGGGAATATCGGCTTTCCTGCTAGTGAAGTTGTTTCAGGCTGC
GGATGATAAAGATATTCTAGTTATGGAATTATCAAGTTTTCAGCTAATGG
GAGTTAAGGAATTTCTGCTCATATTGCAGTAATTACTAATTTAATGCCA
ACTCATTTAGATTATCATGGGTCTTTTGAAGAATATGTTGCTGCAAAATG
GAATATCCAAAATCAAATGTCTTCATCTGATTTTGGTACTTAATTTTAA
ATCAAGGTATTTCTAAAGAGTTAGCTAAAACCTAAAGCAACAATCGTT
CCTTTCTCTACTACGGAATAAGTTGATGGTCTTACGTACAAGACAAGCA
ACTTTTCTATAAAGGGGAGAATATTATGTTAGTAGATGACATTGGTGTCC
CAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTGTCTAAA
CTAGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAATTTTGG
AGGTGTTAAACACCGCTTGCAATCACTCGGTAAAGTTTCATGGTATTAGTT
TCTATATGACAGCAAGTCAACTAATATATTGGCAACTCAAAAGCATTA
TCTGGCTTTGATAATACTAAAGTTATCCTAATTGCAGGAGGTCTTGATCG
CGGTAAATGAGTTTGTGAATTGATACAGATATCACTGGACTTAAACATA
TGGTTGTTTtagGGGAATCGGCATCTCGAGTAAACGTGCTGCACAAAA
GCAGGAGTAACTTATAGCGATGCTTTAGATGTTAGAGATGCGGTACATAA
AGCTTATGAGGTGGCACAACAGGCGATGTTATCTTGCTAAGTCTTGCAA
ATGCATCATGGGACATGTATAAGAATTTGAAAGTCCGTGGTGTGAATTC
ATTGATACTTTGAAAAGTCTTAGAGGAGAG

SEQ ID NO. 6709

STRAIN 1169NT

CAATAACAACATTTGAAAATAAAAAAGTTTGTAGTCTTGGTTTAGCACGA
TCTGGAGAAGCCGCTGCACGTTTGTAGCTAAGTTAGGAGCAATAGTGAC
AGTTAATGATGGCAAAACATTTGATGAAAATCCAACAGCACAGTCTTTGT
TGGAGAGGGTATTAAAGTGGTTTGTGGTAGTCATCCTTTAGAATTTGTTA
GATGAGGATTTTGTACATGATTAAAAATCCAGGAATACCTTATAACAA
TCTATGGTCAAAAAGCATTAGAAAAACAATCCCTGTTTGGACTGAAG
TGAATTAGCATACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGC
TCTAACGGGAAAACGACAACGACAGATGATTGCAGAAGTCTTGAATGC

Table 67: Comparative Sequences relating to SAG0475

TGGAGGTCAGAGAGGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTG
 AAGTTGTTCAGGCTGCGGATGATAAGATACTCTAGTTATGGAATTATCA
 AGTTTTACAGCTAATGGGAGTTAAGGAATTCGTCCTCATATTGCAGTAAT
 TACTAATTTAATGCCAACTCATTAGATTATCATGGGCTTTTGAAGACT
 ATGTGCTGCAAAATGGAATATCCAAATCAAATGCTTCTCATCTGATTTT
 TTGGTACTTAATTTAATCAAGGTATTTCTAAAGAGTTAGCTAAACTAC
 TAAAGCAACAATCGTTCTTCTCTACTACGGAAGGTTGATGGTGCTT
 ACGTACAAGCAAGCAACTTTCTATAAGGGGAGAAATATTATGTCAGTA
 GACGACATTGGTGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAAC
 TATTGCGGTTGCTAAACTAGCTGGTATCAGTAATCAAGTTATTAGAGAAA
 CTTTAAGCAATTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAG
 GTTCATGGTATTAGTTTCTATAACGACAGTAAGTCAACTAATATATTGGC
 AACTCAAAAGCATTATCTGGCTTTGATAATACTAAAGTTATCTTAATTG
 CAGGAGGCTTGTATCGCGGTAATGAGTTTGTGAAITGATACCATATATC
 ACTGGACTTAAGCATATGGTTGTTTAGGGGAATCGGCATCTCGAGTAAA
 ACGTGTGTCACAAAAGCAGGAGTAACCTTATAGCAATGCTTTAGATGTTA
 GAGATGCGGTACATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATC
 TTGTTAGTCTCGCAATGCATCATGGGACATGTATAAGAATTTCAAGT
 CCGTGGTGATGAATTCATTGATACCTTCG

SEQ ID NO. 6710

STRAIN JM9130013

GGACGAGTAATGAAAACAATAACAACA

TTTGAAAATAAAAAAGTTTGTAGCTTGGTTTAGCAGCATCTGGAGAAGC
 TGCTGCAAGTTTGTAGCTAAGTTAGGAGCAATAGTGACAGTTAATGATG
 GCAAAACCATTTGATGAAAATCCAACAGCACAGTCTTTGTTGGAAGAGGGT
 ATTAAGTGGTTTGTGGTAGTCATCCTTTAGAATTGCTAGATGAGGATT
 TTGTTACATGATTAAAAATCCAGGAATACCTTATAACAATCCTATGGTCA
 AAAAAGCATTAGAAAAACAATCCCTGTTTGTACTGAAGTGAATTAGCA
 TACTTAGTTTCAGAATCTCAGCTAATAGGTATTACAGGCTCTAACGGGAA
 AAGCAACAGCAACGATGATTGCAAGTCTTAAATGCTGGAGGTCAGA
 GAGTTTGTAGCTGGGAATATCGGCTTTCTGCTAGTGAAGTTGTTGAG
 GCTGCGAATGATAAAGATACTCTAGTTATGGAATTATCAAGTTTTCAGCT
 AATGGGAGTTAAGGAATTTCTGCTCATATTGCAAGTAATTACTAATTTAA
 TGCCAACCTATTAGATTATCATGGGCTTTTGAAGATTATGTTGCTGCA
 AATGGAATATCCAAATCAAATGCTTCTCATCTGATTTTTGGTACTTAA
 TTTTAATCAAGGTATTCTAAAGAGTTAGCTAAACTACTAAAGCAACAA
 TCGTTCTTTCTACTACGGAAGGTTGATGGTGTCTACGTACAAGAC
 AAGCAACTTTCTATAAAGGGGAGAAATATTATGTCAGTAGATGACATTGG
 TGTCCAGGAAGCCATAACGTAGAGAATGCTCTAGCAACTATTGCGGTTG
 CTAAACTGGCTGGTATCAGTAATCAAGTTATTAGAGAACTTTAAGCAAT
 TTTGGAGGTGTTAAACACCGCTTGCAATCACTCGGTAAGGTTTCATGGTAT
 TAGTTCTATAACGACAGCAAGTCAACTAATATATTGGCAACTCAAAAG
 CATTATCTGGCTTTGATAATACTAAAGTTATCTTAATGTCAGGAGGCTT
 GATCGCAATGAGTTTGTAGTAATGATACCATATCACTGGACTTAA
 ACATATGGTTGTTTAGGGGAATCGGCATCTCGAGTAAACGTGCTGCAC
 AAAAGCAGGAGTAACCTTATAGCGATGCTTTAGATGTTAGAGATGCGGTA
 CATAAAGCTTATGAGGTGGCAACAGGGCGATGTTATCTTGTAAAGTCC
 TGCAATGCATCATGGGACATGTATAAGAATTTCAAGTCCGTGGTGATG
 AATTCATTGATACCTTCGAAAGTCTTAGAGGAGAG

SEQ ID NO. 6710

STRAIN 2603

ggacgagtaaatgaaaacaataacaacatttgaaaataaaaaagtttagt
 ccttggttagcacgatctggagaagctgctgcacgtttagttagctaagt
 taggagcaatagtgacagttaatgatggcaaacatttgatgaaaatcca
 acagcacagtctttagtggaagagggtattaaagtggtttgggttagtca
 tccttagaattgtagatgaggattttttagtatgatataaaatccag
 gaataccttataacaatcctatggtcaaaaagcattagaaaaacaatc
 cctgttttgactgaagtgggaattagcatacttagttcagaatctcagct
 aatagggtattacagggtctaacgggaaaaagcacaacgacacgatgattg
 cagaagctttaaattgctggagggtcagagagggtttagtagctgggaatct
 ggcttctctgctagtgaaagtgttcagggtgcaaatgataaagatactct
 agttatgggaattatcaagttttcagctaatgggagtttaaggaatttcgtc
 ctcatattgacagtaattactaatttaatgccaactcatttagattatcat
 gggtcttttagaattatgtagctgcaaaatgggaatccaaaatcaa
 gtctcatctgattttttagtacttaatttaatacaaggattttctaaag
 agttagctaaaactactaaagcaacaatcgttctctctactacggaa
 aaagttgatgggtgcttacgtacaagacaagcaactttctataaaggga
 gaattatgtagtgatgacattgggtgtcccaggaagccataacgtag
 agaattgcttagcaactatgctgggtgctaaactgggtggtatcagta
 caagttattagagaaactttaagcaattttggagggtgttaaacacggctt
 gcaatcactcggtaaggttcatgggtatttagtttctataacgacagcaag
 caactaatatattggcaactcaaaaagcatctctggctttgataaact
 aaagttatctcaatttgaggagggtcttgatcgcggttaagtagtttagta
 attgataccagatatactggacttaaacatattggtgttttaggggaat
 cggcatctcaggtaaaacgtgctgcacaaaagcaggagtaacttatagc
 gatgttttagatgttagagatgcggtacataaagcttatgaggtggcaca
 acagggcgatgttatctgctaagtcctgcaaatgcatcatgggacatgt
 ataagaatttcgaagtcctggtgatgaattcattgatactttcgaag
 ctttagggagag

Table 67: Comparative Sequences relating to SAG0475

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa30176.2{*} April 29, 2002 02:09 ..

	1				50
msa30176.2{305_18RS21}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_2603}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_A909}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_H36B}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_JM9130013}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_COH1}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_M781}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305e_M732}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_090}	ggacgagtaa	tgaaaaCAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_CJB110}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
msa30176.2{305_1169NT}	-----	-----CAAT	AACAACATTT	GAAAAATAAAA	AAGTTTTAGT
Consensus	-----	-----****	*****	*****	*****
	51				100
msa30176.2{305_18RS21}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_2603}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_A909}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_H36B}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_JM9130013}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_COH1}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_M781}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305e_M732}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_090}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_CJB110}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
msa30176.2{305_1169NT}	CCTTGGTTTA	GCACGATCTG	GAGAAGCtGC	TGCACGTTTG	TTAGCTAAGT
Consensus	*****	*****	*****	*****	*****
	101				150
msa30176.2{305_18RS21}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_2603}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_A909}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_H36B}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_JM9130013}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_COH1}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_M781}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305e_M732}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_090}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_CJB110}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
msa30176.2{305_1169NT}	TAGGAGCAAT	AGTGACAGTT	AATGATGGCA	AACCATTTGA	TGAAAATCCA
Consensus	*****	*****	*****	*****	*****
	151				200
msa30176.2{305_18RS21}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_2603}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_A909}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_H36B}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_JM9130013}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_COH1}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_M781}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305e_M732}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_090}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_CJB110}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
msa30176.2{305_1169NT}	ACAGCACAGT	CTTTGTTTGA	AGAGGGTATT	AAAGTGGTTT	GTGGTAGTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa30176.2{305_18RS21}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_2603}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_A909}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_H36B}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_JM9130013}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_COH1}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_M781}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305e_M732}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_090}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_CJB110}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
msa30176.2{305_1169NT}	TCCTTTAGAA	TTGTTAGATG	AGGATTTTTG	TTACATGATT	AAAAATCCAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa30176.2{305_18RS21}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_2603}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_A909}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_H36B}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_JM9130013}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_COH1}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_M781}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305e_M732}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC
msa30176.2{305_090}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCATTAGA	AAAACAAATC

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_CJB110}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
msa30176.2{305_1169NT}	GAATACCTTA	TAACAATCCT	ATGGTCAAAA	AAGCAITAGA	AAAACAAATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	301				350
msa30176.2{305_2603}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_A909}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_H36B}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_JM9130013}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_COH1}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_M781}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305e_M732}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_090}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_CJB110}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
msa30176.2{305_1169NT}	CCTGTTTGA	CTGAAGTGA	ATTAGCATA	TTAGTTTCAG	AATCTCAGCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	351				400
msa30176.2{305_2603}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_A909}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_H36B}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_JM9130013}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_COH1}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_M781}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305e_M732}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_090}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_CJB110}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
msa30176.2{305_1169NT}	AATAGGTATT	ACAGGCTCTA	ACGGGAAAAC	GACAACGACA	ACGATGATTG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	401				450
msa30176.2{305_2603}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_A909}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_H36B}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_JM9130013}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_COH1}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_M781}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305e_M732}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_090}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_CJB110}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
msa30176.2{305_1169NT}	CAGAAGTCTT	aaATGCTGGA	GGTCAGAGAG	GTTTGTAGC	TGGGAATATC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	451				500
msa30176.2{305_2603}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_A909}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_H36B}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_JM9130013}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_COH1}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_M781}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305e_M732}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_090}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_CJB110}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
msa30176.2{305_1169NT}	GGCTTTCCTG	CTAGTGAAGT	TGTTCAAGCT	GCGaATGATA	AAGATAcTCT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	501				550
msa30176.2{305_2603}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_A909}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_H36B}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_JM9130013}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_COH1}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_M781}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305e_M732}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_090}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_CJB110}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
msa30176.2{305_1169NT}	AGTTATGGAA	TTATCAAGTT	TTCAGCTAAT	GGGAGTTAAG	GAATTTTCGTC
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	551				600
msa30176.2{305_2603}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_A909}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_H36B}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_JM9130013}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_COH1}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305_M781}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT
msa30176.2{305e_M732}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATT	AGATTATCAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_090}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_CJB110}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
msa30176.2{305_1169NT}	CTCATATTGC	AGTAATTACT	AATTTAATGC	CAACTCATTT	AGATTATCAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_2603}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_A909}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_H36B}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_JM9130013}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_COH1}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_M781}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305e_M732}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_090}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_CJB110}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
msa30176.2{305_1169NT}	GGGTCCTTTG	AAGATATATG	TGCTGCAAAA	TGGAATATCC	AAAATCAAAT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_2603}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_A909}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_H36B}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_JM9130013}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_COH1}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_M781}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305e_M732}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_090}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_CJB110}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
msa30176.2{305_1169NT}	GTCTTCATCT	GATTTTTTGG	TACTTAATTT	TAATCAAGGT	ATTTCTAAAG
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_2603}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_A909}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_H36B}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_JM9130013}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_COH1}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_M781}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305e_M732}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_090}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_CJB110}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
msa30176.2{305_1169NT}	AGTTAGCTAA	AACTACTAAA	GCAACAATCG	TTCCTTTCTC	TACTACGGAA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_2603}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_A909}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_H36B}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_JM9130013}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_COH1}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_M781}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305e_M732}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_090}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_CJB110}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
msa30176.2{305_1169NT}	AAAGTTGATG	GTGCTTACGT	ACAAGACAAG	CAACTTTTCT	ATAAAGGGGA
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_2603}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_A909}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_H36B}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_JM9130013}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_COH1}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_M781}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305e_M732}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_090}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_CJB110}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
msa30176.2{305_1169NT}	GAATATTATG	TcAGTAGATG	ACATTGGTGT	CCCAGGAAGC	CATAACGTAG
Consensus	*****	*-*****	*****	*****	*****
msa30176.2{305_18RS21}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_2603}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_A909}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_H36B}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_JM9130013}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_COH1}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT
msa30176.2{305_M781}	AGAAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTgGCTGG	TATCAGTAAT

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305e_M732}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_090}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_CJB110}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
msa30176.2{305_1169NT}	AGAATGCTCT	AGCAACTATT	GCGGTTGCTA	AACTaGCTGG	TATCAGTAAT
Consensus	*****	*****	*****	****_****	*****
msa30176.2{305_18RS21}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_2603}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_A909}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_H36B}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_JM9130013}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_COH1}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_M781}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305e_M732}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_090}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_CJB110}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
msa30176.2{305_1169NT}	CAAGTTATTA	GAGAAACTTT	AAGCAATTTT	GGAGGTGTTA	AACACCGCTT
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_2603}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_A909}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_H36B}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_JM9130013}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_COH1}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_M781}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305e_M732}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_090}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_CJB110}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
msa30176.2{305_1169NT}	GCAATCACTC	GGTAAGGTTT	ATGGTATTAG	TTTCTATAAc	GACAGcAAGt
Consensus	*****	*****	*****	*****	*****
msa30176.2{305_18RS21}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_2603}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_A909}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_H36B}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_JM9130013}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_COH1}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_M781}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305e_M732}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_090}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_CJB110}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
msa30176.2{305_1169NT}	caactaatat	attggcaact	caaaaagcat	tatctggcctt	tgataataact
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_2603}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_A909}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_H36B}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_JM9130013}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_COH1}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_M781}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305e_M732}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_090}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_CJB110}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
msa30176.2{305_1169NT}	aaagttatcc	taattgcagg	aggtccttgat	cgcggtaatg	agtttgatga
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_2603}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_A909}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_H36B}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_JM9130013}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_COH1}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_M781}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305e_M732}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_090}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_CJB110}	attgatacca	gatatactg	gacttaaaaca	tatggttggtt	ttaggggaat
msa30176.2{305_1169NT}	attgatacca	gatatactg	gacttaagca	tatggttggtt	ttaggggaat
Consensus	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_2603}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_A909}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_H36B}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_JM9130013}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc
msa30176.2{305_COH1}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc

Table 67: Comparative Sequences relating to SAG0475

msa30176.2{305_M781}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc		
msa30176.2{305e_M732}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc		
msa30176.2{305_090}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc		
msa30176.2{305_CJB110}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc		
msa30176.2{305_1169NT}	cggcatctcg	agtaaaacgt	gctgcacaaa	aagcaggagt	aacttatagc		
Consensus	-----	-----	-----	-----	-----		
msa30176.2{305_18RS21}	1201	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca	1250
msa30176.2{305_2603}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_A909}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_H36B}	-----	-----	-----	-----	-----		
msa30176.2{305_JM9130013}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_COH1}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_M781}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305e_M732}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_090}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_CJB110}	gatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
msa30176.2{305_1169NT}	aatgcttttag	atgttagaga	tgcggtacat	aaagcttatg	aggtggcaca		
Consensus	-----	-----	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	1251	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt	1300
msa30176.2{305_2603}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_A909}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_H36B}	-----	-----	-----	-----	-----		
msa30176.2{305_JM9130013}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_COH1}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_M781}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305e_M732}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_090}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_CJB110}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
msa30176.2{305_1169NT}	acagggcgat	gttatcttgc	taagtccctgc	aaatgcatca	tgggacatgt		
Consensus	-----	-----	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	1301	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt	1350
msa30176.2{305_2603}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_A909}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_H36B}	-----	-----	-----	-----	-----		
msa30176.2{305_JM9130013}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_COH1}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_M781}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305e_M732}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_090}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_CJB110}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
msa30176.2{305_1169NT}	ataagaattt	cgaagtcctg	ggtgatgaat	tcattgatac	tttcgaaagt		
Consensus	-----	-----	-----	-----	-----	-----	-----
msa30176.2{305_18RS21}	1351	cttagaggag	ag				1362
msa30176.2{305_2603}	cttagaggag	ag					
msa30176.2{305_A909}	cttagaggag	ag					
msa30176.2{305_H36B}	-----	-----					
msa30176.2{305_JM9130013}	cttagaggag	ag					
msa30176.2{305_COH1}	-----	-----					
msa30176.2{305_M781}	cttagaggag	ag					
msa30176.2{305e_M732}	cttagaggag	ag					
msa30176.2{305_090}	cttagaggag	ag					
msa30176.2{305_CJB110}	cttagaggag	ag					
msa30176.2{305_1169NT}	-----	-----					
Consensus	-----	-----	-----	-----	-----	-----	-----

SEQ ID NO. 6711

STRAIN 090 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVAADDKDILVMESSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMLVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHLRQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6712

STRAIN A909 frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLEEGI KVVCGS
HPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQIIGITGSNGK
TTTTTMAIEVLNAGGQRLLAGNIGFPASEVVAANDKDTLMESSSFQLMGVKEFRPHI
AVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVXNALATIAVAKLAGISNQVIRET
LSNFGGVKHLRQSLGKVHGISFYNDKSTNILATQKALSGFDNTKVILIAGGLDRGNEFD

Table 67: Comparative Sequences relating to SAG0475

ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGDVILLSP
ANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6713

STRAIN H36B frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD

SEQ ID NO. 6714

STRAIN 18RS21 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6715

STRAIN M732 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6716

STRAIN COH1 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFE

SEQ ID NO. 6717

STRAIN M781 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6718

STRAIN CJB110 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGI
KVVCGSHPLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
TGSNGKTTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
EFRPHIAVITNLMPTHLDDYHGSFEYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTK
ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISN
QVIRETLSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
RGNEFDELI PDITGLKHMVVLGESASRVKRAAQKAGVTYS DALDVRDAVHKAYEVAQQGD
VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6719

STRAIN 1169NT frame: 3

ITTFENKKVLVLGLARSGEAAARLLAKLGAIVTVNDGKPFDENPTAQSLLLEGIKVVCGS
HLELLDEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGITGSNGK
TTTTTMAEVLNAGGQGRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVKEFRPHI
AVITNLMPTHLDDYHGSFEDYVAAKWNIONQMSSSDFLVLNFNQGISKELAKTTKATIVPF
STTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIAVAKLAGISNQVIRET
LSNFGGVKHLRQLSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLDRGNEF
ELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSN ALDVRDAVHKAYEVAQQGDVILXSP
ANASWDMYKNFEVRGDEFIDTF

Table 67: Comparative Sequences relating to SAG0475

SEQ ID NO. 6720

STRAIN JM9130013 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKEKAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
 RSNFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

SEQ ID NO. 6721

STRAIN 2603 frame: 1

GRVMKTIITTFENKKVLVLGLARSGEAAARLLAKLGAIIVTVNDGKPFDENPTAQSLLLEEGI
 KVVCGSHPLELLEDFCYMIKNPGIPYNNPMVKKALEKQIPVLTEVELAYLVSESQILIGI
 TGSNGKTTTTMTIAEVLNAGGQRLLAGNIGFPASEVVQAANDKDTLVMELSSFQLMGVK
 EFRPHIAVITNLMPTHLDYHGSFEDYVAAKWNINQMSSSDFLVLNFNQGISKEKAKTTK
 ATIVPFSTTEKVDGAYVQDKQLFYKGENIMSVDDIGVPGSHNVENALATIIVAKLAGISN
 QVIRETLSNFGGVKHLQSLGKVHGISFYNDKSTNIIATQKALSGFDNTKVILTAGGLD
 RSNFDELIPDITGLKHMVVLGESASRVKRAAQKAGVTYSDALDVRDAVHKAYEVAQQGD
 VILLSPANASWDMYKNFEVRGDEFIDTFESLRGE

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa25243.2{*} April 29, 2002 02:20 ..

	1		50
msa25243.2{305_18RS21}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_2603}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_JM9130013}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_COH1}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M732}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_M781}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_1169NT}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_A909}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_CJB110}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_090}	-----ITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
msa25243.2{305_H36B}	grvmktITTF	ENKKVLVLGL	ARSGEAAARL LAKLGAIIVTV NDGKPFDENP
Consensus	-----****	*****	*****
	51		100
msa25243.2{305_18RS21}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_2603}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_JM9130013}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_COH1}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M732}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_M781}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_1169NT}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_A909}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_CJB110}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_090}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
msa25243.2{305_H36B}	TAQSLLEEGI	KVVCGSHPLE	LLEDDFCYMI KNPGIPYNNP MVKKALEKQI
Consensus	*****	*****	*****
	101		150
msa25243.2{305_18RS21}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_2603}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_JM9130013}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_COH1}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M732}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_M781}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_1169NT}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_A909}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_CJB110}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_090}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
msa25243.2{305_H36B}	PVLTEVELAY	LVSESQILIGI	TGSNGKTTTT TMIAEVLNAG GQRGLLAGNI
Consensus	*****	*****	*****
	151		200
msa25243.2{305_18RS21}	GFPASEVVQA	AnDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_2603}	GFPASEVVQA	AnDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_JM9130013}	GFPASEVVQA	AnDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_COH1}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M732}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_M781}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_1169NT}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_A909}	GFPASEVVQA	AnDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_CJB110}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_090}	GFPASEVVQA	AdDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
msa25243.2{305_H36B}	GFPASEVVQA	AnDKDcLVME	LSSFQLMGVK EFRPHIAVIT NLMPTHLDYH
Consensus	*****	*-***-*****	*****

Table 67: Comparative Sequences relating to SAG0475

	201		250
msa25243.2{305_18RS21}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_2603}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_JM9130013}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_COH1}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_M732}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_M781}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_1169NT}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_A909}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_CJB110}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_090}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
msa25243.2{305_H36B}	GSFEdYVAAK WNIQNMSSS DFLVLNFNQG ISKELAKTTK ATIVPFSTTE		
Consensus	****-*****	*****	*****
	251		300
msa25243.2{305_18RS21}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_2603}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_JM9130013}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_COH1}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_M732}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_M781}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_1169NT}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_A909}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_CJB110}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_090}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
msa25243.2{305_H36B}	KVDGAYVQDK QLIFYKGENIM sVDDIGVPGS HNveNALATI AVAKLAGISN		
Consensus	*****	*****	*****
	301		350
msa25243.2{305_18RS21}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_2603}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_JM9130013}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_COH1}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_M732}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_M781}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_1169NT}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_A909}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_CJB110}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_090}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
msa25243.2{305_H36B}	QVIRETLSNF GGVKHLRLQSL GKVHGISFYN DSKstnilat qkalsgfdnt		
Consensus	*****	*****	*****
	351		400
msa25243.2{305_18RS21}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_2603}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_JM9130013}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_COH1}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_M732}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_M781}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_1169NT}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_A909}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_CJB110}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_090}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
msa25243.2{305_H36B}	kvliaggld rgnefdelip ditglkhmvv lgesasrvkr aakgagvtys		
Consensus	-----	-----	-----
	401		450
msa25243.2{305_18RS21}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_2603}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_JM9130013}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_COH1}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_M732}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_M781}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_1169NT}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_A909}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_CJB110}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_090}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
msa25243.2{305_H36B}	daldvrdavh kayevagggd villspanas wdmyknfevr gdefidtfes		
Consensus	-----	-----	-----
	451		
msa25243.2{305_18RS21}	lrge		
msa25243.2{305_2603}	lrge		
msa25243.2{305_JM9130013}	lrge		
msa25243.2{305_COH1}	----		
msa25243.2{305_M732}	lrge		
msa25243.2{305_M781}	lrge		
msa25243.2{305_1169NT}	----		
msa25243.2{305_A909}	lrge		
msa25243.2{305_CJB110}	lrge		
msa25243.2{305_090}	lrge		
msa25243.2{305_H36B}	----		
Consensus	----		

Table 68: Comparative Sequences relating to SAG 0499

SEQ ID NO. 6801

STRAIN 2603

ATGGCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGGGACTTTTGTATACACGAGAG
CAAGCGAAACGTTGGTGTATGGCAGGAATGGTGTATTAACGTTATCAATGGAGAACGTTAT
GATAAACCCAGGTGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTA
AAATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTACTGATGTTATG
CTACAATCAGGAGCGCGTTTAGTTTACGCGAGTAGATGTAGGAACAAATCAATTAGTTTGG
AAGTTACGTCAGGATCATCGTGTCTGTTCTATGGAACAATATAATTTTAGGTATGCCCAA
AAAGAAGATTTCAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCT
CTTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAACCCAAATTTGAAGCAGGTGCTGAGCAAATTTGGTAAATATGTTATGTCAAA
GACAAGTTGGTTTCATGAAAAGGTTTGGACAACAGTGACCAATTTACGAAAGATTATGGA
TATACGGTTAAACATCTTGATTTTTCGCCATTCAGGTGGACATGGAAATATTGAGTTT
TTAATGCATTTGCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAAGAT
GTTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6802

STRAIN 090

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATG
GCAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGG
TGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA
AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTT
GAAATTTAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
TGGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCG
TAGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGT
GTTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGAGATT
CAAGGAGGAGCTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
TTAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAA
GTAGTGGCATTAAATTAACCCAAATTTGAAGCAGGTGCTGAGCAAATTTG
TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAA
CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTT
GCAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAAGATG
TTATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6803

STRAIN A909

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGG
GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTG
AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCG
AGATGTAGGAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTG
TTGCTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTC
AAGGAGGAGCTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
TAGTGGCATTAAATTAACCCAAATTTGAAGCAGGTGCTGAGCAAATTTGGT
AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC
AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
TTTTCGCCCATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTG
CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAATACAAGATGT
TATAGAAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6804

STRAIN H36B

GCTAAAGAGAGGGTAGATGTTCTTGCCTATAAACAGG

GACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGGCAGGAATG
GTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGGTGAAAAGGT
TGCAAGCAGATACTGAATTAAAACTAAAAGGTGAAAACTAAAATATGTTA
GTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTTGAAATTTCA
GTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGTGGTTTTAC
TGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCGAGTAGATGTAG
GAACAAATCAATTAGTTTGAAGTTACGTCAGGATCATCGTGTCTGTTCT
ATGGAACAATATAATTTTAGGTATGCCCAAAAGAGATTTCAGGAGGG
ACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCTTAATTTGA
TTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAGTAGTGGCA
TTAATTAACCCAAATTTGAAGCAGGTGCTGAGCAAATTTGGTAAAAATGG
TATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAACAGTGACCA
ATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATTTTTCGCCC
ATTCAGGTGGACATGGAATATTGAGTTTTTAATGCATTTGCAAAAGTG
TCAAGATCCACAAAATCTTGTGCTTGACCAATACAAGATGTTATAGAAA
AAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6805

STRAIN 18RS21

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCGAAACGTTGGTGTATGG
CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACCCAGG

Table 68: Comparative Sequences relating to SAG 0499

GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG
 AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC
 AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCCGCCATTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTGG
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATCAAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6806

STRAIN M732

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGACTGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGC
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG
 AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGTG
 TTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC
 AAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCCGCCATTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTGG
 CAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATCAAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6807

STRAIN COH1

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGC
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT
 GAAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC
 CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATGG
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCGTTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTG
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATCAAGATG
 TTATAGAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6808

STRAIN M781

GCTAAAGAGAGGGTAGATGTTCTTGCCT

ATAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATG
 GCAGGACTGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGC
 CGAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAA
 AATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGT
 GAAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGG
 TGGTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAG
 TAGATGTAGGAACAAATCAATTAGTTTGGAAAGTTACGT CAGGATCATCGT
 GTTCGTTCTATGGAACAAATATAATTTAGGTATGCCCAAAAGAAGATTTC
 CAAGGAGGACTGCCTGAATTTGCATCGATAGATGTCTCATTATCTCTC
 TTAATTTGATTTTACCAGCTCTAAAAGAAATTTAGTGGATGGTGGACAA
 GTAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATGG
 TAAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTGGACAAC
 CAGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGAT
 TTTTCGCCCGTTCAAGGTGGACATGGAATATTGAGTTTAAATGCATTG
 GCAAAAGTGTCAAGATCCACAAATCTTGTGCTTGACCAAAATCAAGATG
 TTATAGAAAAGCACATAAGGAATTTAAGAAAAATGAAGAAGAG

SEQ ID NO. 6809

STRAIN CJB110

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACAGAGAGCAAGCGAAACGTGGTGTATGG
 CAGGAATGGTGATTAACTTATCAATGGAGAACGTTATGATAAACAGGC
 GAAAAGGTTGCAGACGATACTGAATTAAAACTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTGTG
 AAATTTCAAGTTGCAGATAAGCTAACTATAGATATTGGCGCCTCTACGGGT

Table 68: Comparative Sequences relating to SAG 0499

GGTTTTACTGATGTTATGCTACAATCAGGAGCGGTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAAGATTTC
 AAGGAGGGACTGCGCTGAATTTGCATCGATAGATGTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTATTAACCACAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCCGCCATTCAAGGTGGACATGGAAATATTGAGTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6810

STRAIN 1169NT

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCAACGTTGGTGTATGG
 CAGGACTGGTGATTACGTTATCAATGGAGAACGTTATGATAAACAGGC
 GAAAAGGTTGCAGACGATACTGAATTAACCTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAAGATTTC
 AAGGAGGGACTGCGCTGAATTTGCATCGATAGATGTCATTATCTCTCT
 TAATTTGATTTTCCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCCGCCATTCAAGGTGGACATGGAATATTGAGTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

SEQ ID NO. 6811

STRAIN JM9130013

GCTAAAGAGAGGGTAGATGTTCTTGCCTA

TAAACAGGGACTTTTGTATACACGAGAGCAAGCAACGTTGGTGTATGG
 CAGGAATGGTGATTAAACGTTATCAATGGAGAACGTTATGATAAACAGGT
 GAAAAGGTTGCAGACGATACTGAATTAACCTAAAAGGTGAAAACTAAA
 ATATGTTAGTAGAGGTGGATTGAAATTAGAAAAAGCTTTACAAGTTTTG
 AAATTTTCAGTTGCAGATAAGCTAACTATAGATATTGGCGCTCTACGGGT
 GGTTTTACTGATGTTATGCTACAATCAGGAGCGCGTTTAGTTTACGCAGT
 AGATGTAGGAACAAATCAATTAGTTTGGAGTTACGTCAGGATCATCGTG
 TTCGTTCTATGGAACAATATAATTTTAGGTATGCCCAAAAGAAGATTTC
 AAGGAGGGACTGCGCTGAATTTGCATCGATAGATGTCATTATCTCTCT
 TAATTTGATTTTACCAGCTCTAAAAGAAATTTTAGTGGATGGTGGACAAG
 TAGTGGCATTAAATTAACCAAAATTTGAAGCAGGTCGTGAGCAAATTGGT
 AAAAATGGTATTGTCAAAGACAAGTTGGTTTCATGAAAAGGTTTTGACAAC
 AGTGACCAATTTACGAAAGATTATGGATATACGGTTAAACATCTTGATT
 TTTCCGCCATTCAAGGTGGACATGGAATATTGAGTTTTAATGCATTTG
 CAAAAGTGTCAAGATCCACAAAATCTTGTGCTTGACCAAATACAAGATGT
 TATAGAAAAGCACATAAGGAATTTAAGAAAATGAAGAAGAG

PRETTY of: /biotmp/msa236683.2{*} May 14, 2003 02:57 ..

	1		50
msa236683.2{310_090}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_18R521}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_2603}	atgGCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_A909}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_CJB110}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_H36B}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_JM9130013}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_COH1}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M732}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_M781}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
msa236683.2{310_1169NT}	---GCTAAAG	AGAGGGTAGA	TGTTCTTGCC TATAAACAGG GACTTTTTGA
Consensus	*****	*****	*****
	51		100
msa236683.2{310_090}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_18R521}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_2603}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_A909}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_CJB110}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_H36B}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_JM9130013}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_COH1}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M732}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_M781}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
msa236683.2{310_1169NT}	TACACGAGAG	CAAGCGAAAC	GTGGTGTTAT GGCAGGAaTG GTGATTAAACG
Consensus	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		101			150
msa236683.2{310_090}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_18RS21}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_2603}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_A909}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_CJB110}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_H36B}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_JM9130013}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GtGAAAAGGT	TGCAGACGAT
msa236683.2{310_COH1}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M732}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_M781}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
msa236683.2{310_1169NT}	TTATCAATGG	AGAACGTTAT	GATAAACCAG	GcGAAAAGGT	TGCAGACGAT
Consensus		*****	*****	*****	*****
		151			200
msa236683.2{310_090}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_18RS21}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_2603}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_A909}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_CJB110}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_H36B}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_JM9130013}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_COH1}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_M732}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_M781}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
msa236683.2{310_1169NT}	ACTGAATTAA	AACATAAAGG	TGAAAAACTA	AAATATGTGA	GTAGAGGTGG
Consensus		*****	*****	*****	*****
		201			250
msa236683.2{310_090}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_18RS21}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_2603}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_A909}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_CJB110}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_H36B}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_JM9130013}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_COH1}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M732}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_M781}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
msa236683.2{310_1169NT}	ATTGAAATTA	GAAAAAGCTT	TACAAGTTTT	TGAAATTTCA	GTTGCAGATA
Consensus		*****	*****	*****	*****
		251			300
msa236683.2{310_090}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_18RS21}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_2603}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_A909}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_CJB110}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_H36B}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_JM9130013}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_COH1}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M732}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_M781}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
msa236683.2{310_1169NT}	AGCTAACTAT	AGATATTGGC	GCCTCTACGG	GTGGTTTAC	TGATGTTATG
Consensus		*****	*****	*****	*****
		301			350
msa236683.2{310_090}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_18RS21}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_2603}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_A909}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_CJB110}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_H36B}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_JM9130013}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_COH1}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M732}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_M781}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
msa236683.2{310_1169NT}	CTACAATCAG	GAGCGCGTTT	AGTTTACGCA	GTAGATGTAG	GAACAAATCA
Consensus		*****	*****	*****	*****
		351			400
msa236683.2{310_090}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_18RS21}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_2603}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_A909}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_CJB110}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_H36B}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_JM9130013}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_COH1}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M732}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_M781}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
msa236683.2{310_1169NT}	ATTAGTTTGG	AAGTTACGTC	AGGATCATCG	TGTTCTGTTCT	ATGGAACAAAT
Consensus		*****	*****	*****	*****

Table 68: Comparative Sequences relating to SAG 0499

		401			450
msa236683.2{310_090}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_18RS21}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_2603}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_A909}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_CJB110}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_H36B}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_JM9130013}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_COH1}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M732}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_M781}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
msa236683.2{310_1169NT}	ATAAATTTAG	GTATGCCCAA	AAAGAAGATT	TCAAGGAGGG	ACTGCCTGAA
Consensus	*****	*****	*****	*****	*****
		451			500
msa236683.2{310_090}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_18RS21}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_2603}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_A909}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_CJB110}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_H36B}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_JM9130013}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_COH1}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M732}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_M781}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
msa236683.2{310_1169NT}	TTTGCAATCGA	TAGATGTCTC	ATTTATCTCT	CTTAATTGGA	TTTTaCCAGC
Consensus	*****	*****	*****	*****	*****
		501			550
msa236683.2{310_090}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_18RS21}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_2603}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_A909}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_CJB110}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_H36B}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_JM9130013}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_COH1}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M732}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_M781}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
msa236683.2{310_1169NT}	TCTAAAAGAA	ATTTTAGTGG	ATGGTGGACA	AGTAGTGGCA	TTAATTAAAC
Consensus	*****	*****	*****	*****	*****
		551			600
msa236683.2{310_090}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_18RS21}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_2603}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_A909}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_CJB110}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_H36B}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_JM9130013}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_COH1}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_M732}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_M781}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
msa236683.2{310_1169NT}	CACAATTGGA	AGCAGGTCGT	GAGCAAATG	GTAAAAATGG	TATTGTCAAA
Consensus	*****	*****	*****	*****	*****
		601			650
msa236683.2{310_090}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_18RS21}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_2603}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_A909}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_CJB110}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_H36B}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_JM9130013}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_COH1}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_M732}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_M781}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
msa236683.2{310_1169NT}	GACAAGTTGG	TTCATGAAAA	GGTTTGGACA	ACAGTGACCA	ATTTACAGAA
Consensus	*****	*****	*****	*****	*****
		651			700
msa236683.2{310_090}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_18RS21}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_2603}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_A909}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_CJB110}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_H36B}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_JM9130013}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_COH1}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M732}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_M781}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG
msa236683.2{310_1169NT}	AGATTATGGA	TATACGGTTA	AACATCTTGA	TTTTTCGCCC	aTTCAAGGTG

Table 68: Comparative Sequences relating to SAG 0499

Consensus	*****	*****	*****	*****	*****	*****
	701					750
msa236683.2{310_090}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_18RS21}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_2603}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_A909}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_CJB110}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_H36B}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_JM9130013}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_COH1}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M732}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_M781}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
msa236683.2{310_1169NT}	GACATGGAAA	TATTGAGTTT	TTAATGCATT	TGCAAAAGTG	TCAAGATCCA	
Consensus	*****	*****	*****	*****	*****	*****
	751					800
msa236683.2{310_090}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_18RS21}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_2603}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_A909}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_CJB110}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_H36B}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_JM9130013}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_COH1}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M732}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_M781}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
msa236683.2{310_1169NT}	CAAAATCTTG	TGCTTGACCA	AATACAAGAT	GTTATAGAAA	AAGCACATAA	
Consensus	*****	*****	*****	*****	*****	*****
	801					825
msa236683.2{310_090}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_18RS21}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_2603}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_A909}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_CJB110}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_H36B}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_JM9130013}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_COH1}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M732}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_M781}	GGAATTTAAG	AAAAATGAAG	AAGAG			
msa236683.2{310_1169NT}	GGAATTTAAG	AAAAATGAAG	AAGAG			
Consensus	*****	*****	*****			
SEQ ID NO. 6812						
STRAIN 2603 frame: 1						
MAKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
SEQ ID NO. 6813						
STRAIN 090 frame: 1						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
SEQ ID NO. 6814						
STRAIN A909 frame: 1						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
SEQ ID NO. 6815						
STRAIN 18RS21 frame: 1						
AKERVDVLAYKQGLFDTREQAKRGVMAGMVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						
IKPQFEAGREQIGKNGIVKDKLVHEKVLTTVTNFTKDYGYTTVKHLDFSPIQGGHGNIEFL						
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEB						
SEQ ID NO. 6816						
STRAIN M732 frame: 1						
AKERVDVLAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLLK						
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK						
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL						

Table 68: Comparative Sequences relating to SAG 0499

IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6817

STRAIN COH1 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6818

STRAIN M781 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6819

STRAIN CJB110 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6820

STRAIN 1169NT frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6821

STRAIN JM9130013 frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

SEQ ID NO. 6822

STRAIN H36B frame: 1

AKERVDVLAAYKQGLFDTREQAKRGVMAGLVINVINGERYDKPGEKVADDTTELKLKGEKLG
YVSRGGLKLEKALQVFEISVADKLTIDIGASTGGFTDVMLQSGARLVYAVDVGTNQLVWK
LRQDHRVRSMEQYNFRYAQKEDFKEGLPEFASIDVSFISLNLILPALKEILVDGGQVVAL
IKPQFEAGREIQKNGIVKDKLVHEKVLTTVTNFTKDYGYTVKHLDFSPVQGGHGNIEFL
MHLQKCQDPQNLVLDQIQDVIEKAHKEFKKNEEE

PRETTY of: /biotmp/msa236800.2{*} May 14, 2003 02:58 ..

	1		50
msa236800.2{310_090}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_18RS21}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_2603}	mAKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_A909}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_CJB110}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_H36B}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_JM9130013}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGm VINVINGERY DKPGEKVADD
msa236800.2{310_COH1}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M732}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_M781}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
msa236800.2{310_1169NT}	-AKERVDVLA	YKQGLFDTRE	QAKRGVMAGl VINVINGERY DKPGEKVADD
Consensus	*****	*****	*****
	51		100
msa236800.2{310_090}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_18RS21}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_2603}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_A909}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_CJB110}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_H36B}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_JM9130013}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_COH1}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M732}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_M781}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
msa236800.2{310_1169NT}	TELKLKGEKL	KYVSRGGLKL	EKALQVFEIS VADKLTIDIG ASTGGFTDVM
Consensus	*****	*****	*****
	101		150

Table 68: Comparative Sequences relating to SAG 0499

msa236800.2{310_090}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_18RS21}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_2603}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_A909}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_CJB110}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_H36B}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_JM9130013}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_COH1}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M732}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_M781}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
msa236800.2{310_1169NT}	LQSGARLVYA	VDVGTNQLVW	KLRQDHRVRS	MEQYNFRYAQ	KEDFKKEGLPE
Consensus	*****	*****	*****	*****	*****
151					
msa236800.2{310_090}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_18RS21}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_2603}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_A909}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_CJB110}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_H36B}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_JM9130013}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_COH1}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M732}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_M781}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
msa236800.2{310_1169NT}	FASIDVSFIS	LNLILPALKE	ILVDGGQVVA	LIKPFQFAGR	EQIGKNGIVK
Consensus	*****	*****	*****	*****	*****
201					
msa236800.2{310_090}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_18RS21}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_2603}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_A909}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_CJB110}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_H36B}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_JM9130013}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_COH1}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M732}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_M781}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	vQGGHGNIEF	LMHLQKCQDP
msa236800.2{310_1169NT}	DKLVHEKVLT	TVTNTFKDYG	YTVKHLDFSP	iQGGHGNIEF	LMHLQKCQDP
Consensus	*****	*****	*****	*****	*****
251					
msa236800.2{310_090}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_18RS21}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_2603}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_A909}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_CJB110}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_H36B}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_JM9130013}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_COH1}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M732}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_M781}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
msa236800.2{310_1169NT}	QNLVLDQIQD	VIEKAHKEFK	KNEEE		
Consensus	*****	*****	*****		
275					

Table 69: Comparative Sequences relating to SAG0032

SEQ ID NO. 6901

STRAIN 2603

ATGAATAAAAAGGTACTATTGACATCGACAATGGCAGCTTCGCTATTATCAGTCGCAAGT
 GTTCAAGCACAAAGAACAGATACGACGTGGACAGCAGTACTGTTTCAGAGGTAAGGCT
 GATTGGTAAAGCAAGACAAATAAATCATCATATACTGTGAAATATGGTGATACACTAAGC
 GTTATTTTCAAGCAATGTCAATTGATATGAATGTCTTAGCAAAAATAAATAACATTGCA
 GATATCAATCTATTATCTCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCAT
 ACTGCCACTTCAATGAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGACAGCAAAAAGTTTCTCTCAATACA
 ATTTGGAAGGTATGACACCAGAAGCAGCAACACGATTGTTTCGCCAATGAAGACATAT
 TCTTCGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAGAGCAAGCTGTTAGTCAA
 GCAGCAGCTAATGAACAGGTATCACAGCTCCTGTGAAGTCGATTACTTCAGAAAGTTCCA
 GCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACCCGGTAAGAACT
 GTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCCTAAAGTAGAAACTGGTGCA
 TCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGACTACGACTTCACCAGCTACAGAC
 AGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCA
 ACACCGGTAGCACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCTGAAAATGCA
 GGGCTCCAACCTCATGTTGAGCTTATAAAGAAAAGTAGCGTCAACTTATGGAGTTAAT
 GAATTCAGTACATACCTGCGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAGTTGAC
 TTTATTTAGGTACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTTACACAAAAT
 ATGCAGCAAAATACACTTTTCAATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAAC
 AGTATTTATGGAGCTGCTAATACCTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCCTATGACCAGCTTCAGGTATCATTTAAACAAATAATATAAAAAAGGAAGCTATTG
 GCTTCTTTTATATGCTTGAATAGACTTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6902

STRAIN 090

TGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACTGCCACTT
 CAATGAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACACCAGCT
 ACTGTGGATTTGAAAACCAATCAAGTTTCTGTTGACAGCAAAAAGTTTC
 TCTCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACACAGATTG
 TTTCCGCAATGAAGACATATCTTCTGCGCCAGCTTTGAAATCAAAAGAA
 GTATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGT
 ATCAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAG
 AGGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCA
 CCAGCTTCTGTTGCCGTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GGTAAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTC
 CTAAAGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTT
 CCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAACCGACTGA
 AGTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAG
 CACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
 GGGCTCCAACCTCATGTTGAGCTTATAAAGAAAAGTAGCGTCAACTTA
 TGGAGTTAATGAATTCAGTACATACCGTGCAGGTGATCCAGGTGATCATG
 GTAAGGTTTAGCAGTCGACTTTATTGTAGGTAAAAACCAAGCACTTGGT
 AATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATACATTTT
 ATATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG
 GACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 AACCATTATGACCAGTGTTCAGGTATCATTTAAACAAATAATATAAAAAAGG
 AAGCTATTGGCTTCTTTTATATGCTTGAATAGACTTTCAAGGTTCT
 TATATAATTTTATTA

SEQ ID NO. 6903

STRAIN A909

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAA
 ATATGGTGATACACTAAGCGTTATTTTCAAGCAATGTCAATTGATATGA
 ATGCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCT
 GAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACCTGCTACTTC
 AATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTA
 CTGTCGATTTGAAAACCAATCAAGTTTCTGTTGACAGCAAAAAGTTTCT
 CTCATACAAATTTCCGAAGGTATGACACCAGAAGCAGCAACACAGATTGT
 TTCGCCAATGAAGACATATTTCTTCTGCGCCAGCTTTGAAATCAAAAGAA
 TATTAGCACAAGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTA
 TCACAGCTCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGA
 GGAAGTTAAACCACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCAC
 CAGCTTCTGTTGCCGTGAAAACACCAGCTCCAGTAGCTAAAGTAGCACC
 GTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCC
 TAAAGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTT
 CTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAA
 GTTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGC
 ACAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCA
 GGGCTCCAACCTCATGTTGAGCTTATAAAGAAAAGTAGCGTCAACTTAT
 GGAGTTAATGAATTCAGTACATACCGTGCAGGAGATCCAGGTGATCATGG
 TAAAGGTTTAGCAGTTGACTTTATTGTAGGTAATAAACCAGCACTTGGTA
 ATGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAAATACATTTTCA
 TATGTTATCTGGCAACAAAAGTTTACTCAAATACAAATAGTATTATG
 ACCTGCTAATACTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCC
 ACCCATATGACCAGTGTTCAGGTATCATTTAAACAAATAATATAAAAAAGG
 AGCTATTGGCTTCTTTTATATGCTTGAATAGACTTTCAAGGTTCTT
 ATATAATTTTATTA

SEQ ID NO. 6904

STRAIN H36B

Table 69: Comparative Sequences relating to SAG0032

CTGATTGGTAAAGCAAGACAATAAATCATCATATAcTGTGAAATA
 TGGTGATACAcTAAGCGTTATTTGAGAAGCAATGTCaATTGATATGAATG
 TCTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAG
 ACAACaCTGaCAGTAaCTTACGATCAGAAGAGTCATACTGCTACTTCAAT
 GAAAAATAGAAACACCAGCAACAATGCTGCTGGTCAAAACACAGCTACTG
 TCGATTGAAAACCAATCAAGTTTCTGTTGACAGCAAAAAGTTTCTCTC
 AATACAATTTTCGGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTC
 GCCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTAT
 TAGCACAAGGGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCA
 CCAGCTCCTGTGAAGTCGATTACTTCAAGGTTCCAGCAGCTAAAGAGGA
 AGTTAAACCAACTCAGACCTCAGTCAGTCAGTCAACAACAGTATCACCAG
 CTTCTGTTGCGCTGAAACACCAGCTCCAGTAGcTAAAGTAGCACCAGTA
 AGAATCTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTCACTCcTAA
 AGTAGAAACTGGTGATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTG
 TGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGACTGAAGTT
 AAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACA
 ACCAGCTTCAACAACAATGCGAGTAGCTGCACATCCTGAAAAATGCAAGGC
 TCCAACCTCATGTTGCGACTTATAAAGAAAAGTAGCGTCAACTTATGGA
 GTTAATGAATTCAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAA
 AGGTTTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAAATG
 AAGTTGCACAGTACTCTACACAAAATaTGGCAGCAAAATACATTTTCATAT
 GTTATCTGGCaaCAAAAAGTTTTACTCAAAATACAAATAGTATTTATGGACC
 TGCTAATACTTGGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCC
 ACTATGACCAGCTTCAGTATCATTTAACAATAATATAAAAAAGGAAGC
 TATTGGCTTCTTTTATATGCCTTGATAGACcTTCAAGGTTCTTATA
 TAATTTTATTA

SEQ ID NO. 6905

STRAIN 18RS21

CTGATTGGTAAAGCAAGACAAT
 AAATCATCATATACCTGTGAAATATGGTGATACAcTAAGCGTTATTTGAGA
 AGCAATGTCAATTGATATGAATGTCTTAGCAAAAaTAAATAACATTGCAG
 ATATCAATCTTATTTATCcTGAGACAAcCTGaCAGTAACCTTACGATCAG
 AAGAGTCATACTGCCaCTTCAATGAAATAGAAACACCAGCAaCAAAATGC
 TGCTGGTCaaACAaCAGCTACTGTGGATTGAAAACCAATCAAGTTTCTG
 TTGACAGCAAAAAGTTTCTCTCAATACAATTTTCGGAAGGTATGACACCA
 GAAGCAGCAACAACGATTGTTTTCGCCAATGAAGACaTATTCTTCTGCGCC
 AGCTTTGAAaTCAAAAGAAGTATTAGCACAAAGAGCAAGCTGTTAGTCAAG
 CAGCAGCTAATGAACAGGTATCACCAGCTCCTGTGAAGTCGATTACTTCA
 GAAGTTCCAGCAGCTAAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAG
 TCAGTCAACAACAGTATCACCAGCTTCTGTTGCGCTGAAACACCAGCTC
 CAGTAGCTAAAGTAGCACCGGTAAAGAACTGTAGCAGCCCTAGAGTGGCA
 AGTGTTAAGTAGTCACTCCTAAAGTAGAAACTGGTGATCACCAGAGCA
 TGTATCAGCTCCAGCAGTTCCTGTGACTACGACTTACCAGCTACAGACA
 GTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCT
 CCAACAGCAACACCGGTAGCACAAACAGCTTCAACAACAATGCAGTAGC
 TGCACATCCTGAAATGCAGGGCTCCAACCTCATGTTGCGAGCTTATAAAG
 AAAAAGTAGCGTCAACTTATGGAGTTAATGAATTCAATACATACCGTGGC
 GGAGATCCAGGTGATCATGGTAAAGTTTAGCAGTTGACTTTATTGTAGG
 TACTAATCAAGCACTTGGTAATAAAGTTGCACAGTACTcTACACAAAATA
 TGGCAGCAAAATAACATTTATATGTTATCTGGCAACAAAAGTTTACTCA
 AATACAAACAGTATTTATGGACCTGCTAATCTTGAATGCAATGCCAGA
 TCGTGGTGGCGTTACTGCCAACCACTATGACCAGCTTACGTATCATTTA
 ACAATAATATAAAAAAGGAAGCTATTGGCTTCTTTTATATGCCTTG
 AATAGACTTTCAAGGTTCTTATATAATTTTATTA

SEQ ID NO. 6906

STRAIN COH1

CTGATT
 GGTAAAGCAAGACAATAAATCATCATATACCTGTGAAATATGGTGATACAC
 TAAGCGTTATTTGAGAAGCAATGTCAATTGATATGAATGTCTTAGCAAAA
 ATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAACACTGAC
 AGTAACCTTAGCATCAGAAGAGTCATACTGCCACTTCAATGAAATAGAAA
 CACCAGCAACAATGCTGCTGGTCAAAACAACAGcTACTGTGATTGAAA
 ACCAATCAAGTTTTTGTGACAGCAAAAAGTTTCTCTCAATACAATTC
 GGAAGGTATGACACCAGaaGCAGCAACAACGATTGTTTTCGCCAATGAAGA
 CaTATTCTTCTGCGCCAGCTTTGAAATCAAAAGAAGTATTAGCACAAAGAG
 CAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAGCTCCTGT
 GAAGTCGATTACTTCAAGGTTCCAGCAGCTAAAGAGGAAGTTAAACCA
 CTCAGACGTCAGTCAGTCAGTTAACAACAGTATCACCAGCTTCTGTTGCC
 GCTGAAAACACCAGCTCCAGTAGCTAAGTAGCACCGGTAAAGAACTGTAGC
 AGCCCCTAGAGTGGCAAGTGcTAAAGTAGTCACTCcTAAAGTAGAACTG
 GTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCCTGTGACTACGACT
 TCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGAGCGTTCC
 GGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACAGCTTCAA
 CAACAATGCAGTAGCTGCACATCCTGAAATGCAGGGCTCCAACCTCAT
 GTTGACGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAATGAATT
 CAGTACATACCGTGGGGAGATCCAGGTGATCATGGTAAAGGTTTAGCAG
 TTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGTTGCACAG
 TaCTCTACACAAAATATGGCAGCAAAATAACATTTATATGTTATCTGGCA
 ACAAAAGTTTTATTCAAATACAAATAGTATTTATGGACCTGCTAATACTT
 GGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATGACCAC
 GTTCAGTATCATTTAACAATAATATAAAAAAGGAAGCTATTGGCTTCTT

Table 69: Comparative Sequences relating to SAG0032

TTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAATTTTTATT
A

SEQ ID NO. 6907

STRAIN M732

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACAnTAAGCGTTATTTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACCTTACGATCAGAAGAGTCATCTGCCACTTCAATGAAA
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAAGAA
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
TACGACTTCACCAGCTACAGACAGTAAGTTACAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTAttgtaggtaaaaaaccAAGCACTTGGTAATGAAGT
TGCACAGTACTcTACACAAAATATGGCAGCAAAATAACATTTTATATGTTA
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATATGGACCTGCT
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTTACGTATCATTTAAACAAATAATATAAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6908

STRAIN M781

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGT
GATACACTAAGCGTTATTTTTCAGAAGCAATGTCAATTGATATGAATGTCTT
AGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTGAGACAA
CACTGACAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCAATGAAA
ATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTACTGTcGA
TTTGAAAACCAATCAAGTTTGTGTTGCAGACCAAAAAGTTTCTCTCAATA
CAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTTTCGCCA
ATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGTATTAGC
ACAAGAGCAAGCTGTTAGTCAAGTAGCAGCTAATGAACAGGTATCACCAG
CTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAGGAAGTT
AAACCACTCAGACGTCAGTCAGTCAGTTAAACAACAGTATCACCAGCTTC
TGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGGTAAAGAA
CTGTAGCAGCCCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCCTAAAGTA
GAAACTGGTGGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCTGTGAC
TACGACTTCACCAGCTACAGACAGTaaGTTACAAAGCGACTGAAGTTAAGA
GCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCACAAACCA
GCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGGGCTCCA
ACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTA
ATGAATTCAAGTACATACCGTGCGGGAGATCCAGGTGATCATGGTAAAGGT
TTAGCAGTTGACTTTATTGTAGGTAAAAACCAAGCACTTGGTAATGAAGT
TGCACAGTACTCTACACAAAATATGGCAGCAAAATAACATTTTATATGTTA
TCTGGCAACAAAAGTTTATTCAAATACAAATAGTATTATATGGACCTGCT
AATACCTTGAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTA
TGACCACGTTTACGTATCATTTAAACAAATAATATAAAAAAGGAAGCTATT
TGGCTTCTTTTTTATATGCCTTGAATAGACTTTTCAAGGTTCTTATATAAT
TTTTATTA

SEQ ID NO. 6909

STRAIN CJB110

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACTGTGAAA
TATGGTGATACACTAAGCGTTATTTTTCAGAAGCAATGTCAATTGATATGAA
TGCTTTAGCAAAAATTAATAACATTGCAGATATCAATCTTATTTATCCTG
AGACAACACTGCAGTAACCTTACGATCAGAAGAGTCATACTGCCACTTCA
ATGAAAATAGAAAACACCAGCAACAAATGCTGCTGGTCAAACAACAGCTAC
TGTTGGATTTGAAAACCAATCAAGTTTcTGTTGCAGACCAAAAAGTTTCTC
TCAATACAATTTCCGAAGGTATGACACCAGAAGCAGCAACAACGATTGTT
TCGCCAATGAAGACATATTTCTTCTGCCCGAGCTTTGAAATCAAAGAAGT
ATTAGCACAAGAGCAAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTAT
CAACAGCTCCTGTGAAGTCGATTACTTCAGAAGTTCCAGCAGCTAAAGAG
GAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACAACAGTATCACC
AGCTTCTGTTGCCGCTGAAACACCAGCTCCAGTAGCTAAAGTAGCACCGG
TAAGAACTGTAGCAGCCCCCTAGAGTGGCAAGTGTTAAAGTAGTCACTCCT
AAAGTAGAAAACCTGGTGCATCACCAGAGCATGTATCAGCTCCAGCAGTTCC
TGTGACTACGACTTCAACAGcTACAGACAGTaAGTTaCAAGCGACTGAAG
TTAAGAGCGTTCCGGTAGCACAAAAGCTCCAACAGCAACACCGGTAGCA
CAACAGCTTCAACAACAAATGCAGTAGCTGCACATCCTGAAAATGCAGG
GCTCCAACCTCATGTTGCAGCTTATAAAGAAAAAGTAGCGTCAACTTATG
GAGTTAATGAATTCAAGTACATaCCGTGCAGGTGATCCAgGTGATCATGGT
AAAGGTTTAGCAGTcGACTTTATTGTAGTAAAAACCAAGCACTTGGTAA

Table 69: Comparative Sequences relating to SAG0032

TGAAGTTGCACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCAT
 ATGTTTATCTGGCAACAAAAGTTTCTACTCAAATACAAATAGTATTTATGGA
 CCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAA
 CCATTATGACCATGTTTACGATATCATTTTAAACAAATAATATAAAAAAGGAA
 GCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCTTA
 TATAATTTTTATTA

SEQ ID NO. 6910

STRAIN 1169NT

CTGATTTG

GTAAAGCAAGACAATAAATCATCATATACTGTGAAATATGGTGATACACT
 AAGCGTTATTTTTCAGAACCAATGTCAATTGATATGAATGTCTTAGCAAAAA
 TTAATAACATTGTCAGATATCAATCTTATTATCCTGAGACCAACTGACA
 GTAACCTTACGATCAGAGAGTCATCTGCCACTTCAATGAAAAATAGAAAC
 ACCAGCAACAAATGCTGCTGGTCAAACACAGCTACTGTGGATTTGAAAA
 CCAATCAAGTTTCTGTGTCAGACCAAAAAGTTTCTCTCAATCAATTTTCG
 GAAGGTATGACACCAAGAGCAGCAACAACGATTGTTTCGCCAATGAAGAC
 ATATTTCTTCTGCGCCAGCTTTGAAATCAAAGAGTATTAGCACAAGAGC
 AAGCTGTTAGTCAAGCAGCAGCTAATGAACAGGTATCACCAGCTCCTGTG
 AAGTCGATTACTTCAAGAGTTCCAGCAGCTAAAGAGGAAGTTAGACCAAC
 TcAGACGTCAGTCAGTCAGTCAACACAGTATCACCAGCTTCTGTGCGCG
 CTGAAACACCCAGCTCCAGTAGCTAAAGTAGCACCGGTAAGAACTGTAGCA
 GCCCCAGCCCTAGAGTGGCAAGTGCTAAAGTAGTCACTCTTAAAGTAGA
 AACTGGTGATCACCAGAGCATGTACCAGCTCCAGCAGTTCTGTGACTA
 CGACTTCAACAGCTACAGACAAAGTTTCAAGCGACTGAAGTTAAAGAGC
 GTCCGGTGGCAAAAAGCTTCAACAGCAACACCGGTAGCAACACAGC
 TTCAACAAACAAATGTCAGTAGCTGCACATCTGAAATGCAGGACTCAAC
 CTCATGTTGTCAGCTTATAAAGAAAAAGTAGCGTCAACTTATGGAGTTAAT
 GAATTCAGTACATAACCGTGGCGGAGATCCAGGTGATCATGGTAAAGGTTT
 AGCAGTTGACTTTATTGTAGTAAACCAAGCACTTGGTAATGAAGTTG
 CACAGTACTCTACACAAAATATGGCAGCAAATAACATTTTCATATGTTATC
 TGGCAACAAAAGTTTCTCAATACAAATAGTATTTATGGACCTGCTAA
 TACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTACTGCCAACCACTATG
 ACCAGGTTACGATCATTTTAAACAAATAATATAAAAAAGGAAGCTATTTG
 GCTTCTTTTATATGCCTTGAATAGACTTCAAGGTTCTTATATAATTT
 TTATTA

SEQ ID NO. 6911

STRAIN JM9130013

CTGATTTGGTAAAGCAAGACAATAAATCATCATATACT

GTGAAATATGGTGATACACTAAGCGTTATTTTCAGAAAGCAATGTCAATTGA
 TATGAATGTCTTAGCAAAAAATAAATCAATTCAGATATCAATCTTATTT
 ATCCTGAGACAACACTGACAGTAACCTACGATCAGAAGAGTCATACCTGCC
 ACTTCAATGAAAAATAGAAACACCAGCAACAAATGCTGCTGGTCAAACAC
 AGCTACTGTGGATTTGAAAAACCAATCAAGTTTCTGTTGTCAGACCAAAAAG
 TTTCTCTCAATCAATTTGGAAGGTATGACACCAGAAGCAGCAACCAACG
 ATTGTTTCCGCAATGAAGACATATTCTTCTGCGCCAGCTTTGAAATCAA
 AGAAGTATTAGCACAAAGCAAGCTGTAGTCAAGCAGCAGCTAATGAAC
 AGGTATCACCAGCTCCTGTGAAGTCGATTACTTCAAGAGTTCCAGCAGCT
 AAAGAGGAAGTTAAACCAACTCAGACGTCAGTCAGTCAGTCAACACAGT
 ATCACCAGCTTCTGTTGCGGCTGAAACACCAGCTCCAGTAGCTAAAGTAG
 CACCGGTAAGAACTGTAGCAGCCCTAGAGTGGCAAGTGTAAAGTAGTC
 ACTCTAAAGTAGAACTGGTGCATCACCAGAGCATGTATCAGCTCCAGC
 AGTTCTGTGACTACGACTTCAACAGCTACAGACAGTAAGTTACAAGCGA
 CTGAAGTTAAGAGCGTTCCGGTAGCACAAAAGCTTCAACAGCAACACCG
 GTAGCAACACAGCTTCAACAAATGCAGTAGCTGCACATCTGAAAA
 TGCAGGCTCCAACCTCATGTTGTCAGCTTATAAAGAAAAAGTAGCGTCAA
 CTTATGGAGTTAATGAATTCAGTACATACCGTGGCGGAGATCCAGGTGAT
 CATGGTAAAGGTTAGCAGTTGACTTTATTGTAGGTACTAATCAAGCACT
 TGGTAATAAAGTTGACAGTACTCTACACAAAATATGGCAGCAAATAACA
 TTTCTATATGTTATCTGGCAACAAAAGTTTCTCAATACAAACAGTATT
 TATGGACCTGCTAATACTTGGAAATGCAATGCCAGATCGTGGTGGCGTTAC
 TGCCAACCACTATGACCAGCTTACGATCATTTAAACAAATAATATAAAA
 AAGGAAGCTATTTGGCTTCTTTTATATGCCTTGAATAGACTTCAAGG
 TTCTTATATAATTTTTATTA

PRETTY of: /biotmp/msa167919.2{*} March 11, 2003 08:55 ..

	1	50
msa167919.2{322_COH1}	-----	-----
msa167919.2{322_M781}	-----	-----
msa167919.2{322_M732}	-----	-----
msa167919.2{322_18RS21}	-----	-----
msa167919.2{322_2603}	atgaataaaa aggtactatt gacatcgaca atggcagctt cgctattatc	
msa167919.2{322_JM9130013}	-----	-----
msa167919.2{322_090}	-----	-----
msa167919.2{322_CJB110}	-----	-----
msa167919.2{322_A909}	-----	-----
msa167919.2{322_H36B}	-----	-----
msa167919.2{322_1169NT}	-----	-----
Consensus	*****	*****

51

100

Table 69: Comparative Sequences relating to SAG0032

msa167919.2{322_COH1}	-----	-----	-----	-----	-----
msa167919.2{322_M781}	-----	-----	-----	-----	-----
msa167919.2{322_M732}	-----	-----	-----	-----	-----
msa167919.2{322_18RS21}	-----	-----	-----	-----	-----
msa167919.2{322_2603}	agtcgcaagt	gttcaagcac	aagaaacaga	tacgacgtgg	acagcacgta
msa167919.2{322_JM9130013}	-----	-----	-----	-----	-----
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----	-----	-----	-----
msa167919.2{322_A909}	-----	-----	-----	-----	-----
msa167919.2{322_H36B}	-----	-----	-----	-----	-----
msa167919.2{322_1169NT}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
101					
msa167919.2{322_COH1}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_M781}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_M732}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_18RS21}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_2603}	ctgtttcaga	ggtaaaggct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_JM9130013}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_A909}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_H36B}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
msa167919.2{322_1169NT}	-----	-----ct	gatttggtaa	agcaagacaa	taaatcatca
Consensus	*****	*****-	-----	-----	-----
151					
msa167919.2{322_COH1}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M781}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_M732}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_18RS21}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_2603}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_JM9130013}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_A909}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_H36B}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
msa167919.2{322_1169NT}	tatactgtga	aatatgggtga	tacactaagc	gttatttcag	aagcaatgtc
Consensus	-----	-----	-----	-----	-----
201					
msa167919.2{322_COH1}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M781}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_M732}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_18RS21}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_2603}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_JM9130013}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_090}	-----	-----	-----	-----	-----
msa167919.2{322_CJB110}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_A909}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_H36B}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
msa167919.2{322_1169NT}	aattgatatg	aatgtcttag	caaaaattaa	taacattgca	gatatcaatc
Consensus	-----	-----	-----	-----	-----
251					
msa167919.2{322_COH1}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M781}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_M732}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_18RS21}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_2603}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_JM9130013}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_090}	-----	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_CJB110}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_A909}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_H36B}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
msa167919.2{322_1169NT}	ttattttatcc	TGAGACAACA	CTGACAGTAA	CTTACGATCA	GAAGAGTCAT
Consensus	-----	*****	*****	*****	*****
301					
msa167919.2{322_COH1}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M781}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M732}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_18RS21}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_090}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_CJB110}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_A909}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_H36B}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_1169NT}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
Consensus	*****	*****	*****	*****	*****
350					
msa167919.2{322_COH1}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M781}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_M732}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_18RS21}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_2603}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_JM9130013}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_090}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_CJB110}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_A909}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_H36B}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
msa167919.2{322_1169NT}	ACTGCCACTT	CAATGAAAAT	AGAAACACCA	GCAACAAATG	CTGCTGGTCA
Consensus	*****	*****	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

	351		400
msa167919.2{322_COH1}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M781}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_M732}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTtT GTTGCAGACC
msa167919.2{322_18RS21}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_2603}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_JM9130013}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_090}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_CJB110}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_A909}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_H36B}	AACaACAGCT	ACTGTcGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
msa167919.2{322_1169NT}	AACaACAGCT	ACTGTgGATT	TGAAAACCAA TCAAGTTTcT GTTGCAGACC
Consensus	*****	*****	*****
	401		450
msa167919.2{322_COH1}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M781}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_M732}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_18RS21}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_2603}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_JM9130013}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_090}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_CJB110}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_A909}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_H36B}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
msa167919.2{322_1169NT}	AAAAAGTTTC	TCTCAATACA	ATTTTCGGAAG GTATGACACC AGAAGCAGCA
Consensus	*****	*****	*****
	451		500
msa167919.2{322_COH1}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M781}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_M732}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_18RS21}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_2603}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_JM9130013}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_090}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_CJB110}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_A909}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_H36B}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
msa167919.2{322_1169NT}	ACAACGATTG	TTTCGCCAAT	GAAGACATAT TCTTCTGCGC CAGCTTTGAA
Consensus	*****	*****	*****
	501		550
msa167919.2{322_COH1}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_M781}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_M732}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GtAGCAGCTA
msa167919.2{322_18RS21}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_2603}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_JM9130013}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_090}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_CJB110}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_A909}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_H36B}	ATCAAAAGAA	GTATTAGCAC	AAGgGCAAGC TGTTAGTCAA GcAGCAGCTA
msa167919.2{322_1169NT}	ATCAAAAGAA	GTATTAGCAC	AAGaGCAAGC TGTTAGTCAA GcAGCAGCTA
Consensus	*****	*****	*****
	551		600
msa167919.2{322_COH1}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M781}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_M732}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_18RS21}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_2603}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_JM9130013}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_090}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_CJB110}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_A909}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_H36B}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
msa167919.2{322_1169NT}	ATGAACAGGT	ATCAcCAGCT	CCTGTGAAGT CGATTACTTC AGAAGTTCCA
Consensus	*****	*****	*****
	601		650
msa167919.2{322_COH1}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTtAAC
msa167919.2{322_M781}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTtAAC
msa167919.2{322_M732}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTtAAC
msa167919.2{322_18RS21}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_2603}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_JM9130013}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_090}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_CJB110}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_A909}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_H36B}	GCAGCTAAAG	AGGAAGTTAa	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
msa167919.2{322_1169NT}	GCAGCTAAAG	AGGAAGTTAg	ACCAACTCAG ACCTCAGTCA GTCAGTcAAC
Consensus	*****	*****	*****

Table 69: Comparative Sequences relating to SAG0032

		651			700
msa167919.2{322_COH1}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M781}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_M732}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_18RS21}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_2603}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_JM9130013}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_090}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_CJB110}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_A909}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_H36B}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
msa167919.2{322_1169NT}	AACAGTATCA	CCAGCTTCTG	TTGCCGCTGA	AACACCAGCT	CCAGTAGCTA
Consensus		*****	*****	*****	*****
		701			750
msa167919.2{322_COH1}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M781}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_M732}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_18RS21}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_2603}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_JM9130013}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_090}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_CJB110}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_A909}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_H36B}	AAGTAGCACC	GGTAAGAACT	GTAG.....	CAGCCCCTAG	AGTGGCAAGT
msa167919.2{322_1169NT}	AAGTAGCACC	GGTAAGAACT	GTAGcagccc	CAGCCCCTAG	AGTGGCAAGT
Consensus		*****	*****	*****	*****
		751			800
msa167919.2{322_COH1}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M781}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_M732}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_18RS21}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_2603}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_JM9130013}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_090}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_CJB110}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_A909}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_H36B}	GtTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
msa167919.2{322_1169NT}	GcTAAAGTAG	TCACCTCCTAA	AGTAGAAACT	GGTGCATCAC	CAGAGCATGT
Consensus		*..*****	*****	*****	*****
		801			850
msa167919.2{322_COH1}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M781}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_M732}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_18RS21}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_2603}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_JM9130013}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_090}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_CJB110}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_A909}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_H36B}	AtCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACAgTA
msa167919.2{322_1169NT}	AcCAGCTCCA	GCAGTTCCCTG	TGACTACGAC	TTCAcCAGCT	ACAGACaTA
Consensus		*..*****	*****	*****	*****
		851			900
msa167919.2{322_COH1}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M781}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_M732}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_18RS21}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_2603}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_JM9130013}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_090}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_CJB110}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_A909}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_H36B}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTaGCACA	AAAAGCTCCA
msa167919.2{322_1169NT}	AGTTACAAGC	GACTGAAGTT	AAGAGCGTTC	CGGTgGCACA	AAAAGCTCCA
Consensus		*****	*****	*****	*****
		901			950
msa167919.2{322_COH1}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M781}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_M732}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_18RS21}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_2603}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_JM9130013}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_090}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_CJB110}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_A909}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_H36B}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC
msa167919.2{322_1169NT}	ACAGCAACAC	CGGTAGCACA	ACCAGCTTCA	ACAACAAATG	CAGTAGCTGC

Table 69: Comparative Sequences relating to SAG0032

Consensus	*****	*****	*****	*****	*****
	951				1000
msa167919.2{322_COH1}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M781}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_M732}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_18RS21}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_2603}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_JM9130013}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_090}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_CJB110}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_A909}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_H36B}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
msa167919.2{322_1169NT}	ACATCCTGAA	AATGCAGGgC	TCCAACCTCA	TGTTGCAGCT	TATAAAGAAA
Consensus	*****	*****-*	*****	*****	*****
	1001				1050
msa167919.2{322_COH1}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_M781}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_M732}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_18RS21}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_2603}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_JM9130013}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_090}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgt
msa167919.2{322_CJB110}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGgt
msa167919.2{322_A909}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_H36B}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
msa167919.2{322_1169NT}	AAGTAGCGTC	AACCTTATGGA	GTTAATGAAT	TCAGTACATA	CCGTGCgGga
Consensus	*****	*****	*****	*****	*****-*
	1051				1100
msa167919.2{322_COH1}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M781}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_M732}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_18RS21}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_2603}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_JM9130013}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_090}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_CJB110}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_A909}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_H36B}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
msa167919.2{322_1169NT}	GATCCAGGTG	ATCATGGTAA	AGGTTTAGCA	GTtGACTTTA	TTGTAGGTAA
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa167919.2{322_COH1}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M781}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_M732}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_18RS21}	tAaCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_2603}	tAaCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_JM9130013}	tAaCAAGCA	CTTGGTAATa	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_090}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_CJB110}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_A909}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_H36B}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
msa167919.2{322_1169NT}	aAaCAAGCA	CTTGGTAATg	AAGTTGCACA	GTACTCTACA	CAAAATATGG
Consensus	-*-*****	*****	*****	*****	*****
	1151				1200
msa167919.2{322_COH1}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M781}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_M732}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_18RS21}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_2603}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_JM9130013}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_090}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_CJB110}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_A909}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_H36B}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
msa167919.2{322_1169NT}	CAGCAAATAA	CATTTTCATAT	GTTATCTGGC	AACAAAAGTT	TTAcTCAAAT
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa167919.2{322_COH1}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M781}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_M732}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_18RS21}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_2603}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_JM9130013}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_090}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_CJB110}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_A909}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
msa167919.2{322_H36B}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG

Table 69: Comparative Sequences relating to SAG0032

msal67919.2{322_1169NT}	ACAAATAGTA	TTTATGGACC	TGCTAATACT	TGGAATGCAA	TGCCAGATCG
Consensus	*****	*****	*****	*****	*****
	1251				1300
msal67919.2{322_COH1}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M781}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_M732}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_18RS21}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_2603}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_JM9130013}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_090}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_CJB110}	TGGTGGCGTT	ACTGCCAACC	AtTATGACCA	tGTTcACGTA	TCATTTAACA
msal67919.2{322_A909}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_H36B}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
msal67919.2{322_1169NT}	TGGTGGCGTT	ACTGCCAACC	AcTATGACCA	cGTTcACGTA	TCATTTAACA
Consensus	*****	*****	*-*****	-*****	*****
	1301				1350
msal67919.2{322_COH1}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_M781}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_M732}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_18RS21}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_2603}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_JM9130013}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_090}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_CJB110}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_A909}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_H36B}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
msal67919.2{322_1169NT}	AATAATATAA	AAAAGGAAGC	TATTTGGCTT	CTTTTTTATA	TGCCTTGaAT
Consensus	*****	*****	*****	*****	*****_**
	1351				1382
msal67919.2{322_COH1}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_M781}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_M732}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_18RS21}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_2603}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_JM9130013}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_090}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_CJB110}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_A909}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_H36B}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
msal67919.2{322_1169NT}	AGACTTTCAA	GGTTCCTATA	TAATTTTAT	TA	
Consensus	*****	*****	*****	**	
SEQ ID NO. 6912					
STRAIN 2603 frame: 1					
MNKKVLLTSTMAASLLSVASVQAQETDITWTARTVSEVKADLVKQDNKSSYTVKYGDTLS					
VISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSHATSMKIEPATNAAGQTTA					
TVDLKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTYSSAPALKSKEVLQAQVQAVS					
AAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVSPASVAAETPAPVAKVAPVRT					
VAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSPATDSKLQATEVKSVPVQAQKAPTA					
TPVQAQPASTTNAVAHHPENAGLQPHVAAYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVD					
FIVGTNQALGNKVAQYSTQNMAANNISYVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTA					
NHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY					
SEQ ID NO. 6913					
STRAIN 090 frame: 2					
ETTLTVTYDQKSHATSMKIEPATNAAGQTPATVLDKTNQVSVADQKVSNTISEGMTPE					
EAATTIVSPMKTYSSAPALKSKEVLQAQVQAVSQAANEQVSTAPVKSITSEVPAAKEEVK					
PTQTSVSQSTTVSPASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVS					
PAVPVTTTSTATDSKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENAGLQPHVA					
AYKEKVASTYGVNEFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNIS					
YVIWQQKFYSNTNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYAL					
NRLSRFLYNFY					
SEQ ID NO. 6914					
STRAIN A909 frame: 3					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVLDKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENARLQPHVAAYKEKVASTYGVN					
EFSTYRAGDPGDHGKGLAVDFIVGKNQALGNEVAQYSTQNMAANNISYVIWQQKFYSNTN					
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALHRLSRFLYNFY					
SEQ ID NO. 6915					
STRAIN H36B frame: 3					
DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH					
TATSMKIEPATNAAGQTTATVLDKTNQVSVADQKVSNTISEGMTPEAATTIVSPMKTY					
SSAPALKSKEVLQAQVQAVSQAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS					
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVTPKVETGASPEHVSAPAVPVTTTSTATD					
SKLQATEVKSVPVQAQKAPTATPVAQPASTTNAVAHHPENARLQPHVAAYKEKVASTYGVN					

Table 69: Comparative Sequences relating to SAG0032

EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6916

STRAIN 18RS21 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6917

STRAIN M732 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6918

STRAIN COH1 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6919

STRAIN M781 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6920

STRAIN CJB110 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSTAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSTATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6921

STRAIN 1169NT frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASAKVVT PKVETGASPEHVPAPAVPVTTTSTA
TDNKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
VNEFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSN
TNSIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

SEQ ID NO. 6922

STRAIN JM9130013 frame: 3

DLVKQDNKSSYTVKYGDTLSVISEAMSIDMNVLAKINNIADINLIYPETTLTVTYDQKSH
TATSMKIETPATNAAGQTTATVDLKTINQVSVADQKVSINTISEGMTPEAATTIVSPMKTY
SSAPALKSKEVLAEQAVSQAAANEQVSPAPVKSITSEVPAAKEEVKPTQTSVSQSTTVS
PASVAAETPAPVAKVAPVRTVAAPRVASVKVVT PKVETGASPEHVSAPAVPVTTTSPATD
SKLQATEVKSVPVAQKAPTATPVAQPASTTNAAHPENAGLQPHVAAYKEKVASTYGVN
EFSTYRAGDPGDHKGGLAVDFIVGKNQALGNEVAQYSTQNMANNISYVIWQKQFYSNTN
SIYGPANTWNAMPDRGGVTANHYDHVHVSFNK.YKKGSYLASFLYALNRLSRFLYNFY

PRETTY of: /biotmp/msa237049.2{*} May 14, 2003 03:04 ..

	1	50
msa237049.2{322_COH1}	-----	dlvkqdnkss
msa237049.2{322_M781}	-----	dlvkqdnkss
msa237049.2{322_M732}	-----	dlvkqdnkss
msa237049.2{322_A909}	-----	dlvkqdnkss
msa237049.2{322_H36B}	-----	dlvkqdnkss
msa237049.2{322_090}	-----	-----

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_CJB110}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_18RS21}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_2603}	mnkvvlltst	maasllsvas	vqagetdtw	tartvsevka	dlvkqdnkss
msa237049.2{322_JM9130013}	-----	-----	-----	-----	dlvkqdnkss
msa237049.2{322_1169NT}	-----	-----	-----	-----	dlvkqdnkss
Consensus	*****	*****	*****	*****	-----
51 100					
msa237049.2{322_COH1}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M781}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_M732}	ytvkygdtxs	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_A909}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_H36B}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_090}	-----	-----	-----	-----ETT	LTVTYDQKSH
msa237049.2{322_CJB110}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_18RS21}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_2603}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_JM9130013}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
msa237049.2{322_1169NT}	ytvkygdtls	viseamsidm	nvlakinnia	dinliypETT	LTVTYDQKSH
Consensus	-----	-----	-----	-----***	*****
101 150					
msa237049.2{322_COH1}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_M781}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_M732}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_A909}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_H36B}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_090}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_CJB110}	TATSMKIETP	ATNAAGQTpA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_18RS21}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_2603}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_JM9130013}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
msa237049.2{322_1169NT}	TATSMKIETP	ATNAAGQTtA	TVDLKTNQVf	VADQKVS LNT	ISEGMTPEAA
Consensus	*****	*****	*****	*****	*****
151 200					
msa237049.2{322_COH1}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_M781}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_M732}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	VAANEQVSpA	PVKSIITSEVP
msa237049.2{322_A909}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_H36B}	TTIVSPMKTY	SSAPALKSKE	VLAQgQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_090}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_CJB110}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVStA	PVKSIITSEVP
msa237049.2{322_18RS21}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_2603}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_JM9130013}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
msa237049.2{322_1169NT}	TTIVSPMKTY	SSAPALKSKE	VLAQeQAVSQ	AAANEQVSpA	PVKSIITSEVP
Consensus	*****	*****	*****	*****	*****
201 250					
msa237049.2{322_COH1}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M781}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_M732}	AAKEEVkPTQ	TSVSQlTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_A909}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_H36B}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_090}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_CJB110}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_18RS21}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_2603}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_JM9130013}	AAKEEVkPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VA..APRVAS
msa237049.2{322_1169NT}	AAKEEVrPTQ	TSVSQsTTVS	PASVAAETPA	PVAKVAPVRT	VaapAPRVAS
Consensus	*****	*****	*****	*****	*****
251 300					
msa237049.2{322_COH1}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_M781}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_M732}	aKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_A909}	vKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_H36B}	vKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_090}	vKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_CJB110}	vKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_18RS21}	vKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_2603}	vKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_JM9130013}	vKVVTpKVET	GASPEHVsAP	AVPVTTTSpA	TdSKLQATEV	KSVpVAQKAP
msa237049.2{322_1169NT}	aKVVTpKVET	GASPEHVsAP	AVPVTTTStA	TdSKLQATEV	KSVpVAQKAP
Consensus	*****	*****	*****	*****	*****
301 350					
msa237049.2{322_COH1}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M781}	TATpVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_M732}	TAsPVAQPAS	TTNAVAHPE	NagLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_A909}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_H36B}	TATpVAQPAS	TTNAVAHPE	NarLQPHVAA	YKEKVASTYG	VNEFSTYRAG

Table 69: Comparative Sequences relating to SAG0032

msa237049.2{322_090}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_CJB110}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_18RS21}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_2603}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_JM9130013}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
msa237049.2{322_1169NT}	TatPVAQPAS	TTNAVAAHPE	NAGLQPHVAA	YKEKVASTYG	VNEFSTYRAG
Consensus	***-*****	*****	***-*****	*****	*****
351 400					
msa237049.2{322_COH1}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M781}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_M732}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_A909}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_H36B}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_090}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_CJB110}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_18RS21}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_2603}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_JM9130013}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
msa237049.2{322_1169NT}	DPGDHGKGLA	VDFIVGkNQA	LGNeVAQYST	QNMAANNISY	VIWQQKFYSN
Consensus	*****	*****-***	***-*****	*****	*****
401 450					
msa237049.2{322_COH1}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M781}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_M732}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_A909}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_H36B}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALh
msa237049.2{322_090}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_CJB110}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_18RS21}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_2603}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_JM9130013}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
msa237049.2{322_1169NT}	TNSIYGpANT	WNAMPDRGGV	TANHYDHVHV	SFNK.YKKGS	YLASFLYALn
Consensus	*****	*****	*****	*****	*****
451 460					
msa237049.2{322_COH1}	RLSRFLYNFY				
msa237049.2{322_M781}	RLSRFLYNFY				
msa237049.2{322_M732}	RLSRFLYNFY				
msa237049.2{322_A909}	RLSRFLYNFY				
msa237049.2{322_H36B}	RLSRFLYNFY				
msa237049.2{322_090}	RLSRFLYNFY				
msa237049.2{322_CJB110}	RLSRFLYNFY				
msa237049.2{322_18RS21}	RLSRFLYNFY				
msa237049.2{322_2603}	RLSRFLYNFY				
msa237049.2{322_JM9130013}	RLSRFLYNFY				
msa237049.2{322_1169NT}	RLSRFLYNFY				
Consensus	*****				

Table 70: Comparative Sequences relating to SAG 1280

SEQ ID. NO. 7001

STRAIN 2603

ATGGGAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGAGCCACTATTCTC
 GTGATAGAGCCTTGCTTGAGGCATTTTATATATACCAAGCAGAGCATTTTGATGAGGAGT
 GGGATAGTCTTATTATCAGTCTTATGACCAATAGGCAAGAAATAAATAGTCTGTTCAAG
 TACTTCACTTTGAGACAGATGTTTCAGCTTTTGTCCAGGCTAGTCTTATGATAGTCTC
 ATGATCTATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAACTAGATAAAC
 TATCGCCGTCTGAAAAAACTTGGTGTAGAAAGTGGCCTTGTTCAATCTGGCCACTCGTT
 TCAATTATTGGATTCCAATGGACACTACCAAAACCATATCGCCGGATTCACTCTTACAAA
 AGAGTAGGGGAGCTAATTTGGTCAATGTGTATCGTGTGGCTAATAATTAGCGGATCGTA
 TTAGTCCAGATATTGAACAGTTTCTTAACTTACGAGCCTGAGCTTGAAACTAGAGCTG
 ATGAAACTGTTCTAGAAAAATGAAGAACTGTTGATGAGCACAAAACAGTGTTCATCAAG
 CAATATCTTTTCGAGAAGAGGGCTCTCTGGTTATTGTCTAGTTTGGATGTAGATTGTCTC
 AACTAGATGTTCAAAATAGGAAAAACAGTCACTGCCAGCTTATGAAGAGTTATCCTTAC
 GACGTAATTTGAGATTCTAACATATTTTGACCAATTCGAAATGAACGTTCCAAAGTCC
 CAAGTTTGTAGCAGGATGATTTTGACACAGAGATGGAAATGACACAGTCTTTGATGGCG
 AGGAATTTACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAACTGAC
 CTACAGTCGAAGAAAGGAATTAGAAAAAATTTGGACAAGCCATTAGGATAGAAAAATCAAG
 AAAAATTTGACTCAGCTAGGGAATTGATTTATCTCAGTTTGACCCAGACCGAGTGGTATT
 TATTGGATGACAGGTCGTTTTCGTTTAAAAAATGCAGACCTTGTCTTACTAGGTGGTT
 ATCCCAAGGCTCGGTAACTCACTAGCCCTTGCAGACAGAACTACTCCAAATGGGACTAA
 GTCATGAAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATTGAAGAGCTGCGACAAG
 TTGCCTACGCTTTTATACCAAGAACTCAGCAGAGAAGATGCGGAGCAATTGAAAAAG
 ATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTGGAAGCAAGCTAGAGAAAGCTG
 AGGGAAGAGAGTAGATTGATGAAGAAATTCGCGGAAATCCACTGGTTGAGAGATATTGG
 ACATTTATCTCTCGGGGTCACTGGTTTCTTATAAGGGACAGGACTTTGAGGTCACTGCG
 TCAGCGATGCTCGAATTGAACGGTTTGATTGCGATTGAGTTAGTCAATGACTTTTCGGATA
 TCATTGAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGAGTCACTCAGGCACTTC
 ATCAGCCAAAGGCAGAACCAAAAACAGAGTTAGAAGAAGCGGACCAAGAAATTAACCTAT
 TCTCATTTCTGGAAGAGGAGCCAGTTGAGAGTATTGGACTATTGGAACAGATGATTGAG
 AAAATGGTCATAACCATATGATCTTGAAGAAAACAGATAATCAAATTCCTGAAGAGGAAG
 TCGTCGAAACAAATTCAGAGATTCCAGTAACGGACTTTTATTTCCAGAAGATTGACGG
 ACTTTTATCTTAAGACTGCTAGAGATAAGGTTGAGACAAAATTTGTGGCACTCGTTTGG
 TAAAAAATCTAGAAAGTAGAGCACCGCAATGCTTACCAAGTGAACAGAACTCCTTGCCA
 AGTATGTAGGCTGGGTGGACTAGCCCAATGAATTTTGGATGACTATAATCCAAATTTT
 CTAAGGAACGAGAAGAACTGAAGAGCCTAGTCACAGATAAAGAGTATTCGGATATGAAAC
 AGTCTCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTCAGATGTGGGATAAGT
 TGGAAAGAGATGGCTTTACAGGTGGCAAAATCCTAGATCCTTCCATGGGAACAGGGAAT
 TCTTTGCGGTATGCCAAAACACTTAAGAGAAAAGAGTGAAGTTGATGGCTGAGAGTTAG
 ATACTATTACAGGAGCTATTGCCAAAACACCTTCATCCCAATAGTCATATTGAAATTAAG
 GATTGTGAGACGGTGGCTTTTAAACGACAATAGTTTGTATTGGTGATTTCAAATGTGCCCT
 TTGCCAATATACGAATTGGGATAATAGGTACGATAGGCTTACATGATTGATGACTACT
 TTGTCAAAAAGTCACTTGATTGCTTTCATGATGGTGGACAAAGTAGCGATTATCTTCCA
 CAGGAATCTATGGATAAGCGAACAGAAAACATCTTACAAGATATTGCTGAGACAACTGAAT
 TTCTTGGTGGGTGCTGACTGCTGCTTAAAGGCCATTGACGGAACGAGTGTCA
 CAACGGATATGTTATCTTCCAGAAACACTTAGACAAGGATATGTGGCAGACGATTTAG
 CCTTTTCAGGTTCCATTGCTATGACAAGGATAGTGCATTTGGCTCAATCCTTATTTTG
 ATGGAGAATAACAATAGCCAGGTGCTAGGAACCTACGAGGTGAGGAATTTAAACGGAGGA
 CACTTTCTGTTTAAAGGGGACTAGTGATGACTTGATTGCAAGTGTGAAACAGCTCTAAATC
 ACGTTAAGGCCCAAGAGAGATTGATAGAAATGAGGTCACTAATTAACCCAGATGTGTTGA
 CCAAAACAGTCAATCAATCACTCCATTCCAGCTGAATGAGGGAATACTAGGTCAGTACA
 GTTTTGGTTATCAGGGGTCTACAGTTTACTATCGAGATAACAAAGGCATTTCGAGTCGGA
 CCAAGACGGAAGAAATCAGTTACTATGTCGATGAAGAGGGCAACTTCAAGCATGGGACA
 CCAAACTTCTCAAAAGCAGATTGATCGCTTAAATGCCCTAGAAGTGAAGTATGAACTG
 CTCTGGATGTCTATGTGACCGATGATGCAGCCAAACGTGGTCAAGTTAAGGGGTATTATA
 AAAAGACAGTTTCTATGAAGCTCCATTGCTTATAAAGAAGTGGCAGGTATCAAGAGAA
 TGGTCGATATTGCAATGCCATCAAGAAAGTATTGCCATTCAACGCTATTATGACTATG
 ATAGGAGACCTTTAACCACTTGTTAGGCAACTCAATCGTACCTATGATAGCTTTGTCA
 AACACTATGGGTATTGAATAGTCTGTGAACCGCAATCTTTTGTAGTGTATGATAAGT
 ATTCGCTTCTGTAGTTTGGAAAGATGAAAGTCTGGATCCAAGTGGAAAGTCTGTATCT
 ATACTAAATCCCTTGCTTTGAGAAGGCTCTAGTGCCTGCTGAAAAAGAGGTTAAAAAG
 TGCATACCTGCCCTTGATGCCCTTAAATCGAGCTTGGCTGACGAGCAGGTTGTGATTTCG
 CTTATATGATGCTCTATCTACAGTTGAATCGCAGATGACCTGATTGAGGAGTTAGGCG
 ACCTCATTATGCTGATCCTGAGAAGTATTGAATGGAGAATTGACCTATGTTTCTCGCC
 AAGACTTCTTTTCAGGGGATGTCGTCATAAGTTAGAAGTGGTAGATCTATTGCTCAAAC
 AAGACAATCAGGACTTAACTGGTCACTTATGCGGGACTTCTAGAAGCTATCAAAACGAG
 CCCGTATTACTTTGGCAGACATTGATTATCGAATCGGTTACGCTGAGATTCTCTGGCTG
 TTTATGAAAAATTTGCCCAAGAAACCTTTATGGGGAAGCCTATGAAGTGTGAGACCAAG
 AAGTAGCGACAGTCTTGAAGTCAAGTCCATTGACGGGTTTACTACTTACCAATCTAAGT
 TTGCTTACACCTTATTCCAACGCAACGGATAGGAGTTTAGGTGCTCCTGCTTACGCTATG
 ATAGTGTGCAAAAATCTTTGAAAATCTCCTGAATTCCAATCAACCAACCTACAAAAAC
 AAGTTGTGCAAGGGGATAAGAAAAAGATGTGACGGATGTAGAGAAAAACACGGTCTGCTG
 GTGCCAAGGAACACACCTTACAAGAACTCTTTCAAGGTTTGTAGCAAGTATCCAGAAG
 TCCAACAAATGATTGAAGACACCTATAATAGGCTCTACAATCGTACGGTATCAAGTCTCT
 ATGATGTAGTCAATTAACCAATTGATGGAAGTCTCAGAAATCTCCTTACGCTCTCACC
 AAAAGAAATGCCATTCAACGAATTTGTCAGGAAAAACGTCCTTACTAGCTCATGAAGTTG
 GTTCAGGTAACACTTACCATGCTTGGGGCAGGATTCAAACTGAAAGAACTCGGAATGG
 TACATAAACCACTTTATGTGGTGGCTGCTAGTCTGACTGCTCAGTTGGTCAAGAAATCA
 TGAATTTTTCCTTACCAAGAAAGTCTATGTGACTACTAAGAAAGACTTTGCCAAAGCCA
 AACGCAAGCAGTTTGTGCTCCGATATTATACAGGGGACTATGATGCCATTGTTCATTTGGG
 ATTCACAAATTTGAGAAGATACCGATGAGTCTGAAAAACAGGTCACCTATATCAATGACA
 AACTTGAGCAACTCCGAGAAATCAAGCTAGGAAGTACAGTGAATTACAGCGGTGAAGAAG
 CGGAACGTTGATTGAAGGATTAGAACCAGGTTGGAAGAACTCCAAAACTAGAGCGAG